

1261	TCACCAAGCCCACTCAGCAGCCCGGGTGACCCCTCACCCCTCAACCAAGGGCAGTCCC	1320
1141	CTCCCAACCCCAAGGGGACACCTGTCCACACGCCCAAGAGAGACCCCGGTGCGCACGCC	1200
1321	CTCCCAACCCCAAGGGGACACCTGTCCACACGCCCAAGAGAGACCCCGGTGCGCACGCC	1380
1201	AACCCACAGCCCCCGTCCAGCCCCAGCCGTCGAGGGGTGCCTGTGAGGGCGGGCTCAAC	1260
1381	AAACCCACGCGCCCGTCCAGCCCCAGCCGTCGAGGGGTGCCTGTGAGGGCGGGCTCAAC	1440
1261	TCCATCAAGACAGCTTTCTTGGGCTCACCCCGCTTCCACCGCGGAAACTGCAAGTTCCG	1320
1441	TCCATCAAGACAGCTTTCTTGGGCTCACCCCGCTTCCACCGCGGAAACTGCAAGTTCCG	1500
1321	AGCCCGAGGAGATGCCAACCTGCACACAGAGTGTGTCCACAGCTGGCGAAGAGTCC	1380
1501	AGCCCGAGGAGATGCCAACCTGCACACAGAGTGTGTCCACAGCTGGCGAAGAGTCC	1560
1381	TGCTTTGGGAATCTCATCAGCTTGGAGAAGGAGGAGCAGATCTTCGTGGTCATCAAGAC	1440
1561	TGCTTTGGGAATCTCATCAGCTTGGAGAAGGAGGAGCAGATCTTCGTGGTCATCAAGAC	1620
1441	AAACCTCTGAGCTCATCAAGGCTGACATGTGTACACGCTTCCTGTCTCGATTCCACGCTC	1500
1621	AAACCTCTGAGCTCATCAAGGCTGACATGTGTACACGCTTCCTGTCTCGATTCCACGCTC	1680
1501	AGCCACAGCTCATCTCCCAAAACGAGTTCCGGGCGCAGTACAAGGCCACGGGGGGCCA	1560
1681	AGCCACAGCGTCATCTCCCAAAACGAGTTCCGGGCGCAGTACAAGGCCACGGGGGGCCA	1740
1561	GCGTGTTCCAGAAAGCCGCTCAAGTTCCAGGTTGATATCACTACCGAGGGTGGGAG	1620
1741	GCGTGTTCCAGAAAGCCGCTCAAGTTCCAGGTTGATATCACTACCGAGGGTGGGAG	1800
1621	GCGCAGAAAGGAGAACGGCATCTACTCCGTCACCTTCACCTGCTCTCAGGCGCCACGCGT	1680
1801	GCGCAGAAAGGAGAACGGCATCTACTCCGTCACCTTCACCTGCTCTCAGGCGCCACGCGT	1860
1681	GCCTTCAGAGGGTGGTGAGACCATCCAGGCGCCAGCTGCTGAGCACACACGCCGCT	1740
1861	GCCTTCAGAGGGTGGTGAGACCATCCAGGCGCCAGCTGCTGAGCACACACGCCGCT	1920
1741	GGGGCCACGACTTGTTCAGACACCACTAACTGTATGGAATGATGACGGGGCGCTTCC	1800
1921	GGGGCCACGACTTGTTCAGACACCACTAACTGTATGGAATGATGACGGGGCGCTTCC	1980
1801	AAATGTGGAATTATCCGAAAAGTTAA	1827
1981	AAATGTGGAATTATCCGAAAAGTTAA	2007

RESULT 3

US-10-288-798-42
US-10-288-798-42 Application US/10288798
; General Information:
; Sequence 42.
; APPLICANT: BANDMAN, Olga; NGUYEN, Danniell B;
; APPLICANT: WALIA, Narinder K.; HAFALIA, Adril J.A.;
; APPLICANT: YAO, Monique G.; GANDHI, Ameena R.;
; APPLICANT: GURURAJAN, Rajagopal; DING, Li;
; APPLICANT: PATTERSON, Chandra; YUE, Henry;
; APPLICANT: BAUGHN, Mariah R.; TRIBOULEY, Catherine M.;
; APPLICANT: THORNTON, Michael; ELLIOTT, Vicki S.;
; APPLICANT: LU, Yan; ISON, Craig H.;
; APPLICANT: AU-YOUNG, Janice; TANG, Y. Tom;
; APPLICANT: AZIMZAI, Yalda; BURRILL, John D.;
; APPLICANT: MARCUS, Gregory A.; ZINGLER, Kurt A.;
; APPLICANT: LU, Dyung Aina M.; LAL, Prseti G.;
; APPLICANT: RAMKUMAR, Jayalaxmi; WARREN, Bridgett A.;
; APPLICANT: KEARNEY, Liam; POLICKY, Jennifer L.;
; APPLICANT: THANGAVELU, Kavitha; BURFORD, Neil
; APPLICANT: TITLE OF INVENTION: HUMAN KINASES
; FILE REFERENCE: PI-0209 USA

TITLE OF INVENTION: HUMAN K
REFERENCE: PT-0209 USA

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CURRENT APPLICATION NUMBER: US/10/288,798
CURRENT FILING DATE: 2002-11-01
PRIOR APPLICATION NUMBER: PCT/US01/27219
PRIOR FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: US 60/240,542
PRIOR FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: US 60/238,389
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: US 60/236,499
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: US 60/234,902
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: US 60/232,654
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: US 60/231,357
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: US 60/229,873
PRIOR FILING DATE: 2000-08-31
NUMBER OF SEQ ID NOS: 48
SOFTWARE: PERL Program
SEQ ID NO 42
LENGTH: 2647
TYPE: DNA
ORGANISM: Homo sapiens
FEATURES:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No: 4022651CB1
10-288-798-42

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100 0%. score 1827: DB 49: Length 2647;

Query Match	100.0%	Score 1827	DB 49	Length 2647	Matches 1827	Conservative	Mismatches 0	Indels 0	Gaps 0
Best Local Similarity 100.0%; Pred. No. 0;									
1	ATGAAGGTGGAGCGGAGATCCGATCCTGAAAGTCATTGACGACCCCCACGCTCTCTAAAG	60							
169	ATGAAGGTGGAGCGGAGATCCGATCCTGAAAGTCATTGACGACCCCCACGCTCTCTAAAG	228							
61	CTGCACGACGTTTATGAAAAAATAATTTCTACTCGTCTAGAACACGCTGTCAAGT	120							
229	CTGCACGACGTTTATGAAAAAATAATTTCTACTCGTCTAGAACACGCTGTCAAGT	288							
121	GGTAGCTCTTCGACTACCTGTTGAAGAAAGGAGGCTGTACGCTTAAGGAGGCTCGGAAG	180							
289	GGTAGCTCTTCGACTACCTGTTGAAGAAAGGAGGCTGTACGCTTAAGGAGGCTCGGAAG	348							
181	TTCTTTCCGGCAGATCATCTCTGGCGCTGGACTTTGCGCACAGGCACCTCCATATGCCACAGG	240							
349	TTCTTTCCGGCAGATCATCTCTGGCGCTGGACTTTGCGCACAGGCACCTCCATATGCCACAGG	408							
241	GATCTGAAACCTGAAAAACCTCTCTGTGGACGAGAGAAGAACAAATCCGGATCGCAGACTTT	300							
409	GATCTGAAACCTGAAAAACCTCTCTGTGGACGAGAGAAGAACAAATCCGGATCGCAGACTTT	468							
301	GGCATGGGCTCCCTCGAGTTGGCGACAGCCTGTTGGAGACCAAGCTGTGGGTCCCGCCAC	360							
469	GGCATGGGCTCCCTCGAGTTGGCGACAGCCTGTTGGAGACCAAGCTGTGGGTCCCGCCAC	528							
361	TACGCTGGCCCCGAGGTGATCCGGGGGGAGAAATATGACGGCGGAAGCGGAGCTGTGG	420							
529	TACGCTGGCCCCGAGGTGATCCGGGGGGAGAAATATGACGGCGGAAGCGGAGCTGTGG	588							
421	AGCTGGGGGTGATCTCTGTTTCGCCCTTGCTGGTGGGGGCTCTGCCCTTTCGACGATGACAAAC	480							
589	AGCTGGGGGTGATCTCTGTTTCGCCCTTGCTGGTGGGGGCTCTGCCCTTTCGACGATGACAAAC	648							
481	TTGCGACAGCTGCTGGAGAAAGTGAAGCGGGGGGTGTTCCATATCGCGGACCTTATCCCG	540							
649	TTGCGACAGCTGCTGGAGAAAGTGAAGCGGGGGGTGTTCCATATCGCGGACCTTATCCCG	708							
541	CCCGACTGCCAGAGCTGTCTACGGGGCATGATCGAGGTGGACGCCCGACCGCGCTTCAGG	600							
709	CCCGACTGCCAGAGCTGTCTACGGGGCATGATCGAGGTGGACGCCCGACCGCGCTTCAGG	768							

1849	CGCTTCAAGAGGGTGTGAGACCATCCAGGCCAGCTGCTGAGCACACAGACCCGCT	1808
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1741	GGGGCCCGACACTTGTGACACCACTAACTGTATGGAATGATGACGGGGCGCTTTC	1800
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1909	GGGGCCCGACACTTGTGACACCACTAACTGTATGGAATGATGACGGGGCGCTTTC	1968
Db		
1801	AAATGTGGAATTATCCGAAAAGTTAA	1827
QY		
1969	AAATGTGGAATTATCCGAAAAGTTAA	1995
Db		

REC'D 4
ITC-10-362-882-42

US-10-302-032-42 : Sequence 42 Application IIS/10362892

APPLICANT: INCYTE GENOMICS, INC. : BANDMAN, OLGA

APPLICANT: HAFALIA. April J.A.: YAO. Monique/G.

APPLICANT: DING, Li: PATTERSON, Chandra S.

APPLICANT: TRIBOULEY, Catherine M.; THORNTON, Michael

; APPLICANT: ISON, Craig H.; AU-YOUNG, Janice K.

; APPLICANT: BURRILL, John D.; MARCUS, Gregory A.

APPLICANT: LAL, Preeti G.; RAMKUMAR, Jayalaxmi

APPLICANT: POLICKY, JENNIFER L.; THANGAVELU, KAVI

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CURRENT FILING DATE: 2003-02-25

PRIOR FILING DATE: 2001-08-31

;
PRIOR FILING DATE: 2000-08-31

; PRIOR FILING DATE: 2000-09-08 /

; PRIOR FILING DATE: 2000-09-14 /

; PRIOR FILING DATE: 2000-09-22 /

;
 ; PRIOR FILING DATE: 2000-09-29
 ; PRIOR APPLICATION NUMBER: US/2000/0000000

; PRIOR FILING DATE: 2000-10-06
 ; PRIOR APPLICATION NUMBER: US 60/240 542

PRIOR FILING DATE: 2000-10-13
NUMBER OF SEQ ID NOS: 48

DO NOT WRITE IN THESE SPACES
: SEO ID NO 42

TYPE: DNA

FEATURE:

OTHER INFORMATION: Indyte ID No: 4022651CB1

Best Local Similarity /	100.0%;	Pred. No. 0;
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839
840
84

[illegible]

.....

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

nucleic - nucleic search, using sw model

on: November 27, 2003, 04:08:07 ; Search time 3809.85 Seconds
(without alignments)
12803.430 Million cell updates/sec

e: US-10-054-579-1

fect score: 2007

ence: 1 atgacatcagcggggaagga.....gaattatccgaaaagttaa 2007

ing table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

ched: 22781392 seqs, 12152238056 residues

al number of hits satisfying chosen parameters: 45562784

imum DB seq length: 0

imum DB seq length: 2000000000

--processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

abase :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estro:*

6: em_estpl:*

7: em_estro:*

8: em_hic:*

9: gb_est1:*

10: gb_est2:*

11: gb_hic:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_eston:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ult No.	Score	Query Match %	Length	DB	ID	Description
1	763.2	38.0	1201	9	AL538014	AL538014
2	639.4	31.9	769	13	BQ442940	BQ442940 UI-M-EVO-
3	633.2	31.5	791	13	BQ611869	BQ611869 UI-M-FIO-
4	601.4	30.0	732	13	BQ443783	BQ443783 UI-M-EVO-

5	593.4	29.6	723	14	CA315127	CA315127 UI-M-FW0-
6	588.2	29.3	733	13	BQ178695	BQ178695 UI-M-EVO-
7	584.8	29.1	733	10	BG395625	BG395625 602458251
8	583.8	29.1	1882	11	BC017182	BC017182 Homo sapi
9	574.2	28.6	712	13	BQ180079	BQ180079 UI-M-EVO-
10	562.2	28.0	740	10	BF222739	BF222739 7Q32f02.x
11	559.8	27.9	563	10	BE251924	BE251924 601107590
12	550.6	27.4	889	13	BQ434571	BQ434571 AGENCOURT
13	548.2	27.3	693	13	BQ434644	BQ434644 UI-M-EVO-
14	522	26.0	886	13	BQ285204	BQ285204 603601981
15	515	25.7	589	10	BE259121	BE259121 601107773
16	510.6	25.4	728	13	BQ769984	BQ769984 UI-M-FIO-
17	496.8	24.8	699	14	CA319314	CA319314 UI-M-FW0-
18	495.2	24.7	727	12	B1825755	B1825755 603072158
19	478.8	23.9	746	13	BQ394353	BQ394353 603804548
20	476.8	23.8	697	13	BQ392070	BQ392070 603802721
21	445.6	22.2	709	12	B1916891	B1916891 603177863
22	445.2	22.2	546	12	BM944658	BM944658 UI-M-EHOD
23	445	22.2	937	10	BF527021	BF527021 602039908
24	443.8	22.1	730	13	BQ613922	BQ613922 UI-M-FRO-
25	425.6	21.2	947	10	BF525960	BF525960 602070128
26	425.6	21.2	881	13	BQ717903	BQ717903 AGENCOURT
27	421.6	21.0	698	12	BM948524	BM948524 UI-M-EHOD
28	416	20.7	1177	12	BM466629	BM466629 AGENCOURT
29	413.8	20.6	1041	13	BQ882776	BQ882776 AGENCOURT
30	406.2	20.2	701	10	BE256016	BE256016 601113531
31	405.4	20.2	793	9	AI135353	AI135353 GH13047.5
32	403.6	20.1	831	10	BF529743	BF529743 602044002
33	393.6	19.6	639	10	BF342303	BF342303 602013084
34	392.6	19.6	600	13	BQ444032	BQ444032 UI-M-EVO-
35	390.2	19.4	1083	13	BQ067850	BQ067850 AGENCOURT
36	388.2	19.3	651	14	CA368080	CA368080 644147 NC
37	387	19.3	476	14	CD355265	CD355265 UI-M-FYO-
38	385.6	19.2	477	13	BQ554978	BQ554978 H4031D07-
39	379	18.9	742	12	BM944329	BM944329 UI-M-EHOD
40	377	18.8	378	13	EX090836	EX090836 BX090836
41	369.8	18.4	860	13	BQ367263	BQ367263 603788047
42	360.8	18.0	455	14	CD355321	CD355321 UI-M-FYO-
43	357.6	17.8	484	13	BY254507	BY254507 BY254507
44	355.4	17.7	898	10	BF529174	BF529174 602042051
45	355.2	17.7	783	13	BU348106	BU348106 603524982

ALIGNMENTS

RESULT 1
AL538014
LOCUS
DEFINITION
AL538014 Homo sapiens FETAL BRAIN Homo sapiens cdna clone
CS0DF029YC21 5-PRIME, mRNA sequence.
ACCESSION
AL538014
VERSION
AL538014.2 GI:31262615
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE
Full-length cDNA libraries and normalization
JOURNAL
Unpublished
COMMENT
On Feb 13, 2001 this sequence version replaced gi:12801507.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6094.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DF029AB11QPI&cluster=6094.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :

481 GCCTTGCTGGGGGCTGCTGCTTTTATGATGACAACTCGGCGAGTGTCTGGAGAG 540
 582 GTGAAGCGGGCGTGTTCACATCCGACATTTATCCCGCCGAGTCCGAGTGTCTGCTA 741
 541 GTCAAGCGTGTGTGTTCACATCCGACATTTATCCCGCCGAGTGTCTGCTGCTG 600
 742 CGGGCGATGATCGAGTGTGGAGCGCGACCGCGCTCAGCTAGAGCACATTCAGAAAC 801
 601 CGTGGCATGATGAGTGTGGAGTGTGGAGTGTGGAGTGTGGAGTGTGGAGTGTGG 660
 802 ATATGTTATATAGGGGCAAGATGAGCGCGCAACAGAGAGAGAGAGAGAGAGAG 861
 661 ATATGTTATATAGTGTGGAGTGTGGAGTGTGGAGTGTGGAGTGTGGAGTGTGG 720
 862 CAGATCGCTGCTGCGCGAGTGTGGAGTGTGGAGTGTGGAGTGTGGAGTGTGGAG 921
 721 CAGATCGCTGCTGCGCGAGTGTGGAGTGTGGAGTGTGGAGTGTGGAGTGTGGAG 780
 922 TCACTGGGCTG 932
 781 TCACTGGGCTG 791

RESULT 4
 BQ443783
 LOCUS
 DEFINITION
 BQ443783 732 bp mRNA linear EST 29-MAY-2002
 IMAGE:5708522 5', mRNA sequence.
 BQ443783.1 GI:21246895
 EST.
 SOURCE
 Mus musculus (house mouse)
 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 732)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished
 Contact: Robert Strauberg, Ph.D.
 Email: csapbs-remail.nih.gov
 Tissue Procurement: Dr. James Lin, University of Iowa
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LINL at:
 http://image.lnl.gov
 This clone was contributed by the Brain Molecular Anatomy Project
 (BMAP)

Seq primer: pyx-5.
 Location/Qualifiers
 1..732
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6"
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 /tissue_type="whole brain"
 /dev_stage="embryo 15.5 dpc"
 /lab_host="DH10B (T1 phage resistant)"
 /clone_lib="NIH BMAP EWO"
 /note="Organ: brain; Vector: pyx-Asc; Site 1: EcoR I;
 Site 2: Not I; The library was constructed according to
 Bonaldi, Lennon and Soares, Genome Research, 6:791-806,
 1996. Denatured mRNA was size fractionated on a 1% agarose
 gel. First strand cDNA synthesis was primed with an
 oligo-dT primer containing a Not I site. Double stranded
 cDNA was size selected according to mRNA size fraction,
 ligated with EcoR I adaptor, digested with Not I, and then
 cloned directionally into pyx-Asc vector. The library tag
 sequence located between the Not I site and the polyA tail
 , is GTGCGTGGAA. This library was created for the

FEATURES

source

University of Iowa Mouse Brain Molecular Anatomy Project
 (BMAP): 'Gene Discovery in the Developing Mouse Nervous
 System', supported by National Institutes of Mental Health
 (NIMH), Hemin Chin, Ph.D., program coordinator."

BASE COUNT 178 a 240 c 188 g 125 t 1 others
 ORIGIN

Query Match 30.0%; Score 601.4; DB 13; Length 732;
 Best Local Similarity 88.8%; Pred. No. 3.9e-121;
 Matches 650; Conservative 0; Mismatches 82; Indels 0; Gaps 0;
 817 GGCAGAGTATGAGCGCGCGACCGCGCTCAGCTAGAGCACATTCAGAAAC 876
 1 GGCAGAGTATGAGCGCGCGACCGCGCTCAGCTAGAGCACATTCAGAAAC 60
 877 CCCAGCTTGGAGAGACATTCAGCTAGAGTGTGGAGTGTGGAGTGTGGAGTGTGG 936
 61 CCCAGCTTGGAGAGACATTCAGCTAGAGTGTGGAGTGTGGAGTGTGGAGTGTGG 120
 937 CGAGACCGCAACAGCTGTCTGAGAGTGTCTGAGAGTGTCTGAGAGTGTCTGAGAG 996
 121 CGAGACCGCAACAGCTGTCTGAGAGTGTCTGAGAGTGTCTGAGAGTGTCTGAGAG 180
 997 ATTACT 1056
 181 ATTACT 240
 1057 CCCCCCGGAGAGAGATAGACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1116
 241 CCCCCCGGAGAGATAGACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
 1117 CAGGCAAGCGGGGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1176
 301 CATGGCAAGCGGGGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
 1177 TCCCGGCTGCTGCGCGGGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1236
 361 TCCCGGCTGCTGCGCGGGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
 1237 ATCAGCGTGTCT 1296
 421 ATCAGTGTGTCT 480
 1297 CACCCCTTACCAAGGGGAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1356
 481 CACCCCTTACCAAGGGGAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 540
 1357 AAGGAGAGCGCGGTGGCGACCGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1416
 541 AAGGAGAGCGCGGTGGCGACCGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
 1417 GTGCCCTTGGAGGGCGCGGTCTCACTTCACTTCACTTCACTTCACTTCACTTCACTT 1476
 601 GTGCCCTTGGAGGGCGCGGTCTCACTTCACTTCACTTCACTTCACTTCACTTCACTT 660
 1477 CACCGCGGAGAACTGCAAGTTCGAGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAG 1536
 661 CACCGCGGAGAACTGCAAGTTCGAGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
 1537 TCCCCAGAGCTG 1548
 721 TCTCCAGAGCTG 732

RESULT 5
 CA315127
 LOCUS
 DEFINITION
 CA315127 723 bp mRNA linear EST 26-NOV-2002
 IMAGE: 6810176 5', mRNA sequence.
 CA315127
 ACCESSION
 VERSION
 CA315127.1 GI:24533251
 KEYWORDS
 EST.
 Mus musculus (house mouse)

1719 GTACAAGGCCACGGGGGGGGCAGCCGTTGTTCCAGAAGCCGGTCAAGTTCCAGGTTGATAT 1778
362 GTACAAGGCCACGGGGGGGGCAGCCGTTGTTCCAGAAGCCGGTCAAGTTCCAGGTTGATAT 421
1779 CACCTACACGAGGAGTGGGGAGGCGCAGAAGGAGAACGCCATCTACTCCGTCCACCTTCAC 1838
422 CACCTTACACGAGGAGTGGGGAGGCGCAGAAGGAGAACGCCATCTACTCCGTCCACCTTCAC 481
1839 CCTGCTCTCAGGCCCCCAGCCGTCGCTTTCAAGAGGGTGGTGGAGACCATCCAGGCGCCAGCT 1898
482 CCTGCTCTCAGGCCCCCAGCCGTCGCTTCAAGAGGGTGGTGGAGACCATCCAGGCGCCAGCT 541
1899 GCTGAGGCACACAGACCCGCTCGCGCCCGCCAGCAGCCTTGTGCAGACACCAAC 1946
542 GCTGAGGCACACAGACCCGCTCGCGCCCGCCAGCAGCCTTGTGCAGAAACCCC 589
8
82
TION
HON
IDS
NIS
NIS
NCE
IORS
E
UNAL
VRK
IT
1719
362
1779
422
1839
482
1899
542
8
82
TION
HON
IDS
NIS
NIS
NCE
IORS
E
UNAL
VRK
IT

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: <http://image.llnl.gov>
 Series: IRAL plate: 5 Row: j Column: 11
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4103050
 This clone has the following problem: frame shifted.

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IES
source
this clone has the following problem: I have
Location/Qualifiers
1. .1882
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/db_xref="taxon:9606"
/clone="IMAGE:3343795"
/tissue_type="Eye, retinoblastoma"
/clone_lib="NIH MGC 16"
/lab_host="DH10B-R"
/note="Vector: pOTB7"

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352	a	609	c	572	g	349	t
COUNT							
/MODE= VECTOR: POIN							

ORIGIN

Query Match	29.1%;	Score 583.8;	DB 11;	Length 1882;
Best Local Similarity	98.8%;	Pred. No. 3.5e-117;		
Matches 588;	Conservative 0;	Mismatches 7;	Indels 0;	Gaps 0;
QY	1352	CGCCAAAGGAGAGCCGGCTGGCAGCCCCAAACCCACGCCGCCGTCGACGCCCCCGCTCCAGGCCCCAGGGTCG	1411	
Db	3	CACGAGGGAGAGCCGGCTGGCAGCCCCAAACCCACGCCGCCGTCGACGCCCCCGCTCCAGGCCCCAGGGTCG	62	
QY	1412	GAGGGGTGCCCTTGAGGGGCGGGCTCAACTCCATCAAGAAACAGCTTCTTGGGCTCACCCC	1471	
Db	63	GAGGGGTGCCCTTGAGGGGCGGGCTCAACTCCATCAAGAAACAGCTTCTTGGGCTCACCCC	122	
QY	1472	GCTTCCACCGCCGGAACATGCAAGTTCCGACGCCGCGAGGAGATGCCAACCTCACACCAG	1531	
Db	123	GCTTCCACCGCCGGAACATGCAAGTTCCGACGCCGCGAGGAGATGTCAAACCTGACACCAG	182	
QY	1532	AGTCGTCCTCCAGAGCTGGCGGAAGAAGTCTCTGGTTTGGGAACTTTCATCAGCCTCGGAAAGG	1591	
Db	183	AGTCGTCCTCCAGAGCTGGCGGAAGAAGTCTCTGGTTTGGGAACTTTCATCAGCCTCGGAAAGG	242	
QY	1592	AGGAGCAGATCTTCGTGGTCAATCAAGAACAAACCTCTGAGCTCCATCAGGCTGCACATCG	1651	
Db	243	AGGAGCAGATCTTCGTGGTCAATCAAGAACAAACCTCTGAGCTCCATCAGGCTGCACATCG	302	
QY	1652	TGCAGCCCTCTCTGTCGATTCCCGAGTCTCAGCCACAGCGTCATCTCCCAAAACGAGCTTC	1711	
Db	303	TGCAGCCCTCTCTGTCGATTCCCGAGTCTCAGCCACAGCGTCATCTCCCAAAACGAGCTTC	362	
QY	1712	GGGCCGAGTACAGGCCACGGGGGGCCAGCCGTGTTCCAGAGCCCGTCAAGTTCACGG	1771	
Db	363	GGGCCGAGTACAGGCCACGGGGGGCCAGCCGTGTTCCAGAGCCCGTCAAGTTCACGG	422	
QY	1772	TTGATATCACTTACCGGAGGGTGGGGAGCGCCAGAAAGGAGAAACGGGATCTACTCCGTCA	1831	
Db	423	TTGATATCACTTACCGGAGGGTGGGGAGCGCCAGAAAGGAGAAACGGGATCTACTCCGTCA	482	
QY	1832	CCTTCACCTGCTCTCAGAGCCCCAGCCGTCGCTTCAAGAGGGTGGTGAGACCATCCAGG	1891	
Db	483	CCTTCACCTGCTCTCAGAGCCCCAGCCGTCGCTTCAAGAGGGTGGTGAGACCATCCAGG	542	
QY	1892	CCGAGTGTGAGCACACAGACCCGCCCTCGGCCCCAGCACTTGTGACACACAC	1946	
Db	543	CCGAGTGTGAGCACACAGACCCGCCCTCGGCCCCAGCACTTGTGACACACAC	597	

RESULT 9	ACCESSION	REFERENCE
BQ180079	VERSION	AUTHORS
LOCUS	KEYWORDS	TITLE
DEFINITION	SOURCE	JOURNAL
	ORGANISM	COMMENT

BQ180079 712 bp mRNA linear EST 30-APR-2002
 UI-M-5700-Bww-d-22-0-UI.r1 NIH_BMAP_EWO Mus musculus cDNA clone
 IMAGE:5703909 5', mRNA sequence.
 BQ180079
 BQ180079.1 GI:20355571
 EST.
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 712)
 NIH-MGC <http://mgc.nci.nih.gov/>
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Dr. M. Bento Soares, University of Iowa
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 This clone was contributed by the Brain Molecular Anatomy Project

<http://image.umn.gov>
This clone was contributed by the Brain Molecular Anatomy Project

(BMAP)

Seq primer: pyx-5.

ES
source

Location/Qualifiers
1. 712
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/clone="IMAGE:5703909"
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/dev_stage="embryo 15.5 dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH-BMAP_EWO"
/note="Organ: brain; Vector: pyx-Asc; Site 1: EcoR I; Site 2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured mRNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I, and then cloned directionally into pyx-Asc vector. The library tag sequence located between the Not I site and the polyA tail is GTGCGTGGAA. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institutes of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

COUNT 167 a 211 c 193 g 139 t 2 others

Y Match 28.6%; Score 574.2; DB 13; Length 712;

Local Similarity 88.6%; Pred. No. 3.4e-115;

hes 632; Conservative 0; Mismatches 80; Indels 1; Gaps 1;

643 CCTTCGACGATGACCACTGCGACGCTGCTGGAGAGGTGAAGCGGGCTGTCCAC 702

1 CCTTTGATGATGACCACTGCGGCGATGCTGGAGAGGTGACAGCGTGTTCAC 60

703 ATGCCGCACTTTATCCCGCCGACTGCCAGAGTCTGTACCGGGCATGATCAGAGTGAC 762

61 ATGCCACACTTTATCCCAACCACTGCCAGAGTCTCTCGCGCATGATTGAGTGGAT 120

763 GCCGACGCGGCTCAGCTAGACGACATTCAGAACACATATGTTATATAGGGGCAAG 822

121 CGAGCTCGGCGGCTCAGCTAGACGACATTCAGAACACATATGTTATATAGGTGGCAAG 180

823 AATGAGCCGAAACAGACAGCCCACTTCTCGCAAGGTGCAGATCCGCTCGCTGCCACGC 882

181 AATGAGCCGAGCCGACAGCCCACTCCAGCAAGGTGCAGATCCGCTCACTACCCAGC 240

883 CTGGAGGACATGACCCCGACGCTGTGACAGCATGCACTCACTGGGCTGTTCCGAGAC 942

241 TTGGAAGACATTTGACCTGATGTGTGGACAGCATGCACTCACTGGGCTGTTCCGAGAC 300

943 CGCACAGCTGCTCAGACACTGTGTCCGAGGAGGAGACACAGGAGAGATGATTTAC 1002

301 CGCAACAAGCTGCTCGAGATCTGCTATCTGAGGAGGAGATTCAGAAAGATGATTTAT 360

1003 TTCCTCTCTCTGGACCGGAAGAAAGAGTACCCGAGCCAGGAGGATGAGGACCTGCCCCCC 1062

361 TTCCTCTCTCTGGATCGGAAGAAAGAGTATCCAGCCATGAGGATGAGGACCTGCCCCCC 420

1063 CGGAACGAGATAGACCTCCCGGAAGCGTGTGAGTACTCCCGATGCTGAACCGGACGCG 1122

421 AGGAATGAGATAGACCTCCCGGAAGCGTGTGAGTACTCCCGATGCTGAACCGGACGCG 480

1123 AAGCGCGCCGACGAGCAATTCATGAGGTGCTCAGGTGACGCGGCGGCTCCCGG 1182

481 AAGCGCGGACCTGAGCGCAAGTTCATGGAAGTGTCTCAGTGTACAGATGGTGGCTCCCA 540

1183 GTGCTGCGCGCGGCGCATTTAGATGGCCAGCAGCGGACGAGGTCTCGGTCCATCAGC 1242

Db 541 GTCCCTGCAGGAGACCCATTGAGATGGCCAGCATGGCCAGAGATCTCGATCCATCAGT 600

Qy 1243 GGTGCTCTCTCAGGCGCTTTCCACAGCCCACTCAGCAGCCCCCGGGTGACCCCTCACCCC 1302

Db 601 GGTGCGCTCTCAGGCGCTTTCTACAAGTCCACTCAGCAGTCTCTGGGTGACCCCTCACCCC 660

Qy 1303 TCACCAAGGGCAGTCCCTCCACACCCCAAGGGGACACCTGTCCACAGCC 1355

Db 661 TCACCAAGGGGAGT-CCCTTCTACCCCAANAGGAGCGCTGTCCACAGCC 712

RESULT 10
BF222739/c

LOCUS
DEFINITION

7q32f02.x1 NCI CGAP GC6 Homo sapiens cDNA clone IMAGE:369987 3', similar to TR:060843 O60843 PUTATIVE SERINE/THREONINE PROTEIN KINASE 1, mRNA sequence.

ACCESSION
VERSION

BF222739.1 GI:11129830
EST.

KEYWORDS
ORGANISM

Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL
COMMENT

Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov

Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov

High quality sequence stop: 492.
Location/Qualifiers

1. 740
/organism="Homo sapiens"

/mol_type="mRNA"
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/clone="IMAGE:369987"
/tissue_type="pooled germ cell tumors"

/lab_host="DH10B"
/clone_lib="NCI CGAP GC6"

/note="Vector: pF773D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA from the normalized library NCI CGAP GC4 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1257096-1258631, 1469084-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 125 a 206 c 241 g 163 t 5 others

ORIGIN

Query Match 28.0%; Score 562.2; DB 10; Length 740;

Best Local Similarity 97.8%; Pred. No. 1.5e-112;

Matches 578; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

Qy 1401 CCCAGGCTCGGA-GGGGTGCTCGAGGCGCGGCTCAACTCCATCAAGAACAGCTTTC 1459

Db 721 CCCAGGCTCGAGGGGTGCTCGAGGCGCGGCTCAACTCCATCAAGAACAGCTTTC 662

Qy 1460 TGGGCTCACCCCGCTTCCACCGCGGAACTGCAAGTCCGACGCGGAGAGATGTCCA 1519

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DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

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 Technologies."
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 hes 631; Conservative 0; Mismatches 135; Indels 0; Gaps 0;
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RESULT 13
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 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

BQ443644 693 bp mRNA linear EST 29-MAY-2002
 UI-M-EW0-bxh-n-01-0-UI.r1 NIH_BMAP_EW0 Mus musculus CDNA clone
 IMAGE:5708352 5', mRNA sequence.

BQ443644
 BQ443644.1 GI:21246756
 ESI.
 Mus musculus (house mouse)

Mus musculus
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 1 (bases 1 to 693)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished

Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Dr. James Lin, University of Iowa
 CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

This clone was contributed by the Brain Molecular Anatomy Project
 (BMAP)
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 Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
 1996. Denatured mRNA was size fractionated on a 1% agarose
 gel. First strand cDNA synthesis was primed with an
 oligo-dT primer containing a Not I site. Double stranded
 cDNA was size selected according to mRNA size fraction,
 ligated with EcoR I adaptor, digested with Not I, and then
 cloned directionally into pYX-Asc vector. The library tag
 sequence located between the Not I site and the polyA tail
 is GNGCGTGGAA. This library was created for the
 University of Iowa Mouse Brain Molecular Anatomy Project
 (BMAP). Gene Discovery in the Developing Mouse Nervous
 System, supported by National Institutes of Mental Health
 (NIMH), Hemin Chin, Ph.D., program coordinator."

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HORS Pong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
JE A Comprehensive Collection of Chicken cDNAs
RNAL Curr. Biol. 12 (22), 1965-1969 (2002)
3NED 22335534
12445392
WT Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology (UMIST
)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
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Following this first strand reaction, double-stranded cDNA
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compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996) 791, except that a significantly longer
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NCE 1 (bases 1 to 589)
ORS NIH-MGC http://mgi.nci.nih.gov/.
E National Institutes of Health, Mammalian Gene Collection (MGC)
NAL Unpublished
T Contact: Robert Strausberg, Ph.D.
Email: c9apbs@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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Note: this is a NIH_MGC Library."
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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US-09-930-181-1
; Sequence 1, Application US/09930181
; Patent No. 6455292
; GENERAL INFORMATION:
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; TITLE OF INVENTION: Full-Length Serine Protein Kinase in Brain and Pancreas
; FILE REFERENCE: 16U 101 VI
; CURRENT APPLICATION NUMBER: US/09/930,181
; CURRENT FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
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US-09-930-181-1

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Db	346	CTGCACAGCTTTATGAAAACAAAATAATTTGTACTGGTGTAGAACACACGTGTGAGGT	405				
Qy	301	GGTGAAGCTTCTGACCTACCTGGTGAAGAGGGGAGGCTGACGCTAAGGAGGCTCGGAAG	360				
Db	406	GGTGAAGCTTCTGACCTACCTGGTGAAGAGGGGAGGCTGACGCTAAGGAGGCTCGGAAG	465				
Qy	361	TTCTTCCGGCAGATCATCTCTGCGCTGGACTTCTGCGCAGCAGCCATCCATATGCCACAGG	420				

466 TTCTTCCGGCAGATCATCTCTGCGCTGGACTTCTGCCACACGCCACTCCATATGCCACAGG 525

421 GATCTGAATCCTGAAACCTCTCTGCTGGACGAGAAAGAAACAATCCGCGATCGCAGACTTT 480

526 GATCTGAATCCTGAAACCTCTCTGCTGGACGAGAAAGAAACAATCCGCGATCGCAGACTTT 585

481 GGCATGGCGTCCCTGCAGGTTGGCGACAGCTGTGTTGGAGACACAGCTGTGGTCCGCCAC 540

586 GGCATGGCGTCCCTGCAGGTTGGCGACAGCTGTGTTGGAGACACAGCTGTGGTCCGCCAC 645

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646 TACGCCCTGCCCGAGGTGATCCGGGGGAGAAAGTATGACGGCCGGAAGGCGGACGTGG 705

601 AGCTGGCGGTCACTCTGTTTGGCTTTGCTGTGTGGGGGTCTGGCCCTTCGACGATGACAAC 660

706 AGCTGGCGGTCACTCTGTTTGGCTTTGCTGTGTGGGGGTCTGGCCCTTCGACGATGACAAC 765

661 TTGCGACAGCTGCTGGAGAAAGGTGAAGCGGGGCGTGTTCACATGCCGCACTTTATCCCG 720

766 TTGCGACAGCTGCTGGAGAAAGGTGAAGCGGGGCGTGTTCACATGCCGCACTTTATCCCG 825

721 CCCGACTGCCAGATCTGTCTA CGGGGCAATGATCGAGTGGACGCGCACGCCGCTCAAG 780

826 CCCGACTGCCAGATCTGTCTA CGGGGCAATGATCGAGTGGACGCGCACGCCGCTCAAG 885

781 CTAGAGCACATTCAGAAACACATATGGTTATATAGGGGGCAGAAATGAGCCCGAACAGAG 840

886 CTAGAGCACATTCAGAAACACATATGGTTATATAGGGGGCAGAAATGAGCCCGAACAGAG 945

841 CAGCCCATTCCTGCAAGGTGCAGATCCGCTGCTGCCAGCTGCGAGGACATCGACCCC 900

946 CAGCCCATTCCTGCAAGGTGCAGATCCGCTGCTGCCAGCTGCGAGGACATCGACCCC 1005

901 GAGTGTGTGNACGATGCACTCACTGGGCTGTCTCCGAGACCGCAACAAGCTGCTCGAG 960

1006 GAGTGTGTGGACGATGCACTCACTGGGCTGTCTCCGAGACCGCAACAAGCTGCTCGAG 1065

961 GACTGTGTCTCCGAGGAGGAAAC CAGGAGAGATGATTACTTCTCTCTCGACCGG 1020

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1201 ATTGAGATGGCCAGCACGCGCACGAGGTCTCGGTCCATCAGCGGTGCTCTCTCAGGCTT 1260

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1366 TCCACACGCCCACTCAGCAGCCCCCGGGTGACCCCTCACCCCTTCACAAAGGGGAGTCCC 1425

1321 CTCGCCACCCCCAAGGGGACACTGTGTCCACACGCCAAAGAGAGGCCGGCTGGACGCC 1380

1426 CTCGCCACCCCCAAGGGGACACTGTGTCCACACGCCAAAGAGAGGCCGGCTGGACGCC 1485

1381 AACCCACGCCCCCGTCCAGCCCCAGCGTCCGAGGGGTGCTCTGGAGGGCGCGGTCAAC 1440

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Db	1546	TCATCAGAA	CAGCTTTCTGGGCTCACCCGCTTCCACGGCGGAAATGCAAGTTCG	1505
Qy	1501	ACCCCGAGGAGATGTC	CAACCTGACACAGAGTCTGTCCCCAGAGCTGGCGAAGAAGTCC	1560
Db	1606	ACCCGAGGAGATGTC	CAACCTGACACAGAGTCTGTCCCCAGAGCTGGCGAAGAAGTCC	1665
Qy	1561	TGTTTTGGGAACTTCA	TACGCTGGAGAAAGGAGGACAGATCTTCTGTGTCAACAAGAC	1620
Db	1666	TGTTTTGGGAACTTCA	TACGCTGGAGAAAGGAGGACAGATCTTCTGTGTCAACAAGAC	1725
Qy	1621	AAACCTCTGAGCTCCAT	CAAGGCTGACATCGTCGACGCGCTTCTGTGCTCAATCCAGTCTC	1680
Db	1726	AAACCTCTGAGCTCCAT	CAAGGCTGACATCGTCGACGCGCTTCTGTGCTCAATCCAGTCTC	1785
Qy	1681	AGCCACAGCGTCA	TCTCCAAAACGAGCTTCCGGGCGGAGTACAAAGGCCACGGGGGGGCCA	1740
Db	1786	AGCCACAGCGTCA	TCTCCAAAACGAGCTTCCGGGCGGAGTACAAAGGCCACGGGGGGGCCA	1845
Qy	1741	GCCGTGTTCCAGAA	GCGGTCAAGTTCCAGTTTGATATCACTTACACGAGGTTGGGGAG	1800
Db	1846	GCCGTGTTCCAGAA	GCGGTCAAGTTCCAGTTTGATATCACTTACACGAGGTTGGGGAG	1905
Qy	1801	GCGCAGNAGAGAA	CGGCATCTACTCGGTCACTTACCCGTCTCTCAGGCCCCAGCGGT	1860
Db	1906	GCGCAGNAGAGAA	CGGCATCTACTCGGTCACTTACCCGTCTCTCAGGCCCCAGCGGT	1965
Qy	1861	CGCTTCAAGAGGGT	TGGAGACATCCAGGCCCGAGCTGTGTGAGCACACACGACCCGCT	1920
Db	1966	CGCTTCAAGAGGGT	TGGAGACATCCAGGCCCGAGCTGTGTGAGCACACACGACCCGCT	2025
Qy	1921	GCGGCCACGACAT	TGTGACACACCACTTAACTGTATGGAAATGATGACGGGGCGGCTTTC	1980
Db	2026	GCGGCCACGACAT	TGTGACACACCACTTAACTGTATGGAAATGATGACGGGGCGGCTTTC	2085
Qy	1981	AAATGTGGAATTA	TCCGAAAAGTTAA	2007
Db	2086	AAATGTGGAATTA	TCCGAAAAGTTAA	2112

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RESULT 2
US-09-930-181-3
; Sequence 3, Application US/09930181
; Patent No. 6455292
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies
; TITLE OF INVENTION: Full-Length Serine Protein Kinase in Brain and Pancreas
; FILE REFERENCE: 16U 101 V1
; CURRENT APPLICATION NUMBER: US/09/930.181
; CURRENT FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 3364
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (482)..(2239)
US-09-930-181-3

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Query Match	99.3%	Score 1993;	DB 4;	Length 3364;
Best Local Similarity	99.8%	Pred. No. 0;		
Matches 2007;	Conservative 0;	Mismatches 0;	Indels 4;	Gaps 1
QY	1	ATGACATCGACGGGGAAGGACGGCGGGCGGCAGCACGCGCAGTATGTTGGGCCCTTACCGG	60	
DB	229	ATGACATCGACGGGGAAGGACGGCGGGCGGCAGCACGCGCAGTATGTTGGGCCCTTACCGG	288	
QY	61	CTGAGAAAGACCTGTGGGCAAGGGCGCAGACAGGTCTGTTGAAGCTGGGGGTTCACTGCCTC	120	
DB	289	CTGAGAAAGACCTGTGGGCAAGGGCGCAGACAGGTCTGTTGAAGCTGGGGGTTCACTGCCTC	348	
QY	121	ACCTGCCAAGAGGTGGCCATCAAGATCGTCAACCGTGAGAGAGCTCAGCGAGTCGGTGCTG	180	

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349 ACCTGCAGAGGTGGCCATCAAGATCGTCAACCGTGAGAAGCTCAGCGAGTGGTGGCTG 408
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181 ATGAAGTGGAGCGGAGATCGCGATCTCTGAAGCTCATTTAGACACCCCCACGTCCTAAAG 240
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409 ATGAAGTGGAGCGGAGATCGCGATCTCTGAAGCTCATTTAGACACCCCCACGTCCTAAAG 468
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241 CTGCAGACCTTTATGAAACAAATAATTTT---GTACCTGGTGTAGAACACGCTGTC 296
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469 CTGCAGACCTTTATGAAACAAATAATTTTGTAGTACTGTGTGTAGAACACGCTGTC 528
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297 AGTGTGAGCTCTTGCATACCTGTGTGAAGAGGAGGCTGACGCTCTAAAGAGGCTCG 356
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529 AGTGTGTGAGCTCTTGCATACCTGTGTGAAGAGGAGGCTGACGCTCTAAAGAGGCTCG 588
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357 GAAGTCTTCCCGCAGATCATCTCTGGCTGGACTTCTGCCACAGCCACTCCATATGCCA 416
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589 GAAGTCTTCCCGCAGATCATCTCTGGCTGGACTTCTGCCACAGCCACTCCATATGCCA 648
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417 CAGGGATCTGAAACCTGAAACCTCTCTGTGGACGAGAAACAAACATCCGCATCGCAGA 476
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477 CTTTGGCATGGCTCTCTGAGTGTGGCGACGCTCTGTGGAGACAGCTGTGGGTCCCC 536
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709 CTTTGGCATGGCTCTCTGAGTGTGGCGACGCTCTGTGGAGACAGCTGTGGGTCCCC 768
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537 CCACTAGCCTGCCCGAGTGTATCCGGGGGAGAGTATGACGGCGGAGAGCGACGT 596
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769 CCACTAGCCTGCCCGAGTGTATCCGGGGGAGAGTATGACGGCGGAGAGCGACGT 828
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829 GTGGAGCTGGCGGTCTATCTCTGCTTGTGTGGTGGGGCTCTGCCCTTCGACGATGA 888
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657 CAATTTGGCAGACGTCTGGAGAGGTGAAGCGGGCGTGTTCACATGCGCGACATTTAT 716
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889 CAATTTGGCAGACGTCTGGAGAGGTGAAGCGGGCGTGTTCACATGCGCGACATTTAT 948
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717 CCCGCCGACCTGCAGAGTCTGCTACGGGGCATGATCGAGGTGAGCGCGCAGCGCGCT 776
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949 CCCGCCGACCTGCAGAGTCTGCTACGGGGCATGATCGAGGTGAGCGCGCAGCGCGCT 1008
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1197 GGCCATTGAGATGGCCACGACCGCCAGAGGTCTCGGTTCATCAGCGGTGCTCTCTCAGG 1256
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1429 GGCCATTGAGATGGCCAGCACGGCCAGAGGTCTCGGTCCATCAGCGGTGCTCTCTCAGG 1488
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1257 CTTTTCCACGAGCCCACTCAGCAGCCCCCGGGTGAACCTTACCCCTCACCAGGGGCGAG 1316
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1317 TCCCTCTCCCAACCCCAAGGGGACACTGTTCACACGCGCAAGAGGAGAGCCGGCTGGCAC 1376
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1549 TCCCTCTCCCAACCCCAAGGGGACACTGTTCACACGCGCAAGAGGAGAGCCGGCTGGCAC 1608
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1377 GCCCAACCCCAACCCCGCTCCAGCCCCCAGCGTCCGAGGGGTGCCCTGGAGGGCGGGCT 1436
Db
1609 GCCCAACCCCAACCCCGCTCCAGCCCCCAGCGTCCGAGGGGTGCCCTGGAGGGCGGGCT 1668
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1669 CAACTCCATCAAGAACAGCTTTCTGGGTCTCAACCCCGCTTCCACCGCGGAAACTGCAAGT 1728
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1497 TCCGACCGCGGAGGAGATGTCCAACTCTGACACAGAGTCTGCCCGAGAGCTGGCGAAGAA 1556
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1729 TCCGACCGCGGAGGAGATGTCCAACTCTGACACAGAGTCTGCCCGAGAGCTGGCGAAGAA 1788
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1557 GTCTGTGGTTTGGAACTTTCATCAGCCTGGAGAAAGAGGAGAGATCTTGTGGTCAATCAA 1616
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1849 AGACAAACCTCTGAGCTCCATCAAGGCTGACATCTGTCACGCGCTTCTCTGATTTCCAG 1908
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1677 TCTCAGCCACACGCTCATCTCCCAAACGAGCTTCCGGGCGGAGTACAAAGGCCACCGGGGG 1736
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Qy
1737 GCCAGCGGTGTTCAGAAAGCGGTCAAGTTCAGGTTGATATCACTACACGAGAGGTGG 1796
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1969 GCCAGCGGTGTTCAGAAAGCGGTCAAGTTCAGGTTGATATCACTACACGAGAGGTGG 2028
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1797 GGAGCGGAGAGGAGAACGGCATCTACTCGTCACCTTCAACCTGCTCAGGCCCCCAG 1856
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1857 CCGTCGCTTCAAGAGGGTGGTGGAGACCATCCAGGCCAGCTGCTGAGCACACGAGCCC 1916
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2089 CCGTCGCTTCAAGAGGGTGGTGGAGACCATCCAGGCCAGCTGCTGAGCACACGAGCCC 2148
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1917 GCCTGGCGCCAGCACTTGTGCAGACACCACTAACTGTATGGAATGATGACGGGGCGGT 1976
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2149 GCCTGGCGCCAGCACTTGTGCAGACACCACTAACTGTATGGAATGATGACGGGGCGGT 2208
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1977 TTCCAAATGTGAATTATCCCGAAAAGTTAA 2007
Db
2209 TTCCAAATGTGAATTATCCCGAAAAGTTAA 2239

RESULT 3

US-08-557-006C-38
; Sequence 38, Application US/08557006C
; Patent No. 6258547
; GENERAL INFORMATION:
; APPLICANT: Beri, Rajindar K.
; APPLICANT: Carling, David
; APPLICANT: Forder, Robert A.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING AMP-ACTIVATED PROTEIN KINASE
; FILE REFERENCE: NGAP/PHM37588/UST
; CURRENT APPLICATION NUMBER: US/08/557,006C
; CURRENT FILING DATE: 1996-03-06
; PRIOR APPLICATION NUMBER: PCT/GB94/01093
; PRIOR FILING DATE: 1994-05-20
; PRIOR APPLICATION NUMBER: GB 9310489.1
; PRIOR FILING DATE: 1993-05-21
; PRIOR APPLICATION NUMBER: GB 9318010.7
; PRIOR FILING DATE: 1993-08-31

BER OF SEQ ID NOS: 44
TWARE: PatentIn Ver. 2.1
ID NO 38
NGTH: 1742
PE: DNA
GANISM: Human AMP protein kinase
557-006C-38

Y Match 11.2%; Score 225.4; DB 3; Length 1742;
Local Similarity 56.5%; Pred. No. 7.6e-42;
hes 440; Conservative 0; Mismatches 336; Indels 3; Gaps 1;

42 GTATGTTGGGCTTACCGCTCGAGAGACGCTGGGCAAGGGGACAGAGTCTGTGTGAA 101
33 GAAGATCGGACACTAGCTGCTGGGGACACCTTGGGCTGGGACCTTCGGCAAGTGAA 92
102 GCTGGGGGTTCACTGCGTCACTGCGAGAGGTGGCCATCAAGATCGTCAACCGTGAGAA 161
93 GATTGGAGAACATCAATTGACAGGCCATTAAGTGGCAGTTAAGATCTTAAATAGACAGAA 152
162 GCTCAGCAGTGGTGTCTGATG---AAGTGGAGCGGAGATCGGATCCTGAAGCTCAT 218
153 GATTGCGAGTTAGATGTTGTTGGAAAAATNAACGAGAAATTCAAAACTCTTTAACTCTT 212
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213 TGTCTATCTCATATATCAAACTTACCAAGTATCAGCATCTCAACAGACTTTTAT 272
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273 GGTAAATGGAATATGTTCTGGAGGTGAATTTGTTGCACTACATCTGTAAACACGGAGGT 332
339 GAGCCTAAGAGGCTCGAAGTCTTTCGGGAGATCATCTCTGCGTGGACTTCTGCA 398
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693 CTACATCCCGGAGTATCTCAACGTTCTATTGCGCATCTGCTGATGCACTGCTGAGGT 752
759 GGACGCGGACGCGGCTCTCAGCTAGACACATTTCAAGAACACATATGATATAGGGG 817
753 GGAACCTTTGAAGCGAGCACTATCAAGACATACGAGAGCATGATGTTTAAACAGG 811

557-006C-39
ence 39, Application US/0857006C
nt No. 6258547
RAL INFORMATION:
LICANT: Beri, Rajindar K.
LICANT: Carling, David
LICANT: Forder, Robert A.

; TITLE OF INVENTION: NUCLEIC ACID ENCODING AMP-ACTIVATED PROTEIN KINASE
; FILE REFERENCE: NGAP/PM37588/UST
; CURRENT APPLICATION NUMBER: US/08/557,006C
; PRIOR FILING DATE: 1996-03-06
; PRIOR APPLICATION NUMBER: PCT/GB94/01093
; PRIOR FILING DATE: 1994-05-20
; PRIOR APPLICATION NUMBER: GB 9310489.1
; PRIOR FILING DATE: 1993-05-21
; PRIOR APPLICATION NUMBER: GB 9318010.7
; PRIOR FILING DATE: 1993-08-31
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
; LENGTH: 2652
; TYPE: DNA
; ORGANISM: Rat
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)..(1747)
; OTHER INFORMATION: Full length cDNA sequence fragment of Human AMPK -
; OTHER INFORMATION: fragment begins at nucleotide 24 and ends with
; OTHER INFORMATION: nucleotide 1765
US-08-557-006C-39

Query Match 11.2%; Score 225.4; DB 3; Length 2652;
Best Local Similarity 56.5%; Pred. No. 8.6e-42;
Matches 440; Conservative 0; Mismatches 336; Indels 3; Gaps 1;
QY 42 GTATGTTGGGCTTACCGCTCGAGAGACGCTGGGCAAGGGGACAGAGTCTGTGTGAA 101
DB 40 GAAGATCGGACACTAGCTGCTGGGGACACCTTGGGCTGGGACCTTCGGCAAGTGAA 99
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DB 160 GATTGCGAGTTAGATGTTGTTGAAAAATNAACAGAGAAATTCAAAACTTTTAT 219
QY 219 TGAGCACCCCGCTCTAAAGCTGCAGCAGCTTTTATGAAAAACAAAAATATTTGTACCT 278
DB 220 TCGTCACTCTCATATTAATCAAACTCTACCAAGTGTATGTTGCACTACATCTGTAAACACGGGAGGT 279
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DB 400 CAGGCACATGTTGTTCCACAGGGACCTGAAAGCCAGAGAACGTTGTGCTGGACGCCAGAT 459
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557-006C-24
 sence 24, Application US/08557006C
 nt No. 6258547
 RAL INFORMATION:
 LICANT: Beri, Rajindar K.
 LICANT: Carling, David
 LICANT: Forder, Robert A.
 LE OF INVENTION: NUCLEIC ACID ENCODING AMP-ACTIVATED PROTEIN KINASE
 E REFERENCE: NGAP/PHM37588/UST
 RENT APPLICATION NUMBER: US/08/557,006C
 RENT FILING DATE: 1996-03-06
 OR FILING DATE: 1994-05-20
 OR APPLICATION NUMBER: GB 9310489.1
 OR FILING DATE: 1993-05-21
 OR APPLICATION NUMBER: GB 9318010.7
 OR FILING DATE: 1993-08-31
 BER OF SEQ ID NOS: 44
 TWARE: PatentIn Ver. 2.1
 ID NO 24
 ENGT: 2761
 PE: DNA
 GANISM: Artificial Sequence
 NATURE:
 HER INFORMATION: Description of Artificial Sequence: cDNA of rat
 HER INFORMATION: liver AMP protein kinase
 -557-006C-24

Match 11.2%; Score 225.4; DB 3; Length 2761;
 Local Similarity 56.5%; Pred. No. 8.7e-42;
 Matches 440; Conservative 0; Mismatches 336; Indels 3; Gaps 1;
 42 GTATGTTGGCCCTACCGCTGAGAAAGCGTGGCAAGGGGACAGAGTCTGTGTGAA 101
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 476 GAATGCTAAGATAGTCTCGGACTCTTAATATGATGTCAGATGGTGAATTTCTACG 535

QY 519 GACCAGCTGTGGTCCCCCACTAGCTGCTGCCAGGTATCCGGGGGAGAAAGTATGA 578
 Db 536 AACTAGCTGTGGATCGCAAAATATGAGCAACCGAGGTCACTCAGGAAGCTGTATGC 595
 QY 579 CGCCGGAAGCGGACGCTGTGGAGCTGCGGCGTCACTCTGTTTCGCTTGTGGGGGC 638
 Db 596 GGTCTCTGAGGTGATATCTGAGCTGTGGTGTATCTCTGATGCTGCTTCTCTGTGGCAC 655
 QY 639 TCTGCCCTTCGACGATGACAACTTTCGCCGCGACTGCGCAGAGTCTGTCAGGGCATGATCGAGGT 698
 Db 656 CTTCCCGTTGACGATGAGCAGCTGCTTCTTAAAGAGATCCGAGGGGTGTGTT 715
 QY 699 CCACATGCCGCACTTTATCCCGCGCGACTGCGCAGAGTCTGTCAGGGCATGATCGAGGT 758
 Db 716 CTACATCCCGAGTATCTCAACCGTTCTATTGCCACCTGCTGATGACATGCTGCAGGT 775
 QY 759 GGACGCGCACCGCCCTCAGCTAGAGCAATTCAGAAAAACATATATGATATATAGGGG 817
 Db 776 GGACCCCTTGAAGCGGAGCAACTATCAAGAGACATACGAGCATGAATGTTTAAACAGG 834

RESULT 6
 US-09-930-181-5
 ; Sequence 5, Application US/09930181
 ; Patent No. 6455292
 ; GENERAL INFORMATION:
 ; APPLICANT: Origene Technologies
 ; TITLE OF INVENTION: Full-Length Serine Protein Kinase in Brain and Pancreas
 ; FILE REFERENCE: 160 101 V1
 ; CURRENT APPLICATION NUMBER: US/09/930.181
 ; CURRENT FILING DATE: 2001-08-16
 ; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 5
 ; LENGTH: 213
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(213)
 US-09-930-181-5

Query Match 10.6%; Score 213; DB 4; Length 213;
 Best Local Similarity 100.0%; Pred. No. 2.6e-39;
 Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGACATCGACGGGAGGACGCGCGCGCGCAGCAGCAGTATGTTGGGCCCTTACCGG 60
 Db 1 ATGACATCGACGGGAGGACGCGCGCGCGCAGCAGCAGTATGTTGGGCCCTTACCGG 60
 QY 61 CTGGAGAGACGCTGGGCAAGGGGCGAGCAGGTCTGTTGAAGCTGGGGGTTTCACTGCGTC 120
 Db 61 CTGGAGAGACGCTGGGCAAGGGGCGAGCAGGTCTGTTGAAGCTGGGGGTTTCACTGCGTC 120
 QY 121 ACCTGCCAAGAGTGGCCATCAAGATCGTCAACCGTGAGAGCTCAGCGAGTCGGTGTG 180
 Db 121 ACCTGCCAAGAGTGGCCATCAAGATCGTCAACCGTGAGAGCTCAGCGAGTCGGTGTG 180
 QY 181 ATGAAGGTGGAGCGGAGATCGCGATCTGAAG 213
 Db 181 ATGAAGGTGGAGCGGAGATCGCGATCTGAAG 213

RESULT 7
 US-09-101-146-44
 ; Sequence 44, Application US/09101146
 ; Patent No. 6124125
 ; GENERAL INFORMATION:
 ; APPLICANT: Dartmouth College, St. Vincent's Institute of
 ; APPLICANT: Medical Research, Kemp et al.
 ; TITLE OF INVENTION: No. 6124125el AMP Activated Protein Kinase
 ; NUMBER OF SEQUENCES: 64
 ; CORRESPONDENCE ADDRESS:

513 AACAGAGCCTGTGGCTCTGGCCCAATTAATGCTCTGACACAGAGAGTAAATTTGAGAGAGATCTATGCG 517

US-09-984-890-1

QY	457	GCATCGCAGAC	CTTTGGCATG	GGCTCCCT	CGACAGCCT	GTTGGCAGAC	CCTGTTGGAGAC	CAAGCT	526
Db	559	AGATTGCAGAC <th>CTTTGGCTT</th> <th>CAGCAATGA</th> <th>ATTCACCT</th> <th>TTTGGGAA</th> <th>CAAGCTGG</th> <th>ACACCTTCT</th> <th>628</th>	CTTTGGCTT	CAGCAATGA	ATTCACCT	TTTGGGAA	CAAGCTGG	ACACCTTCT	628

527 GTGGTCCCCCAGTACGCTGCCCCGAGGTGATCCGGGGGAGAGTATGACGCGCGGA 586
 629 GTGGCAGTCCCTTATGCTGCTCCCGAGAACTCTTCCAGGGCAAAAAATATGATGGACCG 688
 587 AGGCGGAGTGTGGAGCTGCGGCTGATCTCTGTTGCGCTTCTGTTGGGGGCTCTGCGCT 646
 689 AGGTGGATGTGTGGAGCTGAGGATATCTCTATACACTGCTGAGCGGATCTCTGCGCT 748
 647 TCGAGATGACAACTTGGACAGCTGCTGGGAGAGGTGAAGCGGGCGTGTTCACATGC 706
 749 TTGATGGACAGAACTCAAGAGCTGCGGAAACGGTACTGAGGGGAAAAATACCGTATTC 808
 707 CGCACTTTATCCCGCCGAGTCCAGAGTCTGTACGCGGGCATGATCAGGTGGAGCGCG 766
 809 CATTCTACATGTCCAGCGACTGTGAACCTGCTTAAGAAATTTCTCATCTTAATCCA 868
 767 CAGCGCGCTCAGCTAGACACATTCAGAAACATATGTTATATAGGGGGCAGAAATG 826
 869 GCAAGAGAGGCACTTTAGAGCAAAATCATGAAGATCGATGATGAATGTGGGTCAAG 928
 827 AGCCCGAACACAGC 841
 929 ATGATGAATAAGC 943

AT 9
 i-557-006C-44
 rrence 44, Application US/08557006C
 ent No. 6258547
 ERAL INFORMATION:
 PLICANT: Beri, Rajindar K.
 PLICANT: Carling, David
 PLICANT: Forder, Robert A.
 TLE OF INVENTION: NUCLEIC ACID ENCODING AMP-ACTIVATED PROTEIN KINASE
 LE REFERENCE: NCAP/PH37588/UST
 RRENT APPLICATION NUMBER: US/08/557,006C
 RRENT FILING DATE: 1996-03-06
 RIOR APPLICATION NUMBER: PCT/GB94/01093
 RIOR FILING DATE: 1994-05-20
 RIOR APPLICATION NUMBER: GB 9310489.1
 RIOR FILING DATE: 1993-05-21
 RIOR APPLICATION NUMBER: GB 9318010.7
 RIOR FILING DATE: 1993-08-31
 MBER OF SEQ ID NOS: 44
 FTWARE: PatentIn Ver. 2.1
) ID NO 44
 LENGTH: 1747
 TYPE: DNA
 ORGANISM: Human
 FEATURE:
 NAME/KEY: gene
 LOCATION: (1)..(1747)
 OTHER INFORMATION: Full length cDNA sequence fragment of Human AMPK -
 OTHER INFORMATION: fragment begins at nucleotide 24 and ends with
 OTHER INFORMATION: nucleotide 1765
 i-557-006C-44

try Match 10.0%; Score 200.4; DB 3; Length 1747;
 Local Similarity 56.1%; Pred. No. 3.3e-36;
 ches 440; Conservative 0; Mismatches 336; Indels 8; Gaps 3;
 42 GTATGTTGGGCGCTACCGGCTGGAGAACGCTGGGCAAGGGGAGAGAGTCTGGTGAA 101
 33 GAAGATCGACACTACGCTGGGGGACACCTGGGCGTGGGACCTTCGCAAGTGAA 92
 102 GCTGGGGTTCACCTGCGTCACTGCGCAGAGAGTGGCCATCAAGATGTCACCGTGAGAA 161
 93 GATTGGAGAACATCAATTGACAGGCGCAATAAGTGGCAGTTAAGATCTTAATAGACAGAA 152
 162 GCTCAGCGAGTCCGCTGATG---AAGTGGAGGGAGATCGGATCTCTGAGCTCAT 218
 153 GATTGCGAGTTAGATGTTGTGGAAAAATAAAGCAGAGAAATTCAAAATCTTAACTCTT 212

QY 219 TGAGCACCCCGAGTCTTAAAGCTGACGAGCTTTATGAAAAAATAATTTGTACCT 278
 DB 213 TCGTCACTCTCATATATCAAACTTACCAAGTATCAGCACTCCACAGACTTTTAT 272
 QY 279 GGTGCTAGAACACGCTGTCAGGTGTGAGCTTTCGACTACTCTGGTGAAGAGGGAGCT 338
 DB 273 GGTAAATGGAATATGCTGAGGTGAATTTGTTGCACTACATCTGTAACACAGGGAGGT 332
 QY 339 GACGCTTAAGAGGCTCGGAAGTCTTCGCGAGATCATCTCTGCGCTGAGCTTCTG--C 396
 DB 333 TGAAGAGGTGAAGCTCGCGGCTTTCCAGCAGATTTCTGTCTGCGCTGAGCTACTGTCT 392
 QY 397 CACAGCAGCTCCATATATGCCACAGGGATCTGAAACCTGAAACCTCTCTGCTGGAGCAAG 456
 DB 393 CACAGGACATGTTGTTCCACAGGGACCTGAGCCAGAGAACGTTGCTGGAGCCCGAG 452
 QY 457 AACAAATCCGCATTCGAGACTTTGGCATGCGCTCTCTGAGGTTCGCGACAGCCTGTTG 516
 DB 453 ATGAATGCTAAGATAGCTGACTTCGGACTCTCTAATATGATGTCAATGTTGAATTTCTA 512
 QY 517 GAGACCACTGTGGTCCCCCCTACCTAGCCCTGCGGAGGTGATCCGGGGGAGAACTAT 576
 DB 513 CGAACTAGCTGTGATCGCAAAATTTATGACAGCCGAGGTCTCTCAGGAAGCTGTAT 572
 QY 577 GACGGCGGAGAGCGGACGTGTGGAGCTGCGGCGTCTATCTCTGCTTGCCTTGTGCTGGG 636
 DB 573 GCGGCTCTGAGGTGATATCTGGAGCTGTGGTGTATCTGTATGCGCTTCTCTGTGGC 632
 QY 637 GCTTGCCTT---CGACGATGACAACTTCGACAGCTGCTGGAGAGGTGAAGCGGGC 693
 DB 633 ACCCTCCGTTTCGACGAGCATGAGCAGCTGCTCTTTAAGAGATCCGAGGGGGT 692
 QY 694 GTGTTCCACATCGCGACTTTATCCCGCCGAGTCCGAGAGTCTGCTACGGGGCATGATC 753
 DB 693 GTGTTTACATCCCGAGTATCTCAACCGTTCATTGCGCACTCTGTGATGCACTGCTG 752
 QY 754 GAGGTGACCGCCGACGCGCTCAAGCTAGAGCAGATTCAGAAACACATATGTTATATA 813
 DB 753 CAGGTGACCCCTTGAAGCGAGCACTATCAAGACATACGAGGCAATGATGGTTAAA 812
 QY 814 GGGG 817
 DB 813 CAGG 816

RESULT 10
 US-09-359-161-4
 ; Sequence 4, Application US/09359161A
 ; Patent No. 6342656
 ; GENERAL INFORMATION:
 ; APPLICANT: Bradford, Kent J.
 ; APPLICANT: Dahal, Peetambar
 ; APPLICANT: Yang, Hong
 ; APPLICANT: Cooley, Michael
 ; APPLICANT: Downie, Bruce
 ; APPLICANT: Gee, Oliver
 ; APPLICANT: The Regents of the University of California
 ; TITLE OF INVENTION: Regulation of Source-Sink Relationships and Responses
 ; TITLE OF INVENTION: to Stress Conditions in Plants
 ; FILE REFERENCE: 023070-095900US
 ; CURRENT APPLICATION NUMBER: US/09/359,161A
 ; CURRENT FILING DATE: 1999-07-21
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 4
 ; LENGTH: 1929
 ; TYPE: DNA
 ; ORGANISM: Lycopersicon esculentum
 ; FEATURE:
 ; OTHER INFORMATION: Lycopersicon esculentum plant homolog of yeast
 ; OTHER INFORMATION: SNF1 kinase subunit of protein kinase (LeSNF1)
 US-09-359-161-4

LE REFERENCE: NGAP/PHM37588/UST
RENT APPLICATION NUMBER: US/08/557,006C
RENT FILING DATE: 1996-03-06
IOR APPLICATION NUMBER: PCT/GB94/01093
IOR FILING DATE: 1994-05-20
IOR APPLICATION NUMBER: GB 9310489.1
IOR FILING DATE: 1993-05-21
IOR APPLICATION NUMBER: GB 9318010.7
IOR FILING DATE: 1993-08-31
MBER OF SEQ ID NOS: 44
FTWARE: Patent In Ver. 2.1
ID NO 37
LENGTH: 1736
YPE: DNA
GANISM: Artificial Sequence
ATURE:
THER INFORMATION: Description of Artificial Sequence: Rat liver AMP
THER INFORMATION: protein kinase
-557-006C-37

Query Match 8.8%; Score 176.6; DB 3; Length 1736;
Best Local Similarity 52.6%; Pred. No. 7.8e-31;
Matches 408; Conservative 0; Mismatches 364; Indels 3; Gaps 1;
42 GTATGTTGGCCCTACCGCTGGAGAGACGCTGGCAAGGGCGACAGAGTCTGTGTGAA 101
33 GAAGATCGGACACTAGCTGCTGGCGACACGCTGGCGTGGCACCTTCGGCAAGTGAA 92
102 GCTGGGGTTCACTGCGTCACTCTGGAGAGAGTGGCCATCAAGATCGTCAACCGTGAGAA 161
93 GATTGGAGAACATCAATTAACAGGCCATAAAGTGGCAGTTTAAATCTTAAATAGACAGAA 152
162 GCTCAGCGAGTCCGTCGTGATG---AAGGTGGAGCGGGAGATCGCATCTGAAGCTCAT 218
153 GATTGCGAGTTAGATGTTGTGGAAAAATAAACAGAGAAATTCAAAATCTAAACTCTT 212
219 TGAGCACCCACGTCCTAAGCTGCACGACGTTTATGAAAAAATAATTTGTACCT 278
213 TCCTCATCTCATATTATCAACTATACAGGTGATCAGCACTCCACAGATTTTTTAT 272
279 GGTGCTAGAACAGTGTGAGTGTGAGCTCTTCGACTACTCGTGGTAGAAGGGAGGCT 338
273 GGTATGGAAATATGTTGTGGAGGTGAATTTATTTGACTACATCTGTAAGCATGGACGGT 332
339 GACGCTTAAGAGGCTCGGAAGTTCTTCGGCGAGATCATCTCGCGTGGACTCTTGCCA 398
333 TGAGAGATGGAAGCCAGGCGGCTCTTTAGCAGATCTCTGCTGTGGATTACTGTCA 392
399 CAGCCACTCCATATGCCAGGGATCTGAAACCTGAAACCTCTCTGCTGGACGAGAGAA 458
393 TAGGCATATGTTGTTTCATCGAGACCTGAAACCCAGAGATGTCCTGTTGGATGCACAT 452
459 CAACATCCGATCGCAGACTTTGGCATGGCGTCCCTGACAGTTGGCGACAGCCTGTGGA 518
453 GAATGCCAAGATAGCGGATTCGGAATTAATAATATGATGTCAGATGGTGAATTTCTGAG 512
519 GACAGCTGTGGTCCCGCCACTACGCTCCCGAGGTGATCCGGGGGAGAGATGA 578
513 AACTAGTTCGGATCTCCAAATATAGCAGCACTGAAATCATCTCAGGCAGATGTATGC 572
579 CGCCCGAAGCGGAGCGTGTGGAGCTGCGCGTCACTCTGTTCCGCTTGTGTTGGGGG 638
573 AGGTCTCTGAAGTTGATATCTGGAGCTGTGGTGTATCTTGTATGCTCTCTTTGTGGC 632
639 TGTGCTTCGAGTAGACAACTTTGGACAGCTGTGGAAGAGGTGAGCGGGCGGTGTT 698
633 CCTCCCATTTGATGATGAGCATGTACCTGTTATTTAAGAAATCCGAGGGGTGTCTT 692
699 CCATATCCGCACTTTATCCGCGCCGACTCCAGAGTCTGCTACGGGGCATGATCAGGT 758
693 TTATATCCCAAGATATCTCAATCGTTCTGTGGCAGCTCTCTGATGATATGTCAGGT 752
759 GGACGGCGCAGCGGCTCACGCTAGAGCACATTCAGAAACACATATGGTATATA 813

Db 753 TGACCCACTGAACAGCAACTATCAAGACATAAGAGAGCATGATGTTTAA 807
RESULT 13
US-08-557-006C-36
Sequence 36, Application US/08557006C
Patent No. 6258547
GENERAL INFORMATION:
APPLICANT: Beri, Rajindar K.
APPLICANT: Carling, David
APPLICANT: Forster, Robert A.
TITLE OF INVENTION: NUCLEIC ACID ENCODING AMP-ACTIVATED PROTEIN KINASE
FILE REFERENCE: NGAP/PHM37588/UST
CURRENT APPLICATION NUMBER: US/08/557,006C
CURRENT FILING DATE: 1996-03-06
PRIOR APPLICATION NUMBER: PCT/GB94/01093
PRIOR FILING DATE: 1994-05-20
PRIOR APPLICATION NUMBER: GB 9310489.1
PRIOR FILING DATE: 1993-05-21
PRIOR APPLICATION NUMBER: GB 9318010.7
PRIOR FILING DATE: 1993-08-31
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 36
LENGTH: 1783
TYPE: DNA
ORGANISM: Human AMP protein kinase
US-08-557-006C-36

Query Match 8.8%; Score 176.6; DB 3; Length 1783;
Best Local Similarity 52.6%; Pred. No. 7.8e-31;
Matches 408; Conservative 0; Mismatches 364; Indels 3; Gaps 1;
QY 42 GTATGTTGGCCCTACCGCTGGAGAGACGCTGGCAAGGGCGACAGAGTCTGTGTGAA 101
Db 34 GAAGATCGGACACTAGCTGCTGGCGACACGCTGGCGTGGCACCTTCGGCAAGTGAA 93
QY 102 GCTGGGGTTCACTGCGTCACTCTGGAGAGAGTGGCCATCAAGATCGTCAACCGTGAGAA 161
Db 94 GATTGGAGAACATCAATTAACAGGCCATAAAGTGGCAGTTTAAATCTTAAATAGACAGAA 153
QY 162 GCTCAGCGAGTCCGTCGTGATG---AAGGTGGAGCGGGAGATCGCATCTGAAGCTCAT 218
Db 154 GATTGCGAGTTAGATGTTGTGGAAAAATAAACAGAGAAATTCAAAATCTAAACTCTT 213
QY 219 TGAGCACCCACGTCCTAAGCTGCACGAGCTGTTATGAAAAAATAATTTGTACCT 278
Db 214 TCCTCATCTCATATTATCAACTATACAGGTGATCAGCACTCCACAGATTTTTTAT 273
QY 279 GGTGCTAGAACAGTGTGAGTGTGAGCTCTTCGACTACTCTGCTGTGGAGGGGCT 338
Db 274 GGTATGGAAATATGTTGTGGAGGTGAATTTATTTGACTACATCTGTAAGCATGGACGGT 333
QY 339 GACGCTTAAGAGGCTCGGAAGTTCTTCGGCGAGATCATCTCGCGTGGACTCTTGCCA 398
Db 334 TGAGAGATGGAAGCCAGGCGGCTCTTTAGCAGATCTCTGCTGTGGATTACTGTCA 393
QY 399 CAGCCACTCCATATGCCAGGGATCTGAAACCTGAAACCTCTCTGCTGGACGAGAGAA 458
Db 394 TAGGCATATGTTGTTTCATCGAGACCTGAAACCCAGAGATGTCCTGTTGGATGCACAT 453
QY 459 CAACATCCGATCGCAGACTTTGGCATGGCGTCCCTGACAGTTGGCGACAGCCTGTGGA 518
Db 454 GAATGCCAAGATAGCGGATTTCCGGAATTAATAATATGATGTCAGATGGTGAATTTCTGAG 513
QY 519 GACCACTGTGGTCCCGCCACTACGCTCCCGAGGTGATCCGGGGGAGAGATGATGA 578
Db 514 AACTAGTTCGGATCTCCAAATATAGCAGCACTGAAATCATCTCAGGCAGATGTATGC 573
QY 579 CGCCCGAAGCGGAGCGTGTGGAGCTGCGCGTCACTCTGTTCCGCTTGTGTTGGGGG 638
Db 574 AGGTCTCTGAAGTTGATATCTGGAGCTGTGGTGTATCTTGTATGCTCTCTTTGTGGC 633

GenCore version 5.1.6
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ucleic - nucleic search, using sw model

n: November 27, 2003, 01:57:44 ; Search time 456.512 Seconds
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US-10-054-579-3

ct score: 1827

nce: 1. atgaaggtggagcgggat.....gaattatccgaaagtaa 1827

ng table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

hed: 2552756 seqs, 1349719017 residues

number of hits satisfying chosen parameters: 5105512

um DB seq length: 0

um DB seq length: 2000000000

processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 22: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
- 23: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
- 24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*
- 25: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

t	Score	Query Match	Length	ID	Description
1	1827	100.0	1827	24	ABQ77626 Human kinase NHP #
2	1827	100.0	2007	24	ABQ77625 Human kinase NHP #
3	1827	100.0	2647	24	AAD34315 Human PKIN-18 cDNA
4	1825.4	99.9	2908	25	ABX13583 Human cDNA encodin
5	1813	99.2	3364	25	ABX13584 Human cDNA encodin
6	1759.6	96.3	2025	24	ABA02995 Human protein kina
7	1759.6	96.3	2217	24	ABA02994 Human protein kina
8	904.2	49.5	2799	25	AAL51889 Human cell cycle-r

Human kinase #3 co
Human kinase #1 co
Polynucleotide seq
Human kinase PKIN-
Human kinase #2 co
Novel human cDNA s
Drosophila melanog
Human HrPopK-1 hom
Human lung cancer
Human Ser/Thr kina
Novel protein kina
Murine neuronal se
Murine neuronal se
Human serine/threo
Human microtubule
Human microtubule
Human cDNA SEQ ID
Human full-length
Human microtubule
Human kinase (PKIN
Human MARK cDNA.
Human neuronal ser
Human neuronal ser
Human microtubule
Human protein kina
Human protein kina
Human keratinocyte
Human keratinocyte
Human protein kina
Human kinase PKIN-
Drosophila melanog
Human cDNA 5'-end
Human cDNA clone r
Human expressed po
DNA encoding novel
Polynucleotide seq

ALIGNMENTS

RESULT 1
ABQ77626
ID ABQ77626 standard; cDNA; 1827 BP.
XX ABQ77626;
AC ABQ77626;
XX 21-OCT-2002 (first entry)
XX Human kinase NHP #2-encoding cDNA, SEQ ID NO:3.
DE Human; kinase; NHP; chromosome 11; signal transduction; cytoplasmic;
KW nuclear; brain; pituitary; hypothalamus; adipose; cerebellum;
KW adrenal gland; foetal lung; foetal brain; cancer; drug screening;
KW mental disorder; diagnostic reagent; clinical trial monitoring; cosmetic;
KW nutraceutical; mutation detection; gene expression analysis;
KW chromosome mapping; transgenic animal; cytostatic; gene therapy;
KW gene; ss.
XX Homo sapiens.
XX OS
XX Key Location/Qualifiers
XX CDS 1..1827
XX /tag= a
XX /product= "Human kinase NHP #2"
FT FT
XX WO200259287-A2.
XX
XX
PD 01-AUG-2002.
XX
XX 22-JAN-2002; 2002WO-US01818.
PF
XX

23-JAN-2001; 2001US-263378P.

(LEXI-) LEXICON GENETICS INC.

Turner CA, Mathur B;

4PI; 2002-599780/64.

P-PSDB; ABB09558.

Novel polynucleotide encoding human proteins sharing sequence similarity with animal kinases, useful for drug screening, diagnosis, in gene therapy of disorders and diseases e.g. cancer -

Claim 3; Page 38-39; 40pp; English.

The invention relates to novel human kinases (ABB09557, ABB09558), referred to as NHPs, and to nucleic acids encoding them (ABB07625, ABB07626). The NHPs have structural similarity with animal kinases including serine-threonine kinases, carbon catabolite repressing kinases, calcium/calmodulin-dependent protein kinases, and cAMP-dependent protein kinases. The NHPs do not contain consensus signal sequences, indicating that they may be cytoplasmic or nuclear proteins, and are thought to be involved in signal transduction. Polynucleotides encoding NHPs were obtained using human brain, pituitary, hypothalamus, adipose, cerebellum, adrenal gland, foetal lung, and foetal brain cDNAs and primers derived from human genomic DNA. The gene encoding the NHPs is located on chromosome 11. NHP nucleotides and proteins are useful for treating mental, biological or medical disorders including cancer, and for screening compounds useful in the treatment of such conditions. They can also be used as diagnostic reagents, in clinical trial monitoring and in cosmetic and nutritional applications. NHP nucleotides can additionally be used in the detection of disease-associated mutations, in the analysis of gene expression, for mapping chromosome 11, for the recombinant expression of NHPs, to generate transgenic animals, in gene therapy, and as part of ribozyme and/or triple helix sequences useful in the modulation of NHP gene expression. The present sequence represents cDNA encoding a 608 amino acid NHP (#2).

Sequence 1827 BP; 406 A; 581 C; 535 G; 305 T; 0 other;

CY Match 100.0%; Score 1827; DB 24; Length 1827;
Local Similarity 100.0%; Pred. No. 0;
hes 1827; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 ATGAAGTGGAGCGGAGATCGGATCCTGAAGCTCATTAAGCACCCCGCCTAAAG 60
1 ATGAAGTGGAGCGGAGATCGGATCCTGAAGCTCATTAAGCACCCCGCCTAAAG 60
61 CTGCACGACGTTTATGAACAACAAATATTTGACCTGTGTAGACACGTTGTCAGGT 120
61 CTGCACGACGTTTATGAACAACAAATATTTGACCTGTGTAGACACGTTGTCAGGT 120
121 GGTGAGCTCTTCACTACCTGTTGAAGAGGAGGCTGACGCTGAAGAGGCTCGGAAG 180
121 GGTGAGCTCTTCACTACCTGTTGAAGAGGAGGCTGACGCTGAAGAGGCTCGGAAG 180
181 TTCTTCGGGAGATCATCTCTGGCTGGAATTTGTCACAGCCACTCCATATGCCACAGG 240
181 TTCTTCGGGAGATCATCTCTGGCTGGAATTTGTCACAGCCACTCCATATGCCACAGG 240
241 GATCTGAACCTGAAACCTCTGCTGGACGAGAGAACACATCCGATCGCAGACTTT 300
241 GATCTGAACCTGAAACCTCTGCTGGACGAGAGAACACATCCGATCGCAGACTTT 300
301 GGATGAGCTCCCTGACAGGTTGGGACAGCTGTTGAGACACGAGCTGTGGGTCCCCCAC 360
301 GGATGAGCTCCCTGACAGGTTGGGACAGCTGTTGAGACACGAGCTGTGGGTCCCCCAC 360
361 TAGCCCTGCCCGAGGTGATCCGGGGGAGAGATGATGACCGCGGAGCGGAGCGTGTGG 420
361 TAGCCCTGCCCGAGGTGATCCGGGGGAGAGATGATGACCGCGGAGCGGAGCGTGTGG 420
421 AGCTGGCGGCTATCTCTGTTGCGCTTCTGTTGGGGGCTCTGCCCTTCGACGATGACAC 480

421 AGCTGGCGGCTATCTCTGTTGCGCTTCTGTTGGGGCTCTGCCCTTCGACGATGACAC 480
481 TTGGACAGCTGCTGGAGAGGTGAAGCGGGCGGTGTTCCACATGCCGCACTTTATCCGG 540
481 TTGGACAGCTGCTGGAGAGGTGAAGCGGGCGGTGTTCCACATGCCGCACTTTATCCGG 540
541 CCCGACTGCCAGAGTCTCTACGGGGCATGATCGAGGTGGACGCGCACGCGCCTCAGG 600
541 CCCGACTGCCAGAGTCTCTACGGGGCATGATCGAGGTGGACGCGCACGCGCCTCAGG 600
601 CTAGAGCATTCTAGAAACACATATGTTATATAGGGGCAAGATAGCCCGAACACAGAG 660
601 CTAGAGCATTCTAGAAACACATATGTTATATAGGGGCAAGATAGCCCGAACACAGAG 660
661 CAGCCCATCTCTCGCAAGGTGCAGATCCGCTCGCTGCCCGACCTGGAGGACATGACCCC 720
661 CAGCCCATCTCTCGCAAGGTGCAGATCCGCTCGCTGCCCGACCTGGAGGACATGACCCC 720
721 GACGTGCTGGACAGCATGCACTCACTGGGCTGCTTCCGAGACCGCAACAAAGTGTGCGAG 780
721 GACGTGCTGGACAGCATGCACTCACTGGGCTGCTTCCGAGACCGCAACAAAGTGTGCGAG 780
781 GACGTGCTGGAGAGGAGAACACAGAGAGATGATTTACTTCTCTCTCTGAGACCGG 840
781 GACGTGCTGGAGAGGAGAACACAGAGAGATGATTTACTTCTCTCTCTGAGACCGG 840
841 AAAGAAAGTATCCCGAGCCAGGAGATGAGGACCTGCCCCCGGAAACGAGATAGACCT 900
841 AAAGAAAGTATCCCGAGCCAGGAGATGAGGACCTGCCCCCGGAAACGAGATAGACCT 900
901 CCCCGAAGCGTGTGGACTCCCGATGCTGAACCGGACGCGGCGGCGGCGCAAGCGC 960
901 CCCCGAAGCGTGTGGACTCCCGATGCTGAACCGGACGCGGCGGCGGCGCAAGCGC 960
961 AAATCCATGAGAGTGTCTCAGCGTGAAGACGCGGCTCTCCCGTGTCTGCGGCGGCGG 1020
961 AAATCCATGAGAGTGTCTCAGCGTGAAGACGCGGCTCTCCCGTGTCTGCGGCGGCGG 1020
1021 ATTGAGATGGCCAGCGGCGGAGGCTCTGGTCCATCAGCGGCTCTCTCAGGCGCTT 1080
1021 ATTGAGATGGCCAGCGGCGGAGGCTCTGGTCCATCAGCGGCTCTCTCAGGCGCTT 1080
1081 TCCACAGCCCACTCAGCAGCGCCCGGGTGAGCCCTCACCCCTCACCAAGGGGAGTCCC 1140
1081 TCCACAGCCCACTCAGCAGCGCCCGGGTGAGCCCTCACCCCTCACCAAGGGGAGTCCC 1140
1141 CTCGCCACCCCAAGGAGACCTGTCCACACGCGCAAGAGGAGCGCGCTGGCAGCGCC 1200
1141 CTCGCCACCCCAAGGAGACCTGTCCACACGCGCAAGAGGAGCGCGCTGGCAGCGCC 1200
1201 AACCCAGCGCCCGCTCCAGCGCCAGCGCTCGAGAGGGGTGCCCTGGAGGCGCGGCTCAAC 1260
1201 AACCCAGCGCCCGCTCCAGCGCCAGCGCTCGAGAGGGGTGCCCTGGAGGCGCGGCTCAAC 1260
1261 TCCATCAAGAAACAGCTTTCTGGGCTCAACCCCGCTTCCACCGCGGAAACTGCAAGTTCG 1320
1261 TCCATCAAGAAACAGCTTTCTGGGCTCAACCCCGCTTCCACCGCGGAAACTGCAAGTTCG 1320
1321 AGCCCGGAGGAGATGTCCTGACACGAGTGTCTCCCGAGAGCTGGCGAGAGTCC 1380
1321 AGCCCGGAGGAGATGTCCTGACACGAGTGTCTCCCGAGAGCTGGCGAGAGTCC 1380
1381 TGGTTGGGAACCTTCATCAGCTGGAGAGGAGGAGAGATCTTCTGTTGTTCAATCAAGAC 1440
1381 TGGTTGGGAACCTTCATCAGCTGGAGAGGAGGAGAGATCTTCTGTTGTTCAATCAAGAC 1440
1441 AAACCTCTGAGCTCCATCAAGGCTGACATGCTGACAGCTTCTCTGTTGTTCAATCAAGTTC 1500
1441 AAACCTCTGAGCTCCATCAAGGCTGACATGCTGACAGCTTCTCTGTTGTTCAATCAAGTTC 1500
1501 AGCCACAGGCTATCTCCCAACAGCTTCCGGGCGGAGTACAGGCCACCGGGGGGCA 1560

1501 AGCCACAGCGTCATCTCCAAACGAGCTTCCGGCCGAGTACAAAGGCCACGCGGGGGCCA 1560
1561 GCGGTGTTCCAGAACCGGTCAAGTTCAGGTTGATACACCTACACGAGGGTGGGAG 1620
1561 GCGGTGTTCCAGAACCGGTCAAGTTCAGGTTGATACACCTACACGAGGGTGGGAG 1620
1621 GCGCAGAAGGAGAACGGCATCTACTCCGTACCTTCCACCTGTCTCTCAGGCCCCAGCCGT 1680
1621 GCGCAGAAGGAGAACGGCATCTACTCCGTACCTTCCACCTGTCTCTCAGGCCCCAGCCGT 1680
1681 CGTTCAGAGGGTGTGAGACCATCCAGGCCAGCTGCTGAGCAACACAGACCGGCT 1740
1681 CGTTCAGAGGGTGTGAGACCATCCAGGCCAGCTGCTGAGCAACACAGACCGGCT 1740
1741 GCGGCCAGCACTGTGCAGACACCACTAACTGTATGGAATGATGACGGGGCGCTTCC 1800
1741 GCGGCCAGCACTGTGCAGACACCACTAACTGTATGGAATGATGACGGGGCGCTTCC 1800
1801 AATGTGGAATTATCCGAAAGTTAA 1827
1801 AATGTGGAATTATCCGAAAGTTAA 1827

LT 2
7625

ABQ77625 standard; cDNA; 2007 BP.

ABQ77625;

21-OCT-2002 (first entry)

Human kinase NHP #1-encoding cDNA, SEQ ID NO:1.

Human; kinase; NHP; chromosome 11; signal transduction; cytoplasmic;
nuclear; brain; pituitary; hypothalamus; adipose; cerebellum;
adrenal gland; foetal lung; foetal brain; cancer; drug screening;
mental disorder; diagnostic reagent; clinical trial monitoring; cosmetic;
nutraceutical; mutation detection; gene expression analysis;
chromosome mapping; transgenic animal; cytostatic; gene therapy;
gene; 88.

Homo sapiens.

Key Location/Qualifiers
CDS 1..2007

/tag= a
/product= "Human kinase NHP #1"

WO200259287-A2.

01-AUG-2002.

22-JAN-2002; 2002WO-US01818.

23-JAN-2001; 2001US-263378P.

(LEXI-) LEXICON GENETICS INC.

Turner CA, Mathur B;

WPI; 2002-599780/64.

P-PSDB; ABB09557.

Novel polynucleotide encoding human proteins sharing sequence
similarity with animal kinases, useful for drug screening, diagnosis,
in gene therapy of disorders and diseases e.g. cancer

Claim 1; Page 36; 40pp; English.

The invention relates to novel human kinases (ABB09557, ABB09558),
referred to as NHPs, and to nucleic acids encoding them (ABQ77625,
ABQ77626). The NHPs have structural similarity with animal kinases
including serine-threonine kinases, carbon catabolite repressing kinases,

calcium/calmodulin-dependent protein kinases, and cAMP-dependent protein
kinases. The NHPs do not contain consensus signal sequences, indicating
that they may be cytoplasmic or nuclear proteins, and are thought to be
involved in signal transduction. Polynucleotides encoding NHPs were
obtained using human brain, pituitary, hypothalamus, adipose, cerebellum,
adrenal gland, foetal lung, and foetal brain cDNAs and primers derived
from human genomic DNA. The gene encoding the NHPs is located on
chromosome 11. NHP nucleotides and proteins are useful for treating
mental, biological or medical disorders including cancer, and for
screening compounds useful in the treatment of such conditions. They can
also be used as diagnostic reagents, in clinical trial monitoring and in
cosmetic and nutritional applications. NHP nucleotides can additionally
be used in the detection of disease-associated mutations, in the analysis
of gene expression, for mapping chromosome 11, for the recombinant
expression of NHPs, to generate transgenic animals, in gene therapy,
and as part of ribozyme and/or triple helix sequences useful in the
modulation of NHP gene expression. The present sequence represents cDNA
encoding a 668 amino acid NHP (#1).

Sequence 2007 BP; 445 A; 626 C; 604 G; 332 T; 0 other;

Query Match 100.0%; Score 1827; DB 24; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1827; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAGTGGAGCGGAGATCGCATCTGAAGCTCATTGAGCACCCGCCAGTCTCTAAAG 60
DB 181 ATGAAGTGGAGCGGAGATCGCATCTGAAGCTCATTGAGCACCCGCCAGTCTCTAAAG 240
QY 61 CTGCACGACGTTTATGAAAAACAAAAATATTGTACCTGGTGTAGAACACGTTGTCAGGT 120
DB 241 CTGCACGACGTTTATGAAAAACAAAAATATTGTACCTGGTGTAGAACACGTTGTCAGGT 300
QY 121 GGTGAGCTTTCGACTACCTGCTGAAGAGGGAGGCTGACGCCCTAAGAGGCTCGGAAG 180
DB 301 GGTGAGCTTTCGACTACCTGCTGAAGAGGGAGGCTGACGCCCTAAGAGGCTCGGAAG 360
QY 181 TTCTTCGGCGAGATCATCTCTGCGCTGACCTTCTGCCACACGCACTCCATATGCCACAGG 240
DB 361 TTCTTCGGCGAGATCATCTCTGCGCTGACCTTCTGCCACACGCACTCCATATGCCACAGG 420
QY 241 GATCTGAACCTGAAAAACCTCTCTGCTGGACGAGAGAACAAACATCCGATCGCAGACTTT 300
DB 421 GATCTGAACCTGAAAAACCTCTCTGCTGGACGAGAGAACAAACATCCGATCGCAGACTTT 480
QY 301 GGCATGGCGTCCCTGCGAGGTTGGCGACAGCCTGTTGGAGACAGCTGTGGGTCCCCCACC 360
DB 481 GGCATGGCGTCCCTGCGAGGTTGGCGACAGCCTGTTGGAGACAGCTGTGGGTCCCCCACC 540
QY 361 TACGCTGCCCGGAGGTGATCCGGGGGAGAGTATGACGGCGGAGCGGAGCGAGTGTGG 420
DB 541 TACGCTGCCCGGAGGTGATCCGGGGGAGAGTATGACGGCGGAGCGGAGCGAGTGTGG 600
QY 421 AGCTGCGGCGTCATCTCTGCTGCTGGGGGCTCTGCTGCTTCCGAGATGACAAAC 480
DB 601 AGCTGCGGCGTCATCTCTGCTGCTGGGGGCTCTGCTGCTTCCGAGATGACAAAC 660
QY 481 TTGCGACAGCTGTGCGAAGGTGAAGCGGGGCGTGTTCACATGCCGCCACTTTATCCCG 540
DB 661 TTGCGACAGCTGTGCGAAGGTGAAGCGGGGCGTGTTCACATGCCGCCACTTTATCCCG 720
QY 541 CCCGACTGCCAGAGTCTGTACGGGGCATGATCGAGGTGGAGCGCGCGACCGCCTCAGC 600
DB 721 CCCGACTGCCAGAGTCTGTACGGGGCATGATCGAGGTGGAGCGCGCGACCGCCTCAGC 780
QY 601 CTAGAGCACATTCAGAAACACATATGTTATATAGGGGCAAGAAATGAGCCCGAACACAG 660
DB 781 CTAGAGCACATTCAGAAACACATATGTTATATAGGGGCAAGAAATGAGCCCGAACACAG 840
QY 661 CAGCCCATCTCTCGCAAGGTGAGATCCGCTGCTGCCAGCCTGGAGGACATCGACCCC 720
DB 841 CAGCCCATCTCTCGCAAGGTGAGATCCGCTGCTGCCAGCCTGGAGGACATCGACCCC 900

721 GACGTGCTGGACAGATGCACTCACTGGGCTGCTTCCGAGACCGCAACAAGCTGCTGCAG 780
|||||
901 GACGTGCTGGACAGATGCACTCACTGGGCTGCTTCCGAGACCGCAACAAGCTGCTGCAG 960
|||||
781 GACGTGCTGCTCCGAGGAGGAGAACACGAGAGAGATGATTTACTTCTCTCTCTGGACCGG 840
|||||
961 GACGTGCTGCTCCGAGGAGGAGAACACGAGAGAGATGATTTACTTCTCTCTCTGGACCGG 1020
|||||
841 AAGAAGAGGTACCCGAGCCAGGAGGATGAGACCTGCCCGCCCGGAAACGAGATAGACCTT 900
|||||
1021 AAGAAGAGGTACCCGAGCCAGGAGGATGAGACCTGCCCGCCCGGAAACGAGATAGACCTT 1080
|||||
901 CCCCGGAGGCTGTGGACTCCCGATCTGACCGGACCGGACCGGACCGGACCGGACCGG 960
|||||
1081 CCCCGGAGGCTGTGGACTCCCGATCTGACCGGACCGGACCGGACCGGACCGGACCGG 1140
|||||
961 AATTCATGAGGTGCTCAGCGTACCGGACCGGCGCTCCCGGCTGCTGCGCGCGCGGCC 1020
|||||
1141 AATTCATGAGGTGCTCAGCGTACCGGACCGGCGCTCCCGGCTGCTGCGCGCGGCC 1200
|||||
1021 ATTGAGATGGCCAGCAGCGGACGAGGTCTCGGTCCATCAGCGGTGCTCTCTCAGGCGCTT 1080
|||||
1201 ATTGAGATGGCCAGCAGCGGACGAGGTCTCGGTCCATCAGCGGTGCTCTCTCAGGCGCTT 1260
|||||
1081 TCCACCGCCCACTCAGCAGCGCCCGGGTGACCGCTCACCGCTCACCAAGGGGAGTCCC 1140
|||||
1261 TCCACCGCCCACTCAGCAGCGCCCGGGTGACCGCTCACCGCTCACCAAGGGGAGTCCC 1320
|||||
1141 CTCCCGCAGCCCAAGGGGACACCTGTCCACAGCGCAAGGAGAGCGCGGTGGCAGCGCC 1200
|||||
1321 CTCCCGCAGCCCAAGGGGACACCTGTCCACAGCGCAAGGAGAGCGCGGTGGCAGCGCC 1380
|||||
1201 AACCCCAAGCCCGCTCAGCCCGGCTGAGGGGTGCGCTGAGGGGCGCGCTCAAC 1260
|||||
1381 AACCCCAAGCCCGCTCAGCCCGGCTGAGGGGTGCGCTGAGGGGCGCGCTCAAC 1440
|||||
1261 TCCATCAAGAACAGCTTCTGGGCTCACCGCGCTTCCACCGCGGAACTGCAAGTTCCG 1320
|||||
1441 TCCATCAAGAACAGCTTCTGGGCTCACCGCGCTTCCACCGCGGAACTGCAAGTTCCG 1500
|||||
1321 ACGCCGAGGAGATGTCCAACTGACACAGAGTCGTCCCGCAGAGCTGGCGAAGAGTCC 1380
|||||
1501 ACGCCGAGGAGATGTCCAACTGACACAGAGTCGTCCCGCAGAGCTGGCGAAGAGTCC 1560
|||||
1381 TGTTTGGAACTTCATCAGCTCGAGAGGAGGAGGAGATCTTGTGTGTCATCAAGAGC 1440
|||||
1561 TGTTTGGAACTTCATCAGCTCGAGAGGAGGAGGAGATCTTGTGTGTCATCAAGAGC 1620
|||||
1441 AAACCTCTGAGCTCCATCAAGGCTGACATGTGACCGCTTCTGTGTCGATTCGAGTCTC 1500
|||||
1621 AAACCTCTGAGCTCCATCAAGGCTGACATGTGACCGCTTCTGTGTCGATTCGAGTCTC 1680
|||||
1501 AGCCACAGCGTCACTCTCCAAACGAGCTTCCGGGCGGAGTACAGGCGCACGGGGGGCCCA 1560
|||||
1681 AGCCACAGCGTCACTCTCCAAACGAGCTTCCGGGCGGAGTACAGGCGCACGGGGGGCCCA 1740
|||||
1561 GCGGTGTCAGAGCGGCTCAAGTTCAGGTTGATATACCTACAGCGAGGGTGGGGAG 1620
|||||
1741 GCGGTGTCAGAGCGGCTCAAGTTCAGGTTGATATACCTACAGCGAGGGTGGGGAG 1800
|||||
1621 GCGCAGAGGAGAGCGGATCTACTCTCGTCACTTCCACCTGCTCTCAGGCGCCGAGCGGT 1680
|||||
1801 GCGCAGAGGAGAGCGGATCTACTCTCGTCACTTCCACCTGCTCTCAGGCGCCGAGCGGT 1860
|||||
1681 CGCTTCAAGAGGGTGGTGGAGACCATCAGGCGCCAGCTGTGTGAGCACACGACCCGCGCT 1740
|||||
1861 CGCTTCAAGAGGGTGGTGGAGACCATCAGGCGCCAGCTGTGTGAGCACACGACCCGCGCT 1920
|||||
1741 GCGGCCAGAGCTTGTGTGAGACACCACTAACTGTATGGAATATGATGAGGGGCGGCTTCC 1800
|||||
1921 GCGGCCAGAGCTTGTGTGAGACACCACTAACTGTATGGAATATGATGAGGGGCGGCTTCC 1980
|||||
1801 AAATGTGGAATTATCCCGAAAGTTAA 1827

Db 1981 AAATGTGGAATTATCCCGAAAGTTAA 2007
|||||
RESULT 3
AAD34315
ID AAD34315 standard; cDNA; 2647 BP.
XX
AAD34315;
AC
XX
16-JUL-2002 (first entry)
DT
XX
Human PKIN-18 cDNA.
DE
XX
Human; kinase; enzyme; PKIN-18 protein; immune system disorder; anaemia;
KW acquired immune deficiency syndrome; thymic hypoplasia; Crohn's disease;
KW asthma; neurological disorder; epilepsy; Charcot-Marie-Tooth disease;
KW AIDS; seizures; cell proliferative disorder; cancer; adenocarcinoma;
KW leukaemia; lymphoma; melanoma; sarcoma; developmental disorder;
KW Down's syndrome; gene therapy; protein therapy; cytostatic; gene; ss.
XX
Homo sapiens.
OS
XX
Key Location/Qualifiers
CDS 1..1995
/*tag= a
FT /product= "Human PKIN-18 protein"
FT
XX
WO200218557-A2.
PN
XX
07-MAR-2002.
PD
XX
31-AUG-2001; 2001WO-US27219.
PF
XX
31-AUG-2000; 2000US-329873P.
PR
XX
08-SEP-2000; 2000US-2311357P.
PR
XX
14-SEP-2000; 2000US-232854P.
PR
XX
22-SEP-2000; 2000US-234902P.
PR
XX
29-SEP-2000; 2000US-236499P.
PR
XX
06-OCT-2000; 2000US-238389P.
PR
XX
13-OCT-2000; 2000US-240542P.
XX
(INCY-) INCYTE GENOMICS INC.
XX
Bandman O, Nguyen DB, Hafalia NK, Hafalia AJA, Yao MG, Gandhi AR;
PI Gururajan R, Ding L, Patterson C, Yue H, Baughn MR, Tribouley CM;
PI Thornton M, Elliott VS, Lu Y, Ison CH, Au-Young J, Tang YT;
PI Azimzai Y, Burrill JD, Marcus GA, Zingler KA, Lu DAM, Lal PG;
PI Ramkumar J, Warren BA, Kearney L, Policky JL, Thangavelu K;
PI Burford N;
XX
WPI; 2002-329769/36.
DR P-PSDB; AAE21723.
XX
New human kinases, useful for diagnosing, treating or preventing immune
XX system disorders (e.g. Crohn's disease), neurological disorders (e.g.
XX epilepsy), or cell proliferative disorders (e.g. cancers such as
XX leukemia or lymphoma)
PS Claim 97; Page 212-213; 218pp; English.
XX
The present invention relates to human kinases (PKIN) and polynucleotides
XX encoding such proteins. PKIN sequences of the invention are useful for
XX diagnosing, treating or preventing disorders associated with aberrant
XX expression of PKIN, particularly immune system disorders (e.g. acquired
XX immune deficiency syndrome (AIDS), thymic hypoplasia, Crohn's disease,
XX anaemia, asthma), neurological disorders (e.g. epilepsy, Charcot-Marie-
XX tooth disease or seizures), cell proliferative disorders (e.g. cancers
XX such as adenocarcinoma, leukaemia, lymphoma, melanoma, sarcoma),
XX and developmental disorders (e.g. Down's syndrome). They are also used
XX in gene therapy and protein therapy. The present sequence is a cDNA
XX encoding human PKIN-18 protein.

SQ	Sequence 2647 BP; 525 A; 885 C; 789 G; 448 T; 0 other;	
	Query Match 100.0%; Score 1827; DB 24; Length 2647;	
	Best Local Similarity 100.0%; Pred. No. 0;	
	Matches 1827; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 ATGAAGTGGAGCGGAGATCGCATCTGAAGCTCTGAAGCTCAATTGAGCACCCCAAGTCTCTAAAG 60	
Db	169 ATGAAGTGGAGCGGAGATCGCATCTGAAGCTCTGAAGCTCAATTGAGCACCCCAAGTCTCTAAAG 228	
Qy	61 CTGACGAGCTTTATGAAAAAATAATTTGACCTGGTGTGCTAGAACACGTTGTCAGGT 120	
Db	229 CTGACGAGCTTTATGAAAAAATAATTTGACCTGGTGTGCTAGAACACGTTGTCAGGT 288	
Qy	121 GGTGAGCTCTTCGACTACCTGCTGAAGAGGGAGGCTGAGCCTTAAGAGGCTCGGAAG 180	
Db	289 GGTGAGCTCTTCGACTACCTGCTGAAGAGGGAGGCTGAGCCTTAAGAGGCTCGGAAG 348	
Qy	181 TTCTTCCGCGAGATCATCTCTGCGTGGACTTTGCGCACAGCACTCCATATGCCACAGG 240	
Db	349 TTCTTCCGCGAGATCATCTCTGCGTGGACTTTGCGCACAGCACTCCATATGCCACAGG 408	
Qy	241 GATCTGAACCTGAAAACTCTCTGCTGACGAGAGAAACAATCCGATCGCAGACTTT 300	
Db	409 GATCTGAACCTGAAAACTCTCTGCTGACGAGAGAAACAATCCGATCGCAGACTTT 468	
Qy	301 GGCATGGCGTCCCTGCAGGTTGGGCACAGCCTGTTGGAGACAGCTGTGGTCCGCCAC 360	
Db	469 GGCATGGCGTCCCTGCAGGTTGGGCACAGCCTGTTGGAGACAGCTGTGGTCCGCCAC 528	
Qy	361 TACGCTGCCCGAGGTGATCCGGGGGAGAGTATGACGGCCGGAAGCGGACGTGTGG 420	
Db	529 TACGCTGCCCGAGGTGATCCGGGGGAGAGTATGACGGCCGGAAGCGGACGTGTGG 588	
Qy	421 AGCTGGCGGTCACTCTGTTGCCCTTGTGCTGGGGCTCTGCCCTTCGACGATGACAA 480	
Db	589 AGCTGGCGGTCACTCTGTTGCCCTTGTGCTGGGGCTCTGCCCTTCGACGATGACAA 648	
Qy	481 TTGCGACAGCTGCTGAGAGGTGAAGCGGGCGGTGTTCCACATGCCGCACCTTTATCCG 540	
Db	649 TTGCGACAGCTGCTGAGAGGTGAAGCGGGCGGTGTTCCACATGCCGCACCTTTATCCG 708	
Qy	541 CCGACTGCCAGAGTCTGCTACGGGGCATGATCGAGGTGAGCGCCGACGCGCTCTACG 600	
Db	709 CCGACTGCCAGAGTCTGCTACGGGGCATGATCGAGGTGAGCGCCGACGCGCTCTACG 768	
Qy	601 CTAGAGCACATTCAGAAACACATATGTTATATAGGGGCGAAGATGAGCCGAAACAG 660	
Db	769 CTAGAGCACATTCAGAAACACATATGTTATATAGGGGCGAAGATGAGCCGAAACAG 828	
Qy	661 CAGCCCATTTCTCGCAAGGTGCAGATCCGCTCGCTGCCCGAGCCTGGAGGACATCGACCCC 720	
Db	829 CAGCCCATTTCTCGCAAGGTGCAGATCCGCTCGCTGCCCGAGCCTGGAGGACATCGACCCC 888	
Qy	721 GACGTGCTGGAAGCATGACATCTAGGGCTGCTTCCGAGACCGCAACAAGCTGCTGAG 780	
Db	889 GACGTGCTGGAAGCATGACATCTAGGGCTGCTTCCGAGACCGCAACAAGCTGCTGAG 948	
Qy	781 GACCTGCTGCTCGAGAGGAGAACACAGAGAGATGATTTACTTCTCTCTCTGAGCCGG 840	
Db	949 GACCTGCTGCTCGAGAGGAGAACACAGAGAGATGATTTACTTCTCTCTCTGAGCCGG 1008	
Qy	841 AAAAGAAAGTATCCGAGCGAGGATGAGGACCTGCGCCCGGAAACGAGATAGACCTT 900	
Db	1009 AAAAGAAAGTATCCGAGCGAGGATGAGGACCTGCGCCCGGAAACGAGATAGACCTT 1068	
Qy	901 CCCCAGAAAGCTGTGGACTTCCCGCATGTGTAAACCGGCACGGCAAGCGCGCGCAGAACGC 960	
Db	1069 CCCCAGAAAGCTGTGGACTTCCCGCATGTGTAAACCGGCACGGCAAGCGCGCGCAGAACGC 1128	
Qy	961 AAATCCATGGAGGTCTCAGCTGACGACGCGGCTCCCGGTGCTCTCGCGGGCGGCC 1020	
Db	1129 AAATCCATGGAGGTCTCAGCTGACGACGCGGCTCCCGGTGCTCTCGCGGGCGGCC 1188	

Qy	1021 ATTGAGATGCCCCAGCACGCGCAGAGGTCTCGTCCATCAGCGGTGCTCTCTCAGGCGCTT 1080	
Db	1189 ATTGAGATGCCCCAGCACGCGCAGAGGTCTCGTCCATCAGCGGTGCTCTCTCAGGCGCTT 1248	
Qy	1081 TCACACGACCCACTCAGCAGCCCCCGGGTGACCCCTCACCCCTCACCAAGGGGAGTCCC 1140	
Db	1249 TCACACGACCCACTCAGCAGCCCCCGGGTGACCCCTCACCCCTCACCAAGGGGAGTCCC 1308	
Qy	1141 CTCCCCACCCCAAGGGGACACCTGTCCACGCGCAAGAGAGAGCCCGGTGGGACAGCCC 1200	
Db	1309 CTCCCCACCCCAAGGGGACACCTGTCCACGCGCAAGAGAGAGCCCGGTGGGACAGCCC 1368	
Qy	1201 AACCCCAAGCCCCCGCTCCAGCCCCAGCGGTGGAGGGGTGCCCTGGAGGGCGCGCTCAAC 1260	
Db	1369 AACCCCAAGCCCCCGCTCCAGCCCCAGCGGTGGAGGGGTGCCCTGGAGGGCGCGCTCAAC 1428	
Qy	1261 TCCATCAAGAACAGCTTTTGGGCTCAACCCCGCTTCCACCGCCGGAACCTCAAGTTCCG 1320	
Db	1429 TCCATCAAGAACAGCTTTTGGGCTCAACCCCGCTTCCACCGCCGGAACCTCAAGTTCCG 1488	
Qy	1321 ACGCGGAGAGATGTCACACCTGACACCGAGTCTGCTCCCGAGAGCTGGCGAAGAGTCC 1380	
Db	1489 ACGCGGAGAGATGTCACACCTGACACCGAGTCTGCTCCCGAGAGCTGGCGAAGAGTCC 1548	
Qy	1381 TGGTTTGGGAACTTCATCAGCTCGGAGAGGAGCAGATCTTCGTGGTTCATCAAGAGAC 1440	
Db	1549 TGGTTTGGGAACTTCATCAGCTCGGAGAGGAGCAGATCTTCGTGGTTCATCAAGAGAC 1608	
Qy	1441 AAACCTCTGAGCTCCATCAAGGCTGACATCGTGACAGCCCTTCTGTGATTTCCAGTCTC 1500	
Db	1609 AAACCTCTGAGCTCCATCAAGGCTGACATCGTGACAGCCCTTCTGTGATTTCCAGTCTC 1668	
Qy	1501 AGCCACAGCTCTCTCCCAACGAGCTTCGGGCGAGTACAGGCGCACGGGGGGGCA 1560	
Db	1669 AGCCACAGCTCTCTCCCAACGAGCTTCGGGCGAGTACAGGCGCACGGGGGGGCA 1728	
Qy	1561 GCCGTGTTCCAGAGCGCGTCAAGTTCACGTTGATATCACTACACGAGGGGTGGGGAG 1620	
Db	1729 GCCGTGTTCCAGAGCGCGTCAAGTTCACGTTGATATCACTACACGAGGGGTGGGGAG 1788	
Qy	1621 GCGCAGAGAGAGACGGCATCTACTCCGTCACTTCACTCCCTGTCTCAGGCCCCAGCGGT 1680	
Db	1789 GCGCAGAGAGAGACGGCATCTACTCCGTCACTTCACTCCCTGTCTCAGGCCCCAGCGGT 1848	
Qy	1681 CGCTTCAAGAGGGTGGAGACCATCCAGSCCAGCTGCTGAGCACACAGCCCGCT 1740	
Db	1849 CGCTTCAAGAGGGTGGAGACCATCCAGSCCAGCTGCTGAGCACACAGCCCGCT 1908	
Qy	1741 GCGGCCAGACATTTGTCCAGACACCACTAATGTATGGAATGATGACGGGCGGCTTTCC 1800	
Db	1909 GCGGCCAGACATTTGTCCAGACACCACTAATGTATGGAATGATGACGGGCGGCTTTCC 1968	
Qy	1801 AATGTGGAATTTATCCGAAAAAGTTAA 1827	
Db	1969 AATGTGGAATTTATCCGAAAAAGTTAA 1995	

RESULT 4
ABX13583
ID ABX13583 standard; cDNA; 2908 BP.
XX
AC ABX13583;
XX
XX
DT 10-FEB-2003 (first entry)
XX
DE Human cDNA encoding serine protein kinase KSE336-1.
XX
KW Human; ss; gene; chromosome 11p15.5-pter; astrocytoma; meningioma;
KW pancreatic adenocarcinoma; insulin-dependent diabetes mellitus 2;
KW helioid peripapillary choriorretinal degeneration; brain; pancreas;
KW Beckwith-Wiedemann syndrome; congenital hyperinsulinism; KSE336.
XX

OS Homo sapiens.
PH Key Location/Qualifiers
FT CDS 106..2112
FT /*tag= a
FT /product= "KSE336-1"
XX
XX US6455292-B1.
XX
XX 24-SEP-2002.
XX
XX 16-AUG-2001; 2001US-0930181.
XX PF
XX 16-AUG-2001; 2001US-0930181.
XX PR
XX (ORIG-) ORIGENE TECHNOLOGIES INC.
XX PA
XX Shu Y, Fan W, Kovacs KP, Zidanic M, Jay G;
XX PI
XX WPI; 2003-066233/06.
XX DR P-PSDB; ABG72382.
XX PR
XX New isolated polynucleotide coding without interruption for a human
PT KSE336 polypeptide useful for preventing or treating
PT diseases/conditions relating to brain and pancreas, e.g. meningioma,
PT insulin-dependent diabetes mellitus 2
XX
XX Claim 3; Column 33-40; 34pp; English.
XX
XX The invention relates to an isolated polynucleotide (its complement
CC or a sequence 99% similar to it) coding without interruption for a human
CC KSE336 polypeptide, a serine protein kinase, comprising the KSE336-1 and
CC KSE336-2 splice variants appearing as ABG72382 and ABG72383. Also
CC included is a method of identifying an agent that modulates the
CC expression of KSE336 in brain, pancreas, brain progenitor or pancreas
CC progenitor cells comprising: (a) contacting a cell population comprising
CC the cells with a test agent under conditions effective for the test agent
CC to modulate the expression of KSE336; and (b) determining if the test
CC agent modulates the expression of KSE336. The polynucleotides are useful
CC as molecular targets or drug targets, and for detecting, diagnosing,
CC staging, monitoring, prognosticating, preventing or treating diseases or
CC conditions relating to brain and pancreas, such as astrocytoma,
CC meningioma, pancreatic adenocarcinoma, insulin-dependent diabetes
CC mellitus 2, heliocoid peripapillary chorioretinal degeneration, Beckwith-
CC Wiedemann syndrome or congenital hyperinsulinism. The method and
CC polynucleotides are useful in research, diagnosis, drug discovery,
CC therapy, clinical medicine, forensic science and pathology.
CC The gene for KSE336 is located on chromosome 11p15.5-pter.
CC The present sequence encodes the KSE366 variant KSE366-1.
XX
XX Sequence 2908 BP; 603 A; 948 C; 879 G; 478 T; 0 other;
SQ
Query Match 99.9%; Score 1825.4; DB 25; Length 2908;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1826; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGAAGTGGAGCGGAGATCGCGATCCTGAAGCTATTGAGCACCCCGACGTCCTAAAG 60
DB 286 ATGAGTGGAGCGGAGATCGCGATCCTGAAGCTATTGAGCACCCCGACGTCCTAAAG 345
QY 61 CTGCACGACGTTTATGAAACAAAAATATTTGACCTGTGGTGTAGAACACGTCAGGT 120
DB 346 CTGCACGACGTTTATGAAACAAAAATATTTGACCTGTGGTGTAGAACACGTCAGGT 405
QY 121 GGTGAGCTCTTCGACTACCTGTTGAAGAGGGAGGCTGACCGCTAAGGAGGCTCGGAAG 180
DB 406 GGTGAGCTCTTCGACTACCTGTTGAAGAGGGAGGCTGACCGCTAAGGAGGCTCGGAAG 465
QY 181 TTCTTCGGGAGATCATCTCTGCGCTGACCTTCGCGACAGCCACTCCATATGCCACAGG 240
DB 466 TTCTTCGGGAGATCATCTCTGCGCTGACCTTCGCGACAGCCACTCCATATGCCACAGG 525
QY 241 GATCTGAACCTGAAACCTCTCTGCTGGACGAGAAGAACACATCCGCGATCGCAGACTTT 300

DB 526 GATCTGAACCTGAAACCTCTCTGCTGGACGAGAACAACATCCGATCGCAGACTTT 585
QY 301 GGCATGGCGTCCCTGCAGGTTGGCGACAGCTGTTGGAGACAGCTGTGGTTCCTCCAC 360
DB 586 GGCATGGCGTCCCTGCAGGTTGGCGACAGCTGTTGGAGACAGCTGTGGTTCCTCCAC 645
QY 361 TACGCTCGCCCGAGGTGATCCGGGGGAGAGTATGACGGCGGAGGAGCGACGTGTGG 420
DB 646 TACGCTCGCCCGAGGTGATCCGGGGGAGAGTATGACGGCGGAGGAGCGACGTGTGG 705
QY 421 AGCTCGGCGTCATCTCTGTTGCTGTGGGGGCTCTGCTTTCGACATGACAAAC 480
DB 706 AGCTCGGCGTCATCTCTGTTGCTGTGGGGGCTCTGCTTTCGACATGACAAAC 765
QY 481 TTGCGACAGCTCTCGAGAAAGTGAAGCGGGGCTGTTCCACATGCGGACATTTATCCCG 540
DB 766 TTGCGACAGCTCTCGAGAAAGTGAAGCGGGGCTGTTCCACATGCGGACATTTATCCCG 825
QY 541 CCGGACTGCGAGGTCTGCTACGGGGCATGATCGAGGTGGAGCGCGACGCGCCTCACG 600
DB 826 CCGGACTGCGAGGTCTGCTACGGGGCATGATCGAGGTGGAGCGCGCGCCTCACG 885
QY 601 CTAGAGCATTTTCAGAAACACATATGTTATATAGGGGCAAGAAATGAGCCGAAACAGAG 660
DB 886 CTAGAGCATTTTCAGAAACACATATGTTATATAGGGGCAAGAAATGAGCCGAAACAGAG 945
QY 661 CAGCCCATCTTCGCAAGGTGAGATCGCTGCTGCCCGAGCTGGAGGACATCGACCCC 720
DB 946 CAGCCCATCTTCGCAAGGTGAGATCGCTGCTGCCCGAGCTGGAGGACATCGACCCC 1005
QY 721 GACGTGCTGGACAGATGACACTCTCTGCTGCTTCCGAGACCGCAACAGCTGTGCGAG 780
DB 1006 GACGTGCTGGACAGATGACACTCTCTGCTGCTTCCGAGACCGCAACAGCTGTGCGAG 1065
QY 781 GACCTGCTGCTGGAGGAGAACACAGAGAGATGATTTACTTCTCTCTGAGACCGG 940
DB 1066 GACCTGCTGCTGGAGGAGAACACAGAGAGATGATTTACTTCTCTCTGAGACCGG 1125
QY 841 AAAGAAAGTATCCCGAGCCAGGAGTGAAGGACCTGCCCCCGGAAACAGATAGACCTT 900
DB 1126 AAAGAAAGTATCCCGAGCCAGGAGTGAAGGACCTGCCCCCGGAAACAGATAGACCTT 1185
QY 901 CCCCCGAAACGCTGTGGACTCTCCCGATGCTGAAACCGGACGCAAGCGCGCGGCAAGCGC 960
DB 1186 CCCCCGAAACGCTGTGGACTCTCCCGATGCTGAAACCGGACGCAAGCGCGGCGCAAGCGC 1245
QY 961 AAATCATGAGGAGTGTGACGCTGACGAGCGGCTTCCCGGTGCTGCGCGCGCGGCGC 1020
DB 1246 AAGTCCATGAGGAGTGTGACGCTGACGAGCGGCTTCCCGGTGCTGCGCGCGGCGC 1305
QY 1021 ATTGAGATGGCCAGCAGCGCCAGAGGTCTCGGTCCATCAGCGGTGCTCTCAGGCTTT 1080
DB 1306 ATTGAGATGGCCAGCAGCGCCAGAGGTCTCGGTCCATCAGCGGTGCTCTCAGGCTTT 1365
QY 1081 TCCACAGCCCTCTCAGCAGACCCCGGGTGAACCTCTCACCTCTCAACAGGGGCGAGTCCC 1140
DB 1366 TCCACAGCCCTCTCAGCAGACCCCGGGTGAACCTCTCACCTCTCAACAGGGGCGAGTCCC 1425
QY 1141 CTCCTCCACCTCCCAAGGGGACACTGTGTCCACGCGCAAGAGAGGCGCGGTGCGACGCC 1200
DB 1426 CTCCTCCACCTCCCAAGGGGACACTGTGTCCACGCGCAAGAGAGGCGCGGTGCGACGCC 1485
QY 1201 AACCCCAAGCCCGCTCCAGCCCGGCGGAGGCTGCTGAGGAGGCGCGGTCTCAAC 1260
DB 1486 AACCCCAAGCCCGCTCCAGCCCGGCGGAGGCTGCTGAGGAGGCGCGGTCTCAAC 1545
QY 1261 TCCATCAAGAACAGCTTTCTGGGCTCACCCCGCTTCCACCGCGGAAACTGCAAGTTCCG 1320
DB 1546 TCCATCAAGAACAGCTTTCTGGGCTCACCCCGCTTCCACCGCGGAAACTGCAAGTTCCG 1605
QY 1321 AGCGCGAGGAGATGTCCAACTTGACACAGAGTCTGCTCCCGAGAGCTGCGGAGAGATCC 1380

Db 1606 ACGCGGAGGAGATGTCACACCTGACACAGAGTGTCTCCCGAGAGCTGGCGAAGAGTCC 1665
 QY 1381 TGGTTTGGAACTTCATCAGCTGAGAGAGAGAGAGATCTTCGTGCTCATCAAGAC 1440
 Db 1666 TGGTTTGGAACTTCATCAGCTGAGAGAGAGAGAGATCTTCGTGCTCATCAAGAC 1725
 QY 1441 AAACCTTGAGCTTCATCAGAGCTGACATGTGTGACAGCTTCCTGTGATTCAGAGTTC 1500
 Db 1726 AAACCTTGAGCTTCATCAGAGCTGACATGTGTGACAGCTTCCTGTGATTCAGAGTTC 1785
 QY 1501 AGCCACAGCTCATCTCCCAACAGAGCTTCGGGCGGAGTACAGGCCACAGGGGGGCCA 1560
 Db 1786 AGCCACAGCTCATCTCCCAACAGAGCTTCGGGCGGAGTACAGGCCACAGGGGGGCCA 1845
 QY 1561 GCGGTGTTCCAGAACCGGTCAAGTTCAGAGTTGATATCACTACACAGAGGGTGGGGAG 1620
 Db 1846 GCGGTGTTCCAGAACCGGTCAAGTTCAGAGTTGATATCACTACACAGAGGGTGGGGAG 1905
 QY 1621 GCGCAGAGAGAGAGGATCTACTCCGTACCTTCACCTGCTTCAAGGCCCGAGCGGT 1680
 Db 1906 GCGCAGAGAGAGAGGATCTACTCCGTACCTTCACCTGCTTCAAGGCCCGAGCGGT 1965
 QY 1681 CGCTTCAAGAGGGTGTGAGACCATCAGAGCCAGCTGTGAGCACACAGACCCGCT 1740
 Db 1966 CGCTTCAAGAGGGTGTGAGACCATCAGAGCCAGCTGTGAGCACACAGACCCGCT 2025
 QY 1741 GCGGCCAGCACTTGTTCAGACACCACTAACTGTATGGAATGATGACGGGGCGGCTTTC 1800
 Db 2026 GCGGCCAGCACTTGTTCAGACACCACTAACTGTATGGAATGATGACGGGGCGGCTTTC 2085
 QY 1801 AAATGTGAATATCCCGAAAGTTAA 1827
 Db 2086 AAATGTGAATATCCCGAAAGTTAA 2112

RESULT 5 ABX13584

ID ABX13584 standard; cDNA; 3364 BP.

XX AC ABX13584;

XX 10-FEB-2003 (first entry)

DE Human cDNA encoding serine protein kinase KSE336-2.

XX Human; ss; gene; chromosome 11p15.5-pter; astrocytoma; meningioma;
 KW pancreatic adenocarcinoma; insulin-dependent diabetes mellitus 2;
 KW helicoid peripapillary chorioretinal degeneration; brain; pancreas;
 KW Beckwith-Wiedemann syndrome; congenital hyperinsulinism; KSE336-2.

XX Homo sapiens.

XX Key Location/Qualifiers
 FH CDS 482..2239
 FT /*tag= a
 FT /product= "KSE336-2"

XX US6455292-B1.

XX 24-SEP-2002.

XX 16-AUG-2001; 2001US-0930181.

XX 16-AUG-2001; 2001US-0930181.

XX (ORIG-) ORIGENE TECHNOLOGIES INC.

XX Shu Y, Fan W, Kovacs KF, Zidanic M, Jay G;

XX WPI; 2003-066233/06.

XX P-PSDB; ABG72383.

XX New isolated polynucleotide coding without interruption for a human

PT KSE336 polypeptide useful for preventing or treating
 PT diseases/conditions relating to brain and pancreas, e.g. meningioma,
 PT insulin-dependent diabetes mellitus 2
 XX Claim 4; Column 43-48; 34pp; English.

CC The invention relates to an isolated polynucleotide (its complement
 CC or a sequence 9% similar to it) coding without interruption for a human
 CC KSE336 polypeptide, a serine protein kinase, comprising the KSE336-1 and
 CC KSE336-2 splice variants appearing as ABG72382 and ABG72383. Also
 CC included is a method of identifying an agent that modulates the
 CC expression of KSE336 in brain, pancreas, brain progenitor or pancreas
 CC progenitor cells comprising: (a) contacting a cell population comprising
 CC the cells with a test agent under conditions effective for the test agent
 CC to modulate the expression of KSE336; and (b) determining if the test
 CC agent modulates the expression of KSE336. The polynucleotides are useful
 CC as molecular targets or drug targets, and for detecting, diagnosing or
 CC staging, monitoring, prognosticating, preventing or treating diseases or
 CC conditions relating to brain and pancreas, such as astrocytoma,
 CC meningioma, pancreatic adenocarcinoma, insulin-dependent diabetes
 CC mellitus 2, helicoid peripapillary chorioretinal degeneration, Beckwith-
 CC Wiedemann syndrome or congenital hyperinsulinism. The method and
 CC polynucleotides are useful in research, diagnosis, drug discovery,
 CC therapy, clinical medicine, forensic science and pathology.
 CC The gene for KSE336 is located on chromosome 11p15.5-pter.
 CC The present sequence encodes the KSE336 variant KSE366-2.

XX Sequence 3364 BP; 639 A; 1078 C; 1069 G; 578 T; 0 other;

Query Match 99.2%; Score 1813; DB 25; Length 3364;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1827; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 1 ATGAAGGTGAGCGGGAGATCGCGATCCTCAAGCTCATTCAGCACCCCGCTTAAG 60
 Db 409 ATGAAGGTGAGCGGGAGATCGCGATCCTCAAGCTCATTCAGCACCCCGCTTAAG 468
 QY 61 CTGCACGACGTTTATGAAAAACAAAAATATTT---GTACCTGTGTGTAGAACACGTGTC 116
 Db 469 CTGCACGACGTTTATGAAAAACAAAAATATTTGTAGTACTGTGTGTAGAACACGTGTC 528
 QY 117 AGGTGTGAGCTCTTCGACTACCTGTGTGAAGAGGGAGGCTGACGCTAAGAGGCTCG 176
 Db 529 AGGTGTGAGCTCTTCGACTACCTGTGTGAAGAGGGAGGCTGACGCTAAGAGGCTCG 588
 QY 177 GAAGTTCTCCGCGAGATCATCTCGCTGGAGTTCTGCCACAGCCACCTCATATGCCA 236
 Db 589 GAAGTTCTCCGCGAGATCATCTCGCTGGAGTTCTGCCACAGCCACCTCATATGCCA 648
 QY 237 CAGGGATCTGAAACCTGAAACCTCTCTGTGGAGAGAAACAAACATCCGCATCGCAGA 296
 Db 649 CAGGGATCTGAAACCTGAAACCTCTCTGTGGAGAGAGAAACAAACATCCGCATCGCAGA 708
 QY 297 CTTTGGCATGGCTCCCTGAGGTTGGCGACAGCTGTGGAGACAGCTGTGGTCCCC 356
 Db 709 CTTTGGCATGGCTCCCTGAGGTTGGCGACAGCTGTGGAGACAGCTGTGGTCCCC 768
 QY 357 CCACTACGCTGCCCGGAGGTGATCCGGGGGAGAGTATGACGGCCGGAAGCGGACGT 416
 Db 769 CCACTACGCTGCCCGGAGGTGATCCGGGGGAGAGTATGACGGCCGGAAGCGGACGT 828
 QY 417 GTGAGCTGGGGGTCTCATCTCTGTGTGGTGGGGGTCTGTCCCTTCGACGATGA 476
 Db 829 GTGAGCTGGGGGTCTCATCTCTGTGTGGTGGGGGTCTGTCCCTTCGACGATGA 888
 QY 477 CAACTTGGACAGCTGTGGAGAGGTGAACCGGGGGGTGTTCCACATGCCGACTTTAT 536
 Db 889 CAACTTGGACAGCTGTGGAGAGGTGAACCGGGGGGTGTTCCACATGCCGACTTTAT 948
 QY 537 CCGGCCGAGCTGCCAGAGTCTGTACGGGGCATGATCGAGGTGAGCCGCCGCCCT 596
 Db 949 CCGGCCGAGCTGCCAGAGTCTGTACGGGGCATGATCGAGGTGAGCCGCCGCCCT 1008

QY 597 CAGCTAGACACATTCAGAAACACATATGGTATATAGGGGCAAGATGAGCCGGAACC 656
Db 1009 CAGCTAGACACATTCAGAAACACATATGGTATATAGGGGCAAGATGAGCCGGAACC 1068
QY 657 AGAGCAGCCCATTCCTCGCAAGGTGAGATCCGCTCGCTGCCAGCCTCGAGGACATCGA 716
Db 1069 AGAGCAGCCCATTCCTCGCAAGGTGAGATCCGCTCGCTGCCAGCCTCGAGGACATCGA 1128
QY 717 CCCGAGCGTGTGAGACGATGACATCACTGGGCTGTTCCGAGACCGCAACAGTGTCT 776
Db 1129 CCCGAGCGTGTGAGACGATGACATCACTGGGCTGTTCCGAGACCGCAACAGTGTCT 1188
QY 777 GCAGGACCTCTCTGCCAGAGAGAACACAGAGAGATGATTTACTTCTCTCTCTGA 836
Db 1189 GCAGGACCTCTCTGCCAGAGAGAACACAGAGAGATGATTTACTTCTCTCTCTGA 1248
QY 837 CCGGAAGAAAGTATCCCGAGCCAGGAGGATGAGACCTGCCCCCCCGGAACGAGATAGA 896
Db 1249 CCGGAAGAAAGTATCCCGAGCCAGGAGGATGAGACCTGCCCCCCCGGAACGAGATAGA 1308
QY 897 CCTCTCCCGAAGGTGTGACTCTCCCGATGCTGACCCGACGCGCAAGCGGCGCAGA 956
Db 1309 CCTCTCCCGAAGGTGTGACTCTCCCGATGCTGACCCGACGCGCAAGCGGCGCAGA 1368
QY 957 ACGCAATCCATGAGGTGCTCAGCGTGACGCGCGGCTCCCGGTGCTCGCGGGCG 1016
Db 1369 ACGCAATCCATGAGGTGCTCAGCGTGACGCGCGGCTCCCGGTGCTCGCGGGCG 1428
QY 1017 GGCCATTGAGATGCCCAGCAGCCAGAGGTCTCGGTCCATCAGCGGTGCTCTCAGG 1076
Db 1429 GGCCATTGAGATGCCCAGCAGCCAGAGGTCTCGGTCCATCAGCGGTGCTCTCAGG 1488
QY 1077 CTTTTCACGAGCCACTCAGCAGCCCGCGGTGACCCCTCACCCCTCACAGGGGCGAG 1136
Db 1489 CTTTTCACGAGCCACTCAGCAGCCCGCGGTGACCCCTCACCCCTCACAGGGGCGAG 1548
QY 1137 TCCCTCCCGAAGGTGTGACTCTCCCGATGCTGACCCGACGCGCAAGCGGCGCAGA 1196
Db 1549 TCCCTCCCGAAGGTGTGACTCTCCCGATGCTGACCCGACGCGCAAGCGGCGCAGA 1608
QY 1197 GCCCAACCCACGCCCCGCTCAGCCCCAGCGTGCAGGGGGTGCCTTGAGGGCGGGCT 1256
Db 1609 GCCCAACCCACGCCCCGCTCAGCCCCAGCGTGCAGGGGGTGCCTTGAGGGCGGGCT 1668
QY 1257 CACTCCATCAAGAACAGCTTCTGGGCTCACCCGCTCCACCGCGGAACTGCAAGT 1316
Db 1669 CACTCCATCAAGAACAGCTTCTGGGCTCACCCGCTCCACCGCGGAACTGCAAGT 1728
QY 1317 TCCGACCGGAGGAGATGTCACACCTGACACACAGAGTCTGCCCGAGCTGGCGAAGAA 1376
Db 1729 TCCGACCGGAGGAGATGTCACACCTGACACACAGAGTCTGCCCGAGCTGGCGAAGAA 1788
QY 1377 GTCTGTGTTGGAACTTCATCAGCCTGGAAGAGGAGGAGAGATCTTCGTGTGTCATCAA 1436
Db 1789 GTCTGTGTTGGAACTTCATCAGCCTGGAAGAGGAGGAGAGATCTTCGTGTGTCATCAA 1848
QY 1437 AGACAACTCTGAGCTCCATCAAGGTGACATCGTCAGCGCTTCTCTCGATTCCCGAG 1496
Db 1849 AGACAACTCTGAGCTCCATCAAGGTGACATCGTCAGCGCTTCTCTCGATTCCCGAG 1908
QY 1497 TCTCAGCCACAGCGTCTATCTCCAAACAGGCTTCCGGGCGGAGTACAGGCGCAGGGGG 1556
Db 1909 TCTCAGCCACAGCGTCTATCTCCAAACAGGCTTCCGGGCGGAGTACAGGCGCAGGGGG 1968
QY 1557 GCCAGCGTGTTCAGAAAGCGGTCAAGTTCAGGTTGATATCACTTACAGGAGGTGG 1616
Db 1969 GCCAGCGTGTTCAGAAAGCGGTCAAGTTCAGGTTGATATCACTTACAGGAGGTGG 2028
QY 1617 GGAGCGCAGAAAGGAGAACGCACTTACTCCGTCACTTCACTTCACTTCACTTCACTTCACT 1676
Db 2029 GGAGCGCAGAAAGGAGAACGCACTTACTCCGTCACTTCACTTCACTTCACTTCACTTCACT 2088
QY 1677 CCGTCCGTTCAAGAGGGTGTGGAGACCATCCAGGCCCGAGCTGTGAGCACACAGCACCC 1736

Db 2089 CCGTCCGTTCAAGAGGGTGTGGAGACCATCCAGCCAGCTGTGTGAGCACACAGCACCC 2148
QY 1737 GCCTGCGGCCAGCAGCTTGTGAGACACCACTAACTGTATGAAATGATGACGGGGCGCT 1796
Db 2149 GCCTGCGGCCAGCAGCTTGTGAGACACCACTAACTGTATGAAATGATGACGGGGCGCT 2208
QY 1797 TTCCAAATGTGAAATTATCCCGAAAGTTAA 1827
Db 2209 TTCCAAATGTGAAATTATCCCGAAAGTTAA 2239
RESULT 6
ABA02995
ID ABA02995 standard; cDNA; 2025 BP.
XX
AC ABA02995;
XX
DT 19-FEB-2002 (first entry)
XX
DE Human protein kinase 2246 coding sequence SEQ ID NO 3.
XX
KW Human; protein kinase 2246; cytostatic; immunomodulator; carcinoma;
anti-inflammatory; analgesic; cardiovascular; cancer; sarcoma;
cellular proliferation disorder; cellular differentiation disorder;
metastatic; haematopoietic disorder; leukaemia; immune disorder;
inflammatory disorder; arthritis; autoimmune disease; diabetes mellitus;
psoriasis; Crohn's disease; cardiovascular disease; virus; pain;
gene therapy; ss.
XX
OS Homo sapiens.
XX
PH Key Location/Qualifiers
FT CDS 1..2025
FT /tag= a
FT /product= "protein kinase 2246"
XX
XX WO00181588-A2.
XX
XX 01-NOV-2001.
XX
XX 25-APR-2001; 2001WO-US13784.
XX
XX 25-APR-2000; 2000US-199391P.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Meyers R;
XX
XX WPI; 2002-049281/06.
XX
XX P-PSDB; AAM47830.
XX
XX New protein kinase nucleic acid and polypeptide molecules, designated
PT 2246, useful for diagnosing, preventing or treating cancer or a
PT cellular proliferation/differentiation disorders, e.g. carcinoma,
PT sarcoma or leukaemias
XX
XX Claim 1; Fig 1; 111pp; English.
XX
XX The invention relates to the human protein kinase 2246 gene and the
CC the isolated encoded polypeptide with cytostatic, immunomodulator,
anti-inflammatory, analgesic and cardiovascular activity. The 2246
CC nucleic acid and polypeptide are useful for diagnosing, preventing or
CC treating a subject having cancer or a cellular proliferation and/or
CC differentiation disorder or at risk of developing cancer or a cellular
CC proliferation and/or differentiation disorder. In particular, the
CC disorder includes carcinoma, sarcoma, metastatic or haematopoietic
CC disorders (e.g. leukaemias) or cancers of the lung, breast, thyroid, head
CC neck, prostate or genito-urinary tract. The 2246 nucleic acid and
CC polypeptide are also useful for treating immune disorders, e.g.
CC inflammatory (e.g. respiratory inflammation or arthritis), autoimmune
disease (e.g. diabetes mellitus, psoriasis, Wegener's granulomatosis,
Crohn's disease or Grave's disease), for treating cardiovascular

CC diseases, endothelial cell disorder, viral diseases or pain. The nucleic
CC acid and polypeptide are also useful for evaluating the efficacy of a
CC treatment of cancer or a cellular proliferation and/or differentiation
CC disorder. The nucleic acid is useful for gene therapy. The present
CC sequence is that of the 2346 coding sequence.

Sequence 2025 BP; 442 A; 641 C; 616 G; 326 T; 0 other;

Query Match 96.3%; Score 1759.6; DB 24; Length 2025;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1762; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY	1	ATGAAGTGGAGCGGGAGATCGCGATCTCTGAAGCTCATTTGAGCACACCCCAAGTCTCTAAAG	60
Db	181	ATGAAGGTGGAGCGGGAGATCGCGATCTCTGAAGCTCATTTGAGCACACCCCAAGTCTCTAAAG	240
QY	61	CTGCACGACGTTTATGAACAACAAAAATATTTGTACCTGGTGTCTAGAACACGTTGTCAAGT	120
Db	241	CTGCACGACGTTTATGAACAACAAAAATATTTGTACCTGGTGTCTAGAACACGTTGTCAAGT	300
QY	121	GGTGAGCTCTTTCGACTACCTGGTGAAGAAGGGGAGGCTGACGCTTAAGAGGCTCGGAAG	180
Db	301	GGTGAGCTCTTCGACTACCTGGTGAAGAAGGGGAGGCTGACGCTTAAGAGGCTCGGAAG	360
QY	181	TTCTTTCGGCAGATCATCTCTGCGCTGACATTCTGCCACAGCCACTCCATATGCCACAGG	240
Db	361	TTCTTTCGGCAGATCATCTCTGCGCTGACATTCTGCCACAGCCACTCCATATGCCACAGG	420
QY	241	GATCTGAAACCTGAAACCTCTCTGTCGACGAGAGAAACAACATCCCGATCGCAGACTTT	300
Db	421	GATCTGAAACCTGAAACCTCTCTGTCGACGAGAGAAACAACATCCCGATCGCAGACTTT	480
QY	301	GGCATGCGCTCCCTGCGAGGTTGGCGACAGCCCTGTTGGAGACCAAGTGTGGTCCCGCCAC	360
Db	481	GGCATGCGCTCCCTGCGAGGTTGGCGACAGCCCTGTTGGAGACCAAGTGTGGTCCCGCCAC	540
QY	361	TACGCTGCCCCGAGGTGATCCGGGGGGAAGATGACGCGCGGAAGCGGACGTGTGG	420
Db	541	TACGCTGCCCCGAGGTGATCCGGGGGGAAGATGACGCGCGGAAGCGGACGTGTGTGG	600
QY	421	AGCTGGCGGCTCATCTGTTTCGCCCTTCTGCTGGTGGGGGCTCTGCCCTTCGACGATGACAAC	480
Db	601	AGCTGGCGGCTCATCTGTTTCGCCCTTCTGCTGGTGGGGGCTCTGCCCTTCGACGATGACAAC	660
QY	481	TTGCGACAGCTGCTGGAGAAAGGTGAAGCGGGGCGGTGTTCCACATGCCCGCACTTTATCCCG	540
Db	661	TTGCGACAGCTGCTGGAGAAAGGTGAAGCGGGGCGGTGTTCCACATGCCCGCACTTTATCCCG	720
QY	541	CCGCACTGCCAGAGTCTGTCTACGGGGCATGATCGAGGTGGACGCCGCAACGCCGCTCACG	600
Db	721	CCGCACTGCCAGAGTCTGTCTACGGGGCATGAGCGAGGTGGACGCCGCAACGCCGCTCACG	780
QY	601	CTAGAGCACATTGAGAAACACATATGTTATATAGGGGGGAAGATGAGCCCGGAACAGAG	660
Db	781	CTAGAGCACATTGAGAAACACATATGTTATATAGGGGGGAAGATGAGCCCGGAACAGAG	840
QY	661	CAGCCCAATTCTCGCAAGTGCAGATCCGCTCGCTGCCAGCTGGAGGACATCGACCCC	720
Db	841	CAGCCCAATTCTCGCAAGTGCAGATCCGCTCGCTGCCAGCTGGAGGACATCGACCCC	900
QY	721	GACGTGCTGGACAGCATGCACTCACTGGGCTGCTTCGGAGACGCAACAAGTGTCTGAG	780
Db	901	GACGTGCTGGACAGCATGCACTCACTGGGCTGCTTCGGAGACGCAACAAGTGTCTGAG	960
QY	781	GACCTGCTGTCCGAGGAGGAACCGAGGAGAGATGATTTACTTTCCTCTCTGAGACCGG	840
Db	961	GACCTGCTGTCCGAGGAGGAACCGAGGAGAGATGATTTACTTTCCTCTCTGAGACCGG	1020
QY	841	AAAGAAAGGTACCCGAGCCAGGAGGATGAGGACTGCTGCCCCCGCGGAACGAGATAGACCT	900
Db	1021	AAAGAAAGGTACCCGAGCCAGGAGGATGAGGACTGCTGCCCCCGCGGAACGAGATAGACCT	1080
QY	901	CCCCGGAAGGCTGTGGACTCCCCCGATGCTGAAACCGGCAACGGCAAGCGCGCGCAGAACGC	960

KW metastatic; haematopoietic disorder; leukaemia; immune disorder;
KW inflammatory disorder; arthritis; autoimmune disease; diabetes mellitus;
KW psoriasis; Crohn's disease; cardiovascular disease; virus; pain;
XX gene therapy; ss.
XX Homo sapiens.
XX OS
XX FH Location/Qualifiers
XX CDS 51..2075
XX FT /*tag= a
XX FT /product= "protein kinase 2246"
XX PN WO200181588-A2.
XX OS
XX PD 01-NOV-2001.
XX XX
XX PF 25-APR-2001; 2001WO-US13784.
XX XX
XX PF 25-APR-2000; 2000US-199391P.
XX PR (MILL-) MILLENNIUM PHARM INC.
XX PA
XX PI Meyers R;
XX DR WPI; 2002-049281/06.
XX DR P-PSDB; AAM47830.
XX XX
XX PT New protein kinase nucleic acid and polypeptide molecules, designated
XX FT 2246, useful for diagnosing, preventing or treating cancer or a
XX FT cellular proliferation/differentiation disorders, e.g. carcinoma,
XX PT sarcoma or leukaemias
XX XX
XX PS Claim 1; Fig 1; 11pp; English.
XX CC
XX CC The invention relates to the human protein kinase 2246 gene and the
XX CC the isolated encoded polypeptide with cytosolic, immunomodulator,
XX CC anti-inflammatory, analgesic and cardiovascular activity. The 2246
XX CC nucleic acid and polypeptide are useful for diagnosing, preventing or
XX CC treating a subject having cancer or a cellular proliferation and/or
XX CC differentiation disorder or at risk of developing cancer or a cellular
XX CC proliferation and/or differentiation disorder. In particular, the
XX CC disorder includes carcinoma, sarcoma, metastatic or haematopoietic
XX CC disorders (e.g. leukaemias) or cancers of the lung, breast, thyroid, head
XX CC neck, prostate or genito-urinary tract. The 2246 nucleic acid and
XX CC polypeptide are also useful for treating immune disorders, e.g.
XX CC inflammatory (e.g. respiratory inflammation or arthritis), autoimmune
XX CC disease (e.g. diabetes mellitus, psoriasis, Wegener's granulomatosis,
XX CC Crohn's disease or Grave's disease), for treating cardiovascular
XX CC diseases, endothelial cell disorder, viral diseases or pain. The nucleic
XX CC acid and polypeptide are also useful for evaluating the efficacy of a
XX CC treatment of cancer or a cellular proliferation and/or differentiation
XX CC disorder. The nucleic acid is useful for gene therapy. The present
XX CC sequence is that of the 2246 encoding cDNA.
XX SQ
SQ Sequence 2217 BP; 476 A; 715 C; 682 G; 344 T; 0 other;
Query Match 96.3%; Score 1759.6; DB 24; Length 2217;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1762; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 ATGAAGGTGGAGCGGAGATCGGATCTGAAGCTCATTTAGACACCCCGCTCTAAAG 60
Db 231 ATGAAGGTGGAGCGGAGATCGGATCTGAAGCTCATTTAGACACCCCGCTCTAAAG 290
Qy 61 CTGACAGACGTTTATGAACAAAAATATTTGCTGTGTAGAACACGTTGTCAGGT 120
Db 291 CTGACAGACGTTTATGAACAAAAATATTTGCTGTGTAGAACACGTTGTCAGGT 350
Qy 121 GGTGAGCTCTTCGACTACTCTGCTGAAGAGGGAGGCTGACGCCCTAAGGAGGCTCGGAAG 180
Db 351 GGTGAGCTCTTCGACTACTCTGCTGAAGAGGGAGGCTGACGCCCTAAGGAGGCTCGGAAG 410
Qy 181 TTCTTCGGGCAGATCATCTCTGCGCTGAGACTTGTGCCACAGCCACTCCATATGCCACAGG 240

Db 411 TTCTTCGGGCAGATCATCTCTGCGCTGAGACTTGTGCCACAGCCACTCCATATGCCACAGG 470
Qy 241 GATCTGAACCTGAAACCTCTCTGTGGACGAGAGAAACAATCCGATCCGACGACATTT 300
Db 471 GATCTGAACCTGAAACCTCTCTGTGGACGAGAGAAACAATCCGATCCGACGACATTT 530
Qy 301 GGCATGGGCTCCCTGCAGGTTGGCCGACAGCCTGTTGGAGACAGCTGTGGGTCCCCAC 360
Db 531 GGCATGGGCTCCCTGCAGGTTGGCCGACAGCCTGTTGGAGACAGCTGTGGGTCCCCAC 590
Qy 361 TAGCGCTGCCCGAGGTGATCCGGGGGAGAAAGTATGACGGCGGAAAGCGGACGTTGG 420
Db 591 TAGCGCTGCCCGAGGTGATCCGGGGGAGAAAGTATGACGGCGGAAAGCGGACGTTGG 650
Qy 421 AGCTGGGGCTCATCTCTGTTGCTGTGGGGGCTTGCCTTCGACATGACAAAC 480
Db 651 AGCTGGGGCTCATCTCTGTTGCTGTGGGGGCTTGCCTTCGACATGACAAAC 710
Qy 481 TTGCGACAGCTCTGGAGAGGTGAAGCGGGCGCTGTTCCACATGCGGACATTTATCCG 540
Db 711 TTGCGACAGCTCTGGAGAGGTGAAGCGGGCGCTGTTCCACATGCGGACATTTATCCG 770
Qy 541 CCGCACTGCCAGATCTGCTACGGGCGATGATCGAGGTGGACCGCGCCTCAGC 600
Db 771 CCGCACTGCCAGATCTGCTACGGGCGATGATGAGGTGGACCGCGCCTCAGC 830
Qy 601 CTAGAGCATTCTAGAAACACATATGTTATAGGGGGGAGAAAGTGGAGCCGAGACAGAG 560
Db 831 CTAGAGCATTCTAGAAACACATATGTTATAGGGGGGAGAAAGTGGAGCCGAGACAGAG 890
Qy 661 CAGCCCTCTCTCGCAAGGTGAGATCGCTCGCTGCGCCAGCTGGAGGACATCGACCC 720
Db 891 CAGCCCTCTCTCGCAAGGTGAGATCGCTCGCTGCGCCAGCTGGAGGACATCGACCC 950
Qy 721 GAGCTGCTGGACAGCATGCACTCACTGGGCTGCTTCCGAGACCGCAACAGCTGTGAG 780
Db 951 GAGCTGCTGGACAGCATGCACTCACTGGGCTGCTTCCGAGACCGCAACAGCTGTGAG 1010
Qy 781 GAGCTGCTGCTCGAGGAGGAGAACACAGGAGATGATTTACTTCTCTCTCGACCGG 840
Db 1011 GAGCTGCTGCTCGAGGAGGAGAACACAGGAGATGATTTACTTCTCTCTCGACCGG 1070
Qy 841 AAAGAAAGTACCCGAGCCAGGAGATGAGGACCTGCCCCCGGAAACAGATAGACCT 900
Db 1071 AAAGAAAGTACCCGAGCCAGGAGATGAGGACCTGCCCCCGGAAACAGATAGACCT 1130
Qy 901 CCGCGAAGCGTGTGGAATCCCGATGCTGAACCGGACGCGCAAGCGGCGGCGGAGACGC 960
Db 1131 CCGCGAAGCGTGTGGAATCCCGATGCTGAACCGGACGCGCAAGCGGCGGCGGAGACGC 1190
Qy 961 AAATCCATGGAGGTCTCAGCGTGACGAGCGGGGCTCCCGGCTGCTGCGGGCGGGCC 1020
Db 1191 AAATCCATGGAGGTCTCAGCGTGACGAGCGGGGCTCCCGGCTGCTGCGGGCGGGCC 1250
Qy 1021 ATTGAGATGGCCAGCAGCGCCAGAGGTCTCGGTCCATCAGCGGTGCTCTCAGGCGCTT 1080
Db 1251 ATTGAGATGGCCAGCAGCGCCAGAGGTCTCGGTCCATCAGCGGTGCTCTCAGGCGCTT 1310
Qy 1081 TCCACAGCCCACTCAGCAGCCCGGGGTGACCCCTCACCCCTCAACAAAGGGGAGTCCC 1140
Db 1311 TCCACAGCCCACTCAGCAGCCCGGGGTGACCCCTCACCCCTCAACAAAGGGGAGTCCC 1370
Qy 1141 CTCGCCACCCCAAGGGGACACTGTCACACCGCCAAAGAGAGCCCGGCTGGACGCC 1200
Db 1371 CTCGCCACCCCAAGGGGACACTGTCACACCGCCAAAGAGAGCCCGGCTGGACGCC 1430
Qy 1201 AACCCCAACCCCGCTCCAGCCCGGAGGCTCGGAGGGGCTCCCTGGAGGGCGGGCTCAAC 1260
Db 1431 AACCCCAACCCCGCTCCAGCCCGGAGGCTCGGAGGGGCTCCCTGGAGGGCGGGCTCAAC 1490
Qy 1261 TCATCAAGAAACAGCTTTCTGGGCTCACCCCGCTTCCACCGCGGAAACTGCAAGTTCCG 1320

Db 1491 TCCATCAAGAACAGCTTTCGTGGGTCAACCCCGCTTCCACCCCGGAAACTCAAGTCCG 1550
 QY 1321 AGCGGAGGAGATGCCAACTGACACACAGAGTCGTCCCCAGAGCTGGCGAAGAGTCC 1380
 Db 1551 AGCGGAGGAGATGTCCTCAACTGACACACAGAGTCGTCCCCAGAGCTGGCGAAGAGTCC 1610
 QY 1381 TGGTTTGGAACTTCATCAGCTGGAGAGGAGAGAGATCTTCGTGGTCAATCAAGAC 1440
 Db 1611 TGGTTTGGAACTTCATCAGCTGGAGAGGAGAGAGATCTTCGTGGTCAATCAAGAC 1670
 QY 1441 AAACCTCTGAGCTCCATCAAGCGTGACATCGTCACGCGCTTCCTGTGATTCGCCAGTCTC 1500
 Db 1671 AAACCTCTGAGCTCCATCAAGCGTGACATCGTCACGCGCTTCCTGTGATTCGCCAGTCTC 1730
 QY 1501 AGCCACAGCGTCATCTCCCAACAGAGCTTCGCGGCCGAGTACAAGGCCACCGGGGGGCCA 1560
 Db 1731 AGCCACAGCGTCATCTCCCAACAGAGCTTCGCGGCCGAGTACAAGGCCACCGGGGGGCCA 1790
 QY 1561 GCCGTGTTCCAGAGCCCGTCAAGTTCAGGTTGATATCACTTACACGAGGGTGGGGAG 1620
 Db 1791 GCCGTGTTCCAGAGCCCGTCAAGTTCAGGTTGATATCACTTACACGAGGGTGGGGAG 1850
 QY 1621 GCGCAGAAGGAGAACGGCATCTACTCCGTCACTTCCCTGCTCTCAGGCCCCAGCGGT 1680
 Db 1851 GCGCAGAAGGAGAACGGCATCTACTCCGTCACTTCCCTGCTCTCAGGCCCCAGCGGT 1910
 QY 1681 CGCTTCAAGAGGGTGGAGACCATCAAGGCCAGCTGCTGAGCACAACAGCCCGCT 1740
 Db 1911 CGCTTCAAGAGGGTGGAGACCATCAAGGCCAGCTGCTGAGCACAACAGCCCGCT 1970
 QY 1741 GCGGCCAGAGCTTGTGAGACACAC 1766
 Db 1971 GCGGCCAGAGCTTGTGAGAACCCCC 1996

RESULT 8

AAL51889

ID AAL51889 standard; DNA; 2799 BP.

XX AC AAL51889;

XX DT 08-MAY-2003 (first entry)

XX XX Human cell cycle-regulatory factor Cdr2 coding sequence.

DE Human; cell cycle-regulatory factor; Cdr2; kinase; proliferative disease;

XX Human; cell cycle-regulatory factor; Cdr2; kinase; proliferative disease;

XX anticancer agent; wound-healing drug; gene; ds.

XX OS Homo sapiens.

XX Key Location/Qualifiers

FH 50..2314

FT CDS /tag= a

FT /product= "Human Cdr2 protein"

XX WO200299110-A1.

XX 12-DEC-2002.

XX 03-JUN-2002; 2002WO-JP05411.

XX 04-JUN-2001; 2001JP-0168792.

XX (TAIH) TAIHO PHARM CO LTD.

XX (NAKA/) NAKANISHI M.

XX Nakanishi M;

XX WPI; 2003-156857/15.

XX P-PSDB; AA016604.

XX Cell cycle-regulatory factor Cdr2 with kinase activity and encoded

XX Gene, applicable in diagnosis of and screening drugs for proliferative

PT

PT diseases e.g. anticancer agents and wound-healing drugs -

XX Claim 2; Fig 2 A-C; 63pp; Japanese.

XX The invention comprises the amino acid and coding sequence of the human

CC cell cycle-regulatory factor Cdr2 (with kinase activity). The DNA and

CC protein sequences of the invention are useful in diagnosing and screening

CC drugs for proliferative diseases (e.g. anticancer agents and wound-

CC healing drugs). The present DNA sequence encodes the human cell cycle-

CC regulatory factor Cdr2 protein.

XX Sequence 2799 BP; 570 A; 908 C; 831 G; 490 T; 0 other;

SQ

Query Match 49.5%; Score 904.2; DB 25; Length 2799;

Best Local Similarity 70.9%; Pred. No. 4.6e-188;

Matches 1344; Conservative 0; Mismatches 428; Indels 123; Gaps 6;

QY 1 ATGAAGTGGAGCGGAGATCGCGATCTCTGAAGCTCATGAGCACCCCGCTCTAAAG 60

Db 275 ATGAAGTGGAGCGGAGATCGCGATCTCTGAAGCTCATGAGCACCCCGCTCTCAAG 334

QY 61 CTCACGACGCTTTATGAACAAACAAATATTTCTACCTGGTCTAGAACAGTCTCAGGT 120

Db 335 CTCACGACGCTTTATGAACAAACAAATATTTCTACCTGGTCTAGAACAGTCTCAGGT 394

QY 121 GGTGAGCTTTTCGACTACCTGCTGAGAGGGAGGCTGACGCTTAAGGAGGCTTCGGAAG 180

Db 395 GGTGAGCTTTTCGACTACCTGCTGAGAGGGAGGCTGACGCTTAAGGAGGCTTCGGAAG 454

QY 181 TTCTTCGGCAGATCATCTCTGCGTGGATCTTGCACAGCCATCTCATATGCGCAGG 240

Db 455 TTCTTCGGCAGATCATCTCTGCGTGGATCTTGCACAGCCATCTCATATGCGCAGG 514

QY 241 GATCTGAACCTGAAACCTCTGCTGAGAGAGAGAACCAACATCCGATCGCAGACTTT 300

Db 515 GATCTGAACCTGAAACCTCTGCTGAGAGAGAGAACCAACATCCGATCGCAGACTTT 574

QY 301 GGCATGGCGTCCCTGCGAGTGGCGAGCTGTGGAGACCAAGCTGTGGGTCCCCCAG 360

Db 575 GGCATGGCGTCCCTGCGAGTGGCGAGCTGTGGAGACCAAGCTGTGGGTCCCCCAG 634

QY 361 TAGCCTGCGCGAGTGTATCGCGGGGAGAGATGATGACCGCGGAGAGCGAGCTGTGG 420

Db 635 TAGCCTGCGCGAGTGTATGAGGGGGAGAGATGATGATGCGCGCGGAGAGCATGTGG 694

QY 421 AGCTGCGCGTCTATCTCTGCTGCTGCTGGGGCTCTGCGCTTCGACGATGACAC 480

Db 695 AGCTGCGCGTCTATCTCTGCTGCTGCTGGGGCTCTGCGCTTCGACGATGACAC 754

QY 481 TTGCGACAGCTGTGGAGAGAGTGAAGCGGGGGCTGTTCACATGCGCGACTTTATCCCG 540

Db 755 TTGCGACAGCTGTGGAGAGAGTGAAGCGGGGGCTGTTCACATGCGCGACTTTATCCCT 814

QY 541 CCGAGTCCGAGAGTGTCTACCGGGGATGATGAGGTGACCGCGGAGAGCGCGCTCAGG 600

Db 815 CCGAGTCCGAGAGTGTCTACCGGGGATGATGAGGTGACCGCGGAGAGCGCGCTCAGG 874

QY 601 CTAGAGCACATTCAGAAACACATATGATATAGGGGGGAGAGATGAGCGCGAGCC--- 656

Db 875 CTAGAGCACATTCAGAAACACATATGATATAGGGGGGAGAGATGAGCGCGAGCC--- 934

QY 657 --AGAGCAGCCCATTCCTCGCAAGGTGACATCGCTCGCTGCGCGAGCGAGGAGCATC 714

Db 935 CTGAGCGCAGCCCTGCGCGCGGGTAGCCATCGGAGCGCTGCCATCAACGAGAGAGCTG 994

QY 715 GACCCGAGCTGTGGAGACATGCTACTCTGGCTGCTTCGAGAGCCGCAACAGCTG 774

Db 995 GACCCGAGCTGTGGAGACATGCTACTCTGGCTGCTTCGAGAGCCGCAACAGCTG 1054

QY 775 CTGAGGACCTGCTGCTCGAGAGGAGAGAACACGAGAGAGATGATTTACTTCTCTCTG 834

Db 1055 CATGCGGAGCTGCGCAGTGGAGGAGAGAACCAAGAAAGATGATATATATCTGCTTTG 1114

PT New human kinase proteins useful for diagnosis, drug screening, and
PT clinical trial monitoring, treatment of disorders and diseases, and
XX cosmetic and nutritional applications -

PS Claim 5; Page 39; 47pp; English.

XX The present sequence is the coding sequence for a novel human kinase. The
CC genomic locus encoding the kinase is thought to be on human chromosome
CC 19. The kinase and its coding sequence are useful for diagnosis, drug
CC screening, clinical trial monitoring, treatment of disorders and
CC diseases, and cosmetic and nutritional applications.

XX SQ Sequence 2337 BP; 479 A; 786 C; 686 G; 386 T; 0 other;

Query Match 46.6%; Score 851.4; DB 25; Length 2337;
Best Local Similarity 68.9%; Pred. No. 1.6e-176;
Matches 1356; Conservative 0; Mismatches 416; Indels 195; Gaps 6;

QY	1	ATGAAGTGGAGCGGAGATCGCGATCCTGAAGCTCATTGAGCACCCCAACGTCCTTAAAG	60
DB	226	ATGAGGTGGAGCGGAGATCGCGATCCTGAAGCTCATTGAGCACCCCAACGTCCTTAAAG	285
QY	61	CTGCAGACCTTTATGAAACAAATAATTTGTACTGGTGTAGAACACGTCAGGT	120
DB	286	CTCCAGACCTTACGAGAACAAATAATTTGTACTGGTGTAGAACACGTCAGGT	345
QY	121	GGTGAGCTCTTCGACTACCTGTTGAGAGGGAGGCTGAGCGCTAAGGAGCTCGGAG	180
DB	346	GGTGAGCTATTTCGACTACCTGTTGAGAGGGAGGCTGAGCGCTAAGGAGGCTCGGAG	405
QY	181	TTCTTCCGCGAGATCATCTCTGGCTGGAATTTGTCACAGGCACTTCCATATGCCACAGG	240
DB	406	TTCTTCCGCGAGATTTGTTCTGGCTGGAATTTGTCACAGGCTTCCATATGCCACAGG	465
QY	241	GATCTGAAACCTGAAACCTCTCTGCTGGAAGAGAAACAAATTCGCTATCGAGACTTT	300
DB	466	GACCTAAAGCCGAGAACCTCTCTTGGATGAGAAACAAATTCGCTATCGAGACTTC	525
QY	301	GGCATGCGCTCCCTGAGGTTGGGACAGCTGTTGGAGACCAAGCTGTGGTCCCCCAG	360
DB	526	GGCATGCGCTCCCTGAGGTTGGGAGACAGCTTCTGGAGACCAAGCTGTGGTCCCCCAG	585
QY	361	TACGCTCCGCGAGGTGATCCGCGGAGAGATGATGACGCGCGAGGCGGAGCTGTGG	420
DB	586	TATGCGTGTCCAGAGGTGATTAAGGGGAAATATGATGCGCGCGGAGAGATGTGG	645
QY	421	AGTGTGGGCTCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	480
DB	646	AGTGTGGGCTCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	705
QY	481	TTGCGAGAGCTGTGGAGAGGTGAAAGCGGGGCTGTTCCACATGCGGCACTTTATCCCG	540
DB	706	CTCGCGAGCTGTGGAGAGGTGAAAGCGGGGCTGTTCCACATGCGGCACTTTATCCCT	765
QY	541	CCCGACTGCCAGAGCTGTGCTACGCGGCGATGATGAGGTGAGCGCGCACGCGCTCACG	600
DB	766	CCAGATTGCCAGAGCTCTCTGAGGCGAATGATCGAAGTGGAGCGCGGAGGCTCAGT	825
QY	601	CTAGAGACATTTAGAAACACATATGTTATATAGGGGGGAGAAATGAGCCCGGAAAC	656
DB	826	CTGAGGCAATTTAGAAACACATTTGTTATCTAGGCGGAGAAACACAGAGCCAGCCGTCG	885
QY	657	--AGAGAGCCCATCTCTCGAAGGTGAGATCGCTGCTGCTGCTGCTGCTGCTGCTGCTG	714
DB	886	CTGAGGCGAGCCCTTGGCGCGGGGTAGCCATGCGGAGCTTGCCATCCAAAGGAGAGCTG	945
QY	715	GACCCGAGCTGTGGAGAGATGACCTCATCTGGGCTGCTTCCGAGACCGCAACAGCTG	774
DB	946	GACCCGAGCTGTGGAGAGATGACCTCATCTGGGCTGCTTCCGAGACCGGAGGCTG	1005
QY	775	CTGAGGAGCTGTGCTGCTGAGAGAGAGAACACAGAGAGATGATTACTTCTCTCTCTG	834
DB	1006	CATCGAGCTGCGAGTGAGAGAGAGAACCAAGAAAGATGATATATATCTGCTTTTG	1065

QY	835	GACCGAAGAAAGTATCCGAGCCAGGAGATGAGGACCTGCCCCCGGAAACGAGATA	894
DB	1066	GATCGAAGAGGCGGTATCCAGGCTGTGAGGACCGGACCTGCCCCCGGAAATGATTT	1125
QY	895	GACCTCTCCCGGAAAGCGTGTGGACTCCCCGATGTCTGAAACCGGACGCGAAGCGGCGCA	954
DB	1126	GACCTCTCCCGGAAAGCGTGTGGATTCTCCATGTGTAGCGCTACGGAAGCGGCGCA	1185
QY	955	GACGCAATCATGAGAGTGTCTAGCGTGAAGG-----CGGCGGTCTCCCGGTG	1005
DB	1186	GAGCGAAGTCCATGGAAGTCTTGAGCATACCGATGCCGGGGTGTGGTCCCTCTGA	1245
QY	1006	CTGCGCGCGCGGCATTGAGATGCGCCAGCACGAGAGTCTCGGTCTCATCAGCGGT	1065
DB	1246	CCACCCAGCGGCTTGGAGATGGCCAGCACAGAGATCCCGTAGGCTCAGTGA	1305
QY	1066	GCCTCTCAGGCTTTCCACAGGCCACTCAGAGCCCGG-----	1108
DB	1306	GCCTCCACGGGTCTGTCTCTCAGGCCCTTAAGCAGCCCAAGAGTCCGCTCTTTTCTTT	1365
QY	1109	-----	1108
DB	1366	TCACCGGAGCGGGGCTGAGATGAGGCTCGAGCGGGGCTCCCCGACTTCCAAAG	1425
QY	1109	-----TGACCCCTCACCCT	1122
DB	1426	CAGACGCTGCTTCTCGGGGCCCCAGGGGTGGGGCGCGGGGAGCAGCCCCCGCCCC	1485
QY	1123	TCACCAAGGGGCGTCCCTCCCTC-----ACC	1149
DB	1486	AGTGGCGCTCCACACCCCTGCGCGGCCCCAGGCTCCCGCGCTCTCTGGCGGAGC	1545
QY	1150	CCCAAGGGGACCTGTCCACAGCCAAAGGAGAGCGCGGTGGCAGCCCAACCCACG	1209
DB	1546	CCCTTGCATCGCTCTGACACAGCCCGCGGCGAGTCCACCGGAGCCCGGGGCAACA	1605
QY	1210	CCCCGCTCAGGCCCC-----AGCGTCCGAGGGGTGCGCTGAGGGCGCGGTCAACTCC	1263
DB	1606	CAACCCCGCGCGCGGTGGCTCGGGGAGCGCGCTGGAGGAGTCTCTCACTCC	1665
QY	1264	ATCAAGAACAGTCTTCTGGGCTCAACCGCTTCCACCGCGGAAACTGCAAGTTCGAGG	1323
DB	1666	ATCCGCAACAGCTTCTGGGCTCCCTCGCTTTCACCGCGCAAGATGAGTCTCTTACC	1725
QY	1324	CGGAGGAGATGTCCTGACACAGAGTCTCCCGAGAGCTGCGGAGAGTCTCTCG	1383
DB	1726	GCTGAGGAGATGTCAGCTTGGAGCGCAGAGTCTCCCGGAGCTGGCAACGCTCTCTGG	1785
QY	1384	TTTGGGAACTTCATCAGCTCGAGAGGAGGAGAGATCTTCTGTTGTCATCAAGACAA	1443
DB	1786	TTGCGGAACTTCATCTCTTGGACAAAGAGAAATATCTCTGCTGTAAGGACAA	1845
QY	1444	CTCTGAGCTCATCAAGGCTGACATCGGTGACGCTTCTCTGATTTCCCACTCTCAGC	1503
DB	1846	CTCTCAGCAGCATCAAGCAGACATCGTCTTCTGATGCTTCTGATGCTTCTGATGCT	1905
QY	1504	CACAGCTCATCTCCCAACAGAGTTCGCGGCGGAGTACAAGSCCAGCGGGGCGGCGCC	1563
DB	1906	CACAGTGTCTGTACAGACAGCTTTCAGGCGGAGTACAAGGCGGAGTGGCGGCGCTCC	1965
QY	1564	GTGTTCCAGAACCGGTCAAGTTCCAGGTTGATATACCTTACACGAGGGT-----	1614
DB	1966	GTCTTCCAAAGGCGGTCTCGCTTCCAGGTGGACATCAGCTCTCTGAGGCTCCAGAGCC	2025
QY	1615	-----GGGAGGCGCAGAGGAGAACCGGATCTACTCCGTCACTTCCCTGCTC	1665
DB	2026	TCCCCCGGAGCGGAGGAGTGGTGGTCACTTCTCTGCTCACTTCTCTCTCTCATC	2085
QY	1666	TCAGGCGCCAGCGCTCTTCAAGGGGTGGTGGAGACCATCCAGGCCAGCTGTGTGAGC	1725
DB	2086	TCGGGTCCAGCGCTCGGTTCAAGCGAGTGGTGGAGACCATCCAGGACAGCTCTCTGAGC	2145

Db 1414 TCACCGAGCGGGGCTGGAGATGAGGCTCGAGGCGGGGGCTCCCGAGCTTCCAAAACG 1473
QY 1109 -----TGACCCCTCACCCC 1122
Db 1474 CAGACGCTGCTTCTCGGGGCCCCAGGGGTGGGGGCGCGGGAGCAGCCCCCGCCCCC 1533
QY 1123 TCACCAAGGGGAGTCCCTTCCCC-----ACC 1149
Db 1534 AGTCCCGCTCCACACCCCTGCGCGCCCCCAGGCTCCCGGGCTCTCTGGGGGACC 1593
QY 1150 CCAAGGGGACACTCTTCACACCGCCAAAGGAGAGCCCGGCTGGACGCCCAACCCACG 1209
Db 1594 CCTTGCACCTGCTCTGACACCGCCCGGGCCAGTCCACCGGGACCCCGGGGCAACA 1653
QY 1210 CCCCCCTCAGCCCC-----ACGCTCGAGGGGTGCTTGGAGGGCGGGCTCACTCC 1263
Db 1654 CCACCCCCCAGCCCGCGGTGCGGGGAGCCGCTTGGAGGAGTGGTCTCACTCC 1713
QY 1264 ATCAAGAAACAGCTTCTGGGCTCACCCCGCTTCCACCGCGGAAACTGCAAGTTCCGAGC 1323
Db 1714 ATCGGAACTTCTCTGGGCTCCCTCGCTTTTTCACCGGGGCAAGATGAGTCCCTACC 1773
QY 1324 CCGAGGAGATGTCACACTGACACAGAGTCTGTCACAGAGTCTGCGGAGTGGCGAAGTCTCTGG 1383
Db 1774 GCTGAGGAGATGTCAGTCTGACCGCAGAGTCTTCCCGGAGCTGGCAAAACGCTCTCTGG 1833
QY 1384 TTGGGAACTTCATCAGCTTGGAGAGGAGGAGCAGATCTTCTGTGTCATCAAGACAA 1443
Db 1834 TTGGGAACTTCTCTTGGGCAAGAGAAACAAATATCTCTGTCTGTTAAAGGACAA 1893
QY 1444 CCTCTGAGCTCCATCAAGGCTGACATCGTCAGCGCTTCTGTCGATTTCCAGTCTTCAGC 1503
Db 1894 CCTCTCAGCAGATCAAGCAGACATGCTCCATGCTTCTGTGATCCCGCCTGAGT 1953
QY 1504 CACAGGTATCTCCCAACAGAGCTTCCGGGCGAGTACAAAGCCACGGGGGGCCAGCC 1563
Db 1954 CACAGTGTGTGTACAGACAGCTTCCAGGCGGAGTACAAAGCCAGTGGCGGCCCTCC 2013
QY 1564 GTCTTCCAGAGCGGTTCAGTTCAGTTGATATCACTTACACGAGGGT----- 1614
Db 2014 GTCTTCCAAAGCCGCTCCGCTTCCAGTGGATCAGCTCTCTGAGGGTCCAGAGCCC 2073
QY 1615 -----GGGAGGCGCAGAGAGAGAGCGCATCTTCTCCGTCACCTTCCACCTGCTC 1665
Db 2074 TCCCGGAGCGGAGCGCAGCGAGGTGGTGCATCTACTCCGTCACCTTCACTCTCATC 2133
QY 1666 TCAGGCCCCCGCTGCTTCAAGAGGGTGGTGGAGACCATTCAGGCCCCAGTGTGAGC 1725
Db 2134 TCGGGTCCCGCTCGGTTCAGCGAGTGGTGGAGACCATTCAGGCGACAGCTCTGAGC 2193
QY 1726 ACACACGACCGCTGCGGCCCGACCTTGTGACACACCACTAACTG 1772
Db 2194 ACTCATCAGCAGCCCTCCGTGACGCCCCCTGGCAGAGAGAACCG 2240

RESULT 12
AAD26464
ID AAD26464 standard; cDNA; 2897 BP.
XX AC AAD26464;
XX AC AAD26464;
DT 26-MAR-2002 (first entry)
XX Human kinase PKIN-17 cDNA.
XX Human; kinase; PKIN-17; cancer; leukaemia; adenocarcinoma; osteoporosis;
KW immune disorder; atherosclerosis; Crohn's disease; Hodgkin's disease;
KW Acquired Immune Deficiency Syndrome; AIDS; Addison's disease; anaemia;
KW allergy; asthma; adult respiratory distress syndrome; multiple sclerosis;
KW autoimmune thyroiditis; bronchitis; diabetes mellitus; osteoarthritis;
KW Good pasture's syndrome; Graves' disease; pancreatitis; psoriasis;
KW rheumatoid arthritis; ulcerative colitis; cirrhosis; Cushing's syndrome;
KW hepatitis; hypothyroidism; cerebral palsy; cataract; angina pectoris;

KW cardiovascular disease; hypertension; vasculitis; myocarditis; obesity;
KW congestive heart failure; ischaemic heart disease; lung tumour; gout;
XX fatty liver; Niemann-Pick's disease; gene therapy; ss.
OS Homo sapiens.
XX Key Location/Qualifiers
CDS 1..2385
FT /*tag= a
FT /product= "Human PKIN-17 protein"
XX WO200196547-A2.
XX 20-DEC-2001.
XX 14-JUN-2001; 2001WO-US19444.
XX 15-JUN-2000; 2000US-212073P.
PR 23-JUN-2000; 2000US-213467P.
PR 30-JUN-2000; 2000US-215651P.
PR 07-JUL-2000; 2000US-216605P.
PR 13-JUL-2000; 2000US-218372P.
PR 25-AUG-2000; 2000US-228056P.
XX (INCY-) INCYTE GENOMICS INC.
XX Yue H, Lal P, Bandman O, Borowsky ML, Au-Young J, Lu Y;
PI Gandhi AR, Tribouley CM, Walla NK, Yao MG, Lu DAM, Greenwald SR;
PI Ramkumar J, Griffin JA, Kearney L, Burford N, Nguyen DB, Tang YT;
PI Baughman MR, He A, Thornton M, Hafalia A, Patterson C, Gururajan R;
PI Lo TP, Khan F, Recipon SA, Azimzai Y, Policky JL, Ding L;
PI Grether M, Elliott VS, Thangavelu K, Batra S, Ison CH;
DR WPI: 2002-090207/12.
DR P-PSDB; AAE16271.
XX New polypeptides, useful for diagnosing, treating or preventing
PT disorders of growth and development, cardiovascular and lipid, and
PT diseases such as cancer, comprise human kinase polypeptides -
XX Claim 5; Page 188-189; 197pp; English.
XX The invention relates to human kinase PKIN proteins and their
CC corresponding cDNAs. A composition containing PKIN agonist is useful for
CC treating a disease or condition associated with decreased expression of
CC PKIN and a composition comprising PKIN antagonist is useful for treating
CC a disease or condition associated with overexpression of PKIN. The
CC disorders include cancer (leukaemia, adenocarcinoma, lymphoma, melanoma,
CC myeloma, sarcoma, teratocarcinoma, Hodgkin's disease); asthma, Addison's disease,
CC (Acquired Immune Deficiency Syndrome (AIDS), asthma, Addison's disease,
CC autoimmune thyroiditis, gout, bronchitis, adult respiratory distress syndrome,
CC mellitus, multiple sclerosis, Good pasture's syndrome, Graves' disease,
CC osteoarthritis, osteoporosis, pancreatitis, psoriasis, Reiter's syndrome,
CC rheumatoid arthritis, Sjogren's syndrome, uveitis, ulcerative colitis,
CC bacterial, parasitic, fungal, viral, protozoal and helminthic infections)
CC growth and development disorders (arteriosclerosis, cirrhosis, hepatitis,
CC Cushing's syndrome, hypothyroidism, cerebral palsy, cataracts); cardio
CC vascular disease (arteriovenous fistula, hypertension, vasculitis,
CC aneurysms, congestive heart failure, angina pectoris, myocarditis,
CC ischaemic heart disease, chronic bronchitis, lung tumours); lipid
CC disorder (fatty liver, Fabry's disease, Niemann-Pick's disease,
CC hypocholesterolaemia, obesity). PKIN DNA is useful for assessing
CC toxicity of a test compound and in gene therapy. The present sequence
CC is human PKIN-17 cDNA.
XX Sequence 2897 BP; 599 A; 921 C; 877 G; 500 T; 0 other;
QY Query Match 46.6%; Score 851.4; DB 24; Length 2897;
Best Local Similarity 68.9%; Pred. No. 1.7e-176;
Matches 1356; Conservative 0; Mismatches 416; Indels 195; Gaps 6;
QY 1 ATGAAGGTGGAGGGGAGATCGGATCTCTGAAGCTCATTTGAGACACCCCGCTCTTAAG 60

```
Db 274 ATGAAGGTGAGCGGAGATCGCATCTCTGAAGCTCATCGAACCCACATGCTCTCAAG 333
Qy |||||
Db 61 CTGCACGAGCTTTATGAAGAAATATTTGTACCTGGTCTAGAACACGCTGTCAAGT 120
Qy |||||
Db 334 CTCCACGAGCTCTACGAGAACAGAAATATTTGTACCTGGTCTGTGAGCAGCTCTCGGG 393
Qy |||||
Db 121 GGTGAGCTCTTCGACTACCTGTGTAAGAGGGGAGGCTGACGCCCTAAGGAGGCTCGGAAG 180
Qy |||||
Db 394 GGTGAGCTATTGCACTTACCTGTATGAAGAGGGGAGACTGACGCCCAAGGAGGCCCGGAAG 453
Qy |||||
Db 181 TTCTTCGGCAGATCATCTCTGCTGGACTTTCTGCCACAGCACTTCCATATGCCACAGG 240
Qy |||||
Db 454 TTCTTCGGCAGATGCTGCTGGCTGGACTTTCTGCCACAGCTACTCCATCTGCCACAGA 513
Qy |||||
Db 241 GATCTGAAACCTGAAACCTCTCTGCTGGACGAGAGAACAAATCGCATCGCAGACTTT 300
Qy |||||
Db 514 GACCTAAAGCCCGAGAACCTGCTTTGGATGAGAAACAAATCGCATCGCAGACTTC 573
Qy |||||
Db 301 GGCATGGCGCTCCCTGCGAGGTGGCGACAGCCTGTTGGAGACAGCTGTGGGTCCCCCCAC 360
Qy |||||
Db 574 GGCATGGCGCTCCCTGCGAGGTGGCGACAGCCTCTCTGGAGACAGCTGTGGGTCCCCCCAT 633
Qy |||||
Db 361 TAGCGCTGCCCGAGGTGATCGGGGGGAGAAATATGACGGCCGGAAGCGGACGTGTGG 420
Qy |||||
Db 634 TATGCGTGTCCAGAGGTGATTAAGGGGGAAATATGATGGCCGCGGCGAGACATGTGG 693
Qy |||||
Db 421 AGCTGGGGCTCATCTGTTGCCCTTGTGGTGGGGCTCTGCCCTTGCAGATGACAAAC 480
Qy |||||
Db 694 AGCTGTGGAGTCACTCTCTTCCCTGCTGCTGGGGGGCTCTGCCCTTTGATGACACAAAC 753
Qy |||||
Db 481 TTGCGACAGCTGCTGAGAGGTGAAGCGGGCGGTGTTCCACATGCCGCACCTTTATCCCG 540
Qy |||||
Db 754 CTCGCCAGCTGCTGGAGAGGTGAACCGGGCGTCTTCCACATGCCCCACTTTCACTTCT 813
Qy |||||
Db 541 CCCGACTGCCAGAGTCTGCTACGGGGCATGATCGAGGTGGACCGCGCACCGCGCTCACG 600
Qy |||||
Db 814 CCAGATTGCCAGAGCTCTCTGAGGGGAATGATCGAAGTGGAGCCCGGAAAAAGGCTCAGT 873
Qy |||||
Db 601 CTAGAGCATCTTCAGAAACATATGTTATATAGGGGGCAGAGTACGCCGAAC----- 656
Qy |||||
Db 874 CTGGAGCAATTCAGAAACATCTTTGGTACCTTAGCGGGGAAACACAGACCCAGACCCGTGC 933
Qy |||||
Db 657 --AGAGCAGCCCATCTCTCGAAGGTGCAGATCCGCTGCTGCCAGCCTGGAGGACATC 714
Qy |||||
Db 934 CTGGAGCCAGCCCTTGCGCGCGGTAGCCATGCGAGCCTGCCATCCAAAGGAGCTG 993
Qy |||||
Db 715 GACCCCGAGCTGCTGGACAGCATGCACTACCTGGGCTGCTCCGAGACCGCAACAAAGCTG 774
Qy |||||
Db 994 GACCCCGAGCTCTAGAGAGCATGCGATCACTGGGCTGCTTCAGGGAACCGGAGAGGCTG 1053
Qy |||||
Db 775 CTGAGGACCTGCTGCTCGAGGAGGAGAACAGGAGAGATGATTTACTTCTCTCTCTG 834
Qy |||||
Db 1054 CATCCGAGCTGCGCAGTGTAGAGAGAGAACCAAGAAAGATGATATATATCTGCTTTTG 1113
Qy |||||
Db 835 GACCCGAAAGAAAGGTACCCGAGCCAGGAGGATGAGGACCTGCCCGCCCGGAACGAGATA 894
Qy |||||
Db 1114 GATCGGAGGAGCGGTATCCAGCTGTGAGGACCAAGGACCTGCTCCCGGAGATGATGTT 1173
Qy |||||
Db 895 GACCTTCCCGAAGCGTGTGACTCCCGGATGTGAAACCGGACCGCAAGCGCGGCA 954
Qy |||||
Db 1174 GACCCCGCCCGGAGCGTGTGATTTCTCCATGTGAGCGGTACGCGGAAGCGCGGACCA 1233
Qy |||||
Db 955 GACCCGAAATCCATGGAGTGTCTACGCTGACGGA-----CGGCGGTCCCGGTG 1005
Qy |||||
Db 1234 GAGCGGAAGTCCATGGAAGTCTGAGCATACCCGATGCGCGGGGTGGTGGTCCCGCTGA 1293
Qy |||||
Db 1006 CTTGCGCGCGCGGCTTATGAGATGCCCGACGCGCAGAGGTCTCGGTTCATACGCGGT 1065
Qy |||||
Db 1294 CCCACCCGAGCGGCTTGGAGATGGCCCGACGACGAGAGATCCGTAGCGTCAGTGA 1353
Qy |||||
Db 1066 GCCTCTCTAGGCTTTTCCACAGCCCACTTCAGACGCCCGCGG----- 1108
Qy |||||
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Db 1354 GCCTCCAGGGGTCTGCTCTCCAGCCCTTAAGCAGCCCAAGGAGTCCGGTCTTTTCTCTTT 1413
Qy |||||
Db 1109 ----- 1108
Db 1414 TCACCGGAGCGGGGCTTGAGATGAGGCTCGAGCGGGGCTCCCGACTTCCAAACG 1473
Qy |||||
Db 1109 -----TGACCCCTCACCCC 1122
Db 1474 CAGAGCTGCTCTTCGCGGCCCCAGGGGTGGGGGCGCGGGGAGCAGCCCGCCCGCCCC 1533
Qy |||||
Db 1123 TCACAAAGGGCAGTCCCTCTCC-----ACC 1149
Db 1534 AGTCCCGCTCCACACCCCTGCGCGCCCCCAGGCTCCCGCGCTCTCTCTGCGGGAGC 1593
Qy |||||
Db 1150 CCCAAGGGGACACTGTCTCCACAGCCCAAGAGAGCCCGGTGSCACGCCCAACCCCAAG 1209
Qy |||||
Db 1594 CCCTTGCACTGCTCTGCAACACGCCCGGGCCAGTCCCAACCGGAGCCCGGGGACACA 1653
Qy |||||
Db 1210 CCCCCTGCCAGCCCC-----AGCGTCGAGGGGTGCCCTGGAGGGCGCGGCTCAACTCC 1263
Db 1654 CCACCCCGACCCCGGGGTGGGCTCGGGGAGCCGCTGGAGAGTCTGCTCAACTCC 1713
Qy |||||
Db 1264 ATCAAGAACAGCTTTCTGGGCTCAACCCGCTTCACCCCGCGAAACTGCAAGTTCCGACG 1323
Db 1714 ATCGCAACAGTTCCTGGGCTCCCTCGCTTTCACCGCGCAAGATGCAAGTCCCTTACC 1773
Qy |||||
Db 1324 CCGAGAGAGATGTCACACCTGACACAGAGTCTGCCCGAGAGCTGGCGAGAAAGTCTCTGG 1383
Db 1774 GCTGAGGAGATGTCAGCTTGAAGCCAGAGTCTCTCCCGAGAGTGGCAAAACGCTCTCTGG 1833
Qy |||||
Db 1384 TTTGGGAACCTTCATCAGCTGGAGAGGAGAGCAGATCTTCGTGGTTCATCAAAAGACAAA 1443
Db 1834 TTCGGGAACCTTCATCTCTTGGACAAAGAGAACAAATATTCCTCGTGTAAAGAGACAAA 1893
Qy |||||
Db 1444 CTTCTGAGCTCCATCAAGGCTGACATCGTCACGCCCTTCCTGTCGATTCACAGTCTCAGC 1503
Db 1894 CTTCTGAGCAGCATCAAGCAGACATCGTCCATGCTCTGTCGATCCCGCAGCTGAGT 1953
Qy |||||
Db 1504 CACAGCTCATCTCCCAACGAGCTTCGGGGCCGAGTACAGGCCACGGGGGGGCCAGCC 1563
Db 1954 CACAGTGTGTGTACAGACCAAGCTTCAGGGCCGAGTACAAAGGCCAGTGGCGGCCCTCC 2013
Qy |||||
Db 1564 GTGTTCCAGAAAGCGGTCAAGTTCAGGTTGATATCACCTACACGAGGGT----- 1614
Db 2014 GTCTTCCAAAGCCCGTCCGCTTCAGAGTGACATCAGCTCCTCTGAGGGTCCAGAGCCC 2073
Qy |||||
Db 1615 -----GGGAGGCGCAGAAAGAGAAACGGCATCTACTCCGTCACCTTACCCCTGCTC 1665
Db 2074 TCCCGCGACGGGACGCGAGGTGGTGGCATCTACTCCGTCACCTTCACTCTCATC 2133
Qy |||||
Db 1666 TCAGGCCCCAGCGCTCGCTTCAGAGGGGTGGTGGAGACCATCCAGGCCAGCTGCTGAGC 1725
Db 2134 TCGGGTCCCAAGCCGTCCGTTCAAGCGAGTGGTGGAGACCATCCAGGCACAGCTCTGAGC 2193
Qy |||||
Db 1726 ACACAGCAGCCGCTGCGGCCCGACACTTGTTCAGACACCACTACTG 1772
Db 2194 ACTCATGCCAGCCCTCGGTGCGAGGCCCTGGCAGCAGAGAGAACGG 2240
Qy |||||

RESULT 13
ABV74558
ID ABV74558 standard; cDNA; 2289 BP.
XX
AC ABV74558;
XX
DT 20-JAN-2003 (first entry)
XX
DE Human kinase #2 coding sequence.
XX
KW Human; kinase; chromosome 19; gene; ss.
XX
OS Homo sapiens.
XX
```

PH	Key	Location/Qualifiers	
FT	CDS	1..2289	
FT		/*tag= a	
FT		/product= "Human kinase #2"	
XX	W0200281670-A1.		
XX	PN		
XX	PD	17-OCT-2002.	
XX	XX		
XX	PF	04-APR-2002; 2002MO-US10786.	
XX	PR	06-APR-2001; 2001US-282036P.	
XX	XX	(LEXI-) LEXICON GENETICS INC.	
PA	Turner CA, Mathur B, Friddle CJ;		
XX	PI	WPI; 2003-058538/05.	
XX	DR	P-PSDB; ABB98744.	
XX	DR		
XX	PT	New human kinase proteins useful for diagnosis, drug screening,	
PT	clinical trial monitoring, treatment of disorders and diseases, and		
PT	cosmetic and nutritional applications		
XX	XX		
PS	Claim 5; Page 41-42; 47pp; English.		
XX	XX		
CC	The present sequence is the coding sequence for a novel human kinase. The		
CC	genomic locus encoding the kinase is thought to be on human chromosome		
CC	19. The kinase and its coding sequence are useful for diagnosis, drug		
CC	screening, clinical trial monitoring, treatment of disorders and		
CC	diseases, and cosmetic and nutritional applications.		
XX	XX		
SQ	Sequence 2289 BP; 457 A; 759 C; 666 G; 407 T; 0 other;		
Query Match 42.5%; Score 777.2; DB 25; Length 2289;			
Best Local Similarity 67.9%; Pred. No. 2.6e-160;			
Matches 1277; Conservative 0; Mismatches 408; Indels 195; Gaps 6;			
QY	88	TATTTCTACTGCTGTAGAACACGCTGTACAGGTGTGAGCTTTCGACTACCTGCTGTAAG	147
DB	265	TTTAGGTACCTGTTCTTGGAGCAGCTCTCGGGGGTGAGCTATTGCACTACCTGGTAAAG	324
QY	148	AAGGGAGGCTGACCGCTAAGGAGGCTCGGAAGTCTTCCGGCAGATCATCTCTGCGCTG	207
DB	325	AAGGGAGACTGACGCCCAAGAGGAGCCGGAAGTCTTCCGCAGATTGTCTGCGCTG	384
QY	208	GACTTCTGCCACAGCCACTCCATATGCCACAGGATCTGAAACCTGAAACCTCTGCTG	267
DB	385	GACTTCTGCCACAGTACTCCATCTGCCACAGAGACCTAAAGCCCGAGAACCTGCTTTG	444
QY	268	GACGAGAGAACACATCCCGCATCGCAGACTTTGGCATGGCGTCCCTGCAGGTTGGCGAC	327
DB	445	GATGAGAAACACATCCCGCATTCGACACTTCGGCATGGCGTCCCTGCAGGTTGGCGAC	504
QY	328	AGCTGTGTGAGACCACTGTGGTCCCGCCACTACGCTTCCCGCAGAGTGATCCGCGGG	387
DB	505	AGCTTCTGAGACCACTGTGGTCCCGCCACTATGCGTGTCCAGAGGTGATTAGGGG	564
QY	388	GAGAAGTATGACGCCCGGAAGGCGGAGCTGTGAGCTGCGCGGTCTATCTGTTCGCTTG	447
DB	565	GAATAATATGATGGCCCGCGGAGACATGTGGAGCTGTGGAGTCTATCTTTCGCGCTG	624
QY	448	CTGTGGGGGCTGCGCTTCGAGTACACATTCGAGCAGCTGTGGAGAGGTTGAG	507
DB	625	CTGTGGGGGCTGCGCTTTCGAGTACACATTCGAGCAGCTGTGGAGAGGTTGAA	684
QY	508	CGGGCGGTGTTCACATGCGGCACTTTATCCCGCCGACTGCCAGAGTCTGTACCGGGC	567
DB	685	CGGGCGGTGTTCACATGCGGCACTTTATCCCGCCGACTGCCAGAGTCTGTACCGGGC	744
QY	568	ATGATCAGGTGAGCGCGCCTCAGCGTACGATAGACATTCAGAAACATATGG	627
DB	745	ATGATCAGGTGAGCGCGCCTCAGCGTACGATAGACATTCAGAAACATATGG	804

QY	628	TATATAGGGGCAAGATGAGCCCGAACCC-----AGAGAGCCCATTCCTCGCAAGGTG	681
DB	805	TACCTTAGCGGGAAACACAGAGCCAGACCGTCTGAGAGCCAGCCCTGGCGCGGGTGA	864
QY	682	CAGATCCGCTCGTCCAGCTGAGGAGACATCGACCCGAGCTGCTCGACAGCATGCAC	741
DB	865	GCCATGCGAGCTGCCATCAACGAGAGCTGGACCCCGAGCTCTAGAGAGCATGGCA	924
QY	742	TCATGGGCTGCTCCGAGACCGCAACAAAGTGTGTGAGGACCTGCTGTCCGAGAGGAG	801
DB	925	TCATGGGCTGCTTCAGGAGCCGCGAGAGGTGCTATCGGAGCTCGCAGTGGAGGAG	984
QY	802	RACAGAGAGATGATTTACTTCTCTCTGAGCCGGAAGAGAGTACCCGAGCCAG	861
DB	985	AACCAAGAAAGATGATATATATCTGCTTTTGGATCGGAAGGAGCGGTATCCAGCTGT	1044
QY	862	GAGATGAGGACCTGCCCCCGGAAACGAGATAGACCTCTCCCGGAAGCTGTGACTCC	921
DB	1045	GAGGACGAGGACCTGCTCCCGGAAATGATGTTGACCCCCCGGAGGCTGTGATCT	1104
QY	922	CCGATGCTGAACCGGACCGCAAGCGGCGGCGAGAAACGAAATCCATGAGGTGCTCAGC	981
DB	1105	CCCATGCTGAGCCGTACCGGAAGCGGACCCAGAGCGGAAGTCCATGGAAGTCTCTGAGC	1164
QY	982	GTGAC-----CGACGGGGCTCCCGGTGCTGCGCGGGGGCCATTGAGATGGCC	1032
DB	1165	ATCACCGATGCGGGGGTGGTGGCTCTCCCTGTACCCACCGACCGGGCTTGGAGATGCC	1224
QY	1033	CAGACGCGCAGAGGTCTCGGTTCATCAGCGGTGCTCTCAGGCTTTTCCACACAGCCCA	1092
DB	1225	CAGACAGCCAGAGATCCGTTAGCTCAGTGAGGCTCCACGGGTCTGTCTCCAGCCCT	1284
QY	1093	CTCAGAGCCCGCCG-----	1106
DB	1285	CTAAGCAGCCCAAGAGTACCGGTCTTTCTTTTCCCGGAGCGGGGCTGGAGATGAG	1344
QY	1107	-----	1106
DB	1345	GCTCAGGGGGGGCTCCCGACTTCCAAACGAGAGAGCTGCTCTTCGCGGGCCCCAGG	1404
QY	1107	-----GGTGACCTCTCACCTCTACCAAGGGGAGTCCCCCTCCCC-----	1146
DB	1405	GGTGGGGCGCGGGAGCAGCCCCCGCCCCAGTCCCGCTCCACACCTCTGCGCGGC	1464
QY	1147	-----ACCCCAAGGGGACACCTGTCTCACAGCCA	1176
DB	1465	CCCCCAGGCTCCCCGCTCTCTGCGGGAGCCCCCTTGCACTCGCTCTGCACAGCCCT	1524
QY	1177	NAGGAGCGCGGCTGGCAGCGCCCAACCCCGCCCGTCCAGCCCG-----AGCGTC	1230
DB	1525	CGGGCCAGTCCACCGGGACCCCGGGGACACACACCCCCCGCGCGGGTGGCGTC	1584
QY	1231	GGAGGGGTGCTTGGAGGGCGGGCTCAACTCCATCAAGAAACAGCTTTCTGGGCTCACCC	1290
DB	1585	GGGGAGCGCGCTGGAGGAGTCTCACTCACTCCGCAACAGCTTCTGGGCTCCCT	1644
QY	1291	CGCTTCCACCGCGGAAACTGCAAGTTCCGAGCGCGGAGGAGATGTCCAACTGACACCA	1350
DB	1645	CGCTTTCACCGCGCAAGATGCAAGTCCCTACCGTGGAGGAGATGTCCAGCTTGACGCCA	1704
QY	1351	GAGTCTGCTCCAGAGCTGGCGAAGAGTCTCTGTTTGGAACTTCATCAGCTGGAGAG	1410
DB	1705	GAGTCTCTCCCGAGCTGGCAAAACGCTCTCTGGTTCGGGAACTTCATCTCTTGGACAA	1764
QY	1411	GAGGAGCAGATCTTCTGGTCTATCAAGACAAACCTCTGAGCTCCATCAAGGCTGACATC	1470
DB	1765	GAAGAACAAATATCTCTGCTGCTAAAGGACAAACCTCTCAGCAGCATCAAGCAGACATC	1824
QY	1471	GTGCAGCGCTTCTCTGATTTCCAGTCTCAGCCACAGGCTCATCTCCCAAGAGCTTC	1530
DB	1825	GTCCATGCGCTTTCTGTGATCCCGACCTGAGTCAAGTGTCTGCACAGACCCAGCTTC	1884

QY 1531 CGGCGGAGTACAAAGCCAGCGGGGGCCAGCGGTGTTCAGAAAGCGGTCAAGTTCCAG 1590
Db 1885 AGGCGCGAGTACAAAGCCAGTGGCGGCCCTCGTCTTCCAAAAGCCGCTCCGTTCCAG 1944
QY 1591 GTTGATATCACTACACGGAGGT-----GGGAGGCGCAGAAGGAG 1632
Db 1945 GTGGACATCACTCCCTCTGAGGTCCAGAGCCCTCCCGCGAGCGGACGCGAGGT 2004
QY 1633 AAGCGCATCTACTCCGTCACCTTCAACCTCTCAGGCGCCAGCGCTCGCTTCAAGAGG 1692
Db 2005 GGTGGCATCTACTCCGTCACCTTCACTCTCGGTCCAGCGCTGGTTCAGCGA 2064
QY 1693 GTGGTGAACCATCAGGCGCCAGCTGTGAGCACACAGCCCGCTCGGCGCCAGCAC 1752
Db 2065 GTGGTGAACCATCAGGCGCACAGCTCTGAGCACTCATGACCAGCCCTCGGTGACGGC 2124
QY 1753 TTGTCAGACCACTAATCG 1772
Db 2125 CTGGCAGCAGGAAGACGG 2144

RESULT 14

ABX70994

ID ABX70994 standard; cDNA; 1797 BP.

XX AC ABX70994;

XX DT 05-MAR-2003 (first entry)

XX DE Novel human cDNA sequence #219.

XX KW Human; gene; ss; nervous system disorder; peripheral neuropathy;

XX KW Huntington's disease; amyotrophic lateral sclerosis; haemophilia;

XX KW neurodegenerative disease; Parkinson's disease; Alzheimer's disease;

XX KW autoimmune disease; systemic lupus erythematosus; rheumatoid arthritis;

XX KW insulin-dependent diabetes mellitus; anaemia; thrombocytopaenia; wound;

XX KW ulcer; burn; bone disorder; osteoporosis; osteoarthritis; stroke;

XX KW fibrosis; reperfusion injury; infection; allergic rhinitis; asthma;

XX KW coagulation disorder; cancer; tumour; inflammatory disease;

XX KW septic shock; Crohn's disease; anaphylaxis; proliferation; chemotactic;

XX KW differentiation; stem cell growth factor; haematopoiesis; chemokinetic;

XX KW haemostatic; antiinflammatory; expressed sequence tag; EST.

XX OS Homo sapiens.

XX XX WO200281731-A2.

XX XX 17-OCT-2002.

XX XX 29-JAN-2002; 2002WO-US01222.

XX XX 30-JAN-2001; 2001US-0774528.

XX XX (HYSE-) HYSEQ INC.

XX XX (GOOD/) GOODRICH R. W.

XX XX Tang TY, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;

XX XX Xue AJ, Yang Y, Wehrman T, Wang J, Wang D, Drmanac RT;

XX XX WPI; 2003-058563/05.

XX XX Novel polypeptide useful for treating neurodegenerative diseases,

XX XX myeloid or lymphoid cell disorders, bone disorders, mechanical and

XX XX traumatic disorders, coagulation disorders, and inflammatory diseases

XX XX -

XX XX Claim 1; Page -; 612pp; English.

XX XX This invention relates to the cDNA sequences encoding an isolated

XX XX novel human polypeptide. The protein encoded by the nucleic acid of

XX XX the invention is useful for treating central and peripheral nervous

XX XX system diseases (e.g. peripheral neuropathy, Huntington's disease,

XX XX amyotrophic lateral sclerosis); neurodegenerative diseases (e.g.

CC Parkinson's disease, Alzheimer's disease); autoimmune disease (e.g.
CC systemic lupus erythematosus, rheumatoid arthritis, insulin-dependent
CC diabetes mellitus); myeloid or lymphoid cell disorders (e.g. anemia
CC and thrombocytopaenia); wounds, ulcers, burns; bone disorders (e.g.
CC osteoporosis, osteoarthritis); mechanical and traumatic disorders (e.g.
CC stroke, head trauma); lung or liver fibrosis; reperfusion injury in
CC various tissues; bacterial, viral or fungal infections; allergic
CC conditions such as allergic rhinitis, asthma; coagulation disorders
CC (e.g. haemophilia); cancer and tumours; and inflammatory diseases (e.g.
CC septic shock, Crohn's disease, anaphylaxis). The protein may be used to
CC inhibit the growth, infection or function of infectious agents such as
CC bacteria, fungi, viruses, or to effect bodily characteristics,
CC biorhythms or circadian cycles of rhythms. The protein may also
CC have proliferation/differentiation, stem cell growth factor,
CC haematopoiesis regulation, immune stimulating or suppressing,
CC chemotactic/chemokinetic, haemostatic and thrombolytic, receptor/ligand,
CC and antiinflammatory activities. The cDNA sequences of the invention are
CC useful for expressing recombinant protein for analysis. The present
CC sequence represents a novel human cDNA sequence of the invention.
CC this sequence is an expressed sequence tag (EST) and was identified
CC using subtractive hybridisation.
XX

SQ Sequence 1797 BP; 375 A; 549 C; 520 G; 353 T; 0 other;

Query Match 32.2%; Score 588.8; DB 25; Length 1797;

Best Local Similarity 77.1%; Pred. No. 4e-119;

Matches 748; Conservative 0; Mismatches 207; Indels 15; Gaps 2;

QY 93 GTACCTGTGTAGAACACGTCAGGTGGTGGAGTCTTCGACTACCTGGTGAAGAGG 152

Db 89 GTACCTGTGTTCGGAGCACGTCCTCGGGGGTGAGCTATTTCGACTACCTGGTGAAGAGG 148

QY 153 GAGGCTGACGCTTAGAGGAGGTCGGAAGTCTTCGCGGAGATCATCTCTCGCTGGCTT 212

Db 149 GAGACTGAGCCCAAGAGGAGGCGGAAAGTCTTCGCGCAGATTTGCTCTGCGCTGGACTT 208

QY 213 CTGCCACAGCCACTCATATGTCACAGGGATCTGAAACCTGAAACCTCTCTGCTGAGCA 272

Db 209 CTGCCACAGCTACTCCATCTGCCACAGAGACTTAAAGCCCGAGAACCTGCTTTTGATGA 268

QY 273 GAAGAACAACTCCGATCGCAGACTTTGGGATGCGCTCCCTGCGAGGTGGCGACAGCT 332

Db 269 GAAACAAACATCCGATTCGCACTTCGCGATGCGCTCCCTGCGAGGTGGCGGACAGCT 328

QY 333 GTTGAGACACGAGTGTGGTCTCCCGCTACGCTGCGCGCGAGGTGATCCCGGGGAGAA 392

Db 329 CCTGGAGACAGCTCGGGTCCCCCATTTATGCTGTCCAGAGGTGATTAAGGGGGGAAA 388

QY 393 GTATGACGCGCGGAGAGCGGAGCTGTGGAGCTGCGCGCTCATCTCTGCTTCTGCTGCT 452

Db 389 ATATGATGCGCGCGGCGGAGACATGTGGAGCTGTGAGTCTATCTCTTCCGCTCTGCT 448

QY 453 GGGGCTCTGCGCTTCGACGATGACAACTTGGGACAGCTGTGGAGAGAGGTGAAGCGGG 512

Db 449 GGGGCTCTGCGCTTTGATGACGACAACTCCGCGAGCTGTGGAGAGAGGTGAAGCGGG 508

QY 513 CGTGTTCACATCGCGCACTTTATCCCGCGAGCTGCGAGAGTCTGCTACGGGGCATGAT 572

Db 509 GCTTTCACATGCCCCCACTTCATTCCTCCAGATTGCCAGAGCTCTCTGAGGGGAATGAT 568

QY 573 CGAGTGGAGCGCGCACCGCGCTCACGCTAGAGCACATTCAGAAACACATATGTTATAT 632

Db 569 CGAAGTGAGCGCGGAAAAAGGCTCAGTCTGGAGCAATTCAGAAACATCTCTTGGTACT 628

QY 633 AGGGGGCAAGAAATGAGCCCGAACCA-----GAGCAGGCCATTCCTCGCAAGGTGCAGAT 686

Db 629 AGGCGGAAACACAGGACGAGCCCGCTGCTGTGAGCCAGCCCTCGCGCGGGTGGCCAT 688

QY 687 CGGCTCGCTGCCAGCTGGAGGACATCGACCGAGCTGTGGAGACAGTCACTCACT 746

Db 689 GCGGAGCTGCTCCATCCAAAGGAGAGCTGGAGCCCGAGCTCTTAGAGAGATGGCATCACT 748

QY 747 GGGCTGTCTTCCGAGACCGCCAAAGAGCTGCTGCGAGGACCTGTGCTCCGAGGAGGAGAACCA 806

Db 749 GGGCTGCTTCAGGACCGGAGAGGCTGCATCGGAGCTGCGAGTGCAGTGAGGAGGAGCA 808
Qy 807 GGAGAAGATGATTTACTTCTCTCTGACCGGAAAGAGGTACCCGAGCCAGGAGGA 866
Db 809 AGAAAGATGATATATATCTGCTTTTGGATCGAAGAGCGGTATCCAGCTGTGAGGA 868
Qy 867 TGAGGACCTGCCCCCGGAGAGATAGACCTTCCCGGAGGCTGTGACTTCCCGAT 926
Db 869 CCAGGACCTGCTCCCGGAGATGATGTGACCCCGGAGCGTGTGATTTCCCAT 928
Qy 927 GCTGAACCGGACGCGAGCGCGGCGGACGACGAAATCCATGAGGTGCTCAGCGTGAC 986
Db 929 GCTGAGCGCTCAGCGGAGCGGCGGACGAGCGGAAATCCATGGAATCTTGAGCATCAC 988
Qy 987 -----GGAGCGCGCTCCCGGCTGCTGCGCGCGGCCCATTTGAGATGGGCCAGCA 1037
Db 989 CGATGCGGGGGTGGTGGCTCCCTGTACCCAGCCGAGCGGCGCTTGGAGATGGGCCAGCA 1048
Qy 1038 CGGCGAGAGG 1047
Db 1049 CAGCCAGAGG 1058

RESULT 15

ABL10489
ID ABL10489 standard; cDNA; 2720 BP.
XX AC ABL10489;
XX DT 26-MAR-2002 (first entry)
XX DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 25949.
XX KW Drosophila; developmental biology; cell signalling; insecticide;
XX KW pharmaceutical; gene; ss.
XX OS Drosophila melanogaster.
XX FN WO200171042-A2.
XX PD 27-SEP-2001.
XX PF 23-MAR-2001; 2001WO-US09231.
XX PR 23-MAR-2000; 2000US-191637P.
XX PR 11-JUL-2000; 2000US-0614150.
XX PA (PEKE) PE CORP NY.
XX PI Venter JC, Adams M, Li PWD, Myers EW;
XX WPI; 2001-656860/75.
XX DR P-PSDB; ABB66386.
XX PT New isolated nucleic acid detection reagent for detecting 1000 or more
XX genes from Drosophila and for elucidating cell signalling and cell-cell
XX interactions -
XX Claim 1; SEQ ID NO 25949; 21pp + Sequence Listing; English.
XX The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
XX useful in developmental biology and in elucidating cell signalling and
XX cell-cell interactions in higher eukaryotes for the development of
XX insecticides, therapeutics and pharmaceutical drugs. The invention
XX discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
XX sequences (ABL01840-ABL16175) and the encoded proteins
XX (ABB57737-ABB72072).
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 2720 BP; 661 A; 715 C; 759 G; 585 T; 0 other;
Query Match 24.4%; Score 446.2; DB 23; Length 2720;
Best Local Similarity 70.2%; Pred. No. 6.8e-88;
Matches 614; Conservative 0; Mismatches 258; Indels 3; Gaps 1;
Qy 1 ATGAAGTGGAGCGGGAGATCGGATCTCGAGCTCATTGAGCACCCACCTCCTTAAG 60
Db 178 ATGAAGTGGAGCGGAAATCGCAATATGAACCTAATCGATCATCCACCTCTTGGC 237
Qy 61 CTGACAGACGCTTTATGAAAACAAAATAATTTGTACTCTGCTGCTAGAACACAGTGTGAGT 120
Db 238 CTGAGCGATGTGACGAGAACAGAGTATTTGTATTTGATTTGAGGATGTATCCGCG 297
Qy 121 GGTGAGCTTTTCGACTTACTGTTGAGAGAGGGAGGCTGACGCTTAAGAGGCTCGGAAG 180
Db 298 GGAGAGCTCTTCGATTTACCTGTTGAAGAGGGTCGATTGACGCCGAAGAGGCGCGCAAG 357
Qy 181 TTCTTCCGCGAGATCATCTCTGGCTGGACTTCTGCCACAGCCACTCCATATGCCACAGG 240
Db 358 TTCTTCCAGGCAATCATCTCCGCTCGGATTTCTGCCACTCGCATTCGATTTGCCATCGC 417
Qy 241 GATCTGAAACCTGAAACCTCTCTGTCGACGAGAGAACAAACATCCGATCGCAGACTTT 300
Db 418 GACTTGAAGCGCGGAGATCTGCTGTCGACGAGAGAGATAACATTAAGATAGCGGACTTT 477
Qy 301 GGATGCGCTCCTGTCAGGTGGCGACAGCTGTTGGAGACAGAGTGTGGGTCCCGCCAC 360
Db 478 GGGATGGCTTCCCTGCGAGCGAGCTGGCAGCATGTTGGAGACCTCTCTGCGGACGCCACAC 537
Qy 361 TAGCCCTGCCCGAGGTGATCCGGGGGAGAGTATGAGCGCGGAGGCGGACGCTGTGG 420
Db 538 TAGCCCTGTGTCAGAGGTGATACGGGGCGAGAGTACGATGGCGCGAAGCGGATGTCGG 597
Qy 421 AGTGGCGGCTCATCTCTGTTGCTGCTGGGGGCTCTGCGCTTCGACATGACAAC 480
Db 598 TCCTGTGGGGTCTATCTCTATGCCCTCTCTGTTGGTGGCTTGCCTTCGACGACGACAC 657
Qy 481 TTGCGACAGCTGTGAGAGAGGTGAGCGGGGGTGTTCACATGCGGACATTTATCCCG 540
Db 658 TTGCGCCAGCTGTGAGAGAGGTCAAGCGGGGGCTCTTTCACATACCGCATTTTGTGCGG 717
Qy 541 CCGGACTGCCAGAGTCTGCTAGCGGGCATGATCGAGGTGAGCGCCGACCGCCCTCACG 600
Db 718 CCGGACTGCCAGAGTCTGCTGCGGCGCATGTTGAGGTCAATCCGACCGCGGCGCTCACG 777
Qy 601 CTAGAGCACATTCAGAAACACATATGTTATATA ---GGGGGCAAGAAATGAGCCCGAACCA 657
Db 778 CTGGCTGAAATCAACCGGCATCCGTGGGTCAACAGTGGCGCAAGGGGAGCTGGAGCTG 837
Qy 658 GAGCAGCCCATTCCTCGAAGGTGCGAGATCCGCTCGCTGCCAGCCTGGAGGACATCGAC 717
Db 838 GAGCTGCCAATGATGGAGGTGGTGACACACAGCTTATTTCCACACCCCGCGGTGGAT 897
Qy 718 CCGGAGCTGTGAGACAGCATGCACTCAGCTGGGTGCTTCCGAGACCGCAACAGCTGTG 777
Db 898 CCGGATGTGTGAAACCGGATTTGCTCGCTGGGCTGTTTCAAGGAGAGGAGAACTCATC 957
Qy 778 CAGGACCTGCTGTCCGAGGAGGAGAACCCAGGAGAGATGATTTACTTCTCTCTCTGGAC 837
Db 958 CAGGAACTGCTCAGTTCAAGTCAATACGAGAGGTTATATATTTCTCTGTTGCTCGAG 1017
Qy 838 CGGAAAGAGGTACCCGAGCCAGGAGGATGAGGA 872
Db 1018 CGCAACGAGAGACGACCTCGCTGGAGGATGATGA 1052

Search completed: November 27, 2003, 05:15:03

Job time : 472.512 secs

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OM nucleic - nucleic search, using sw model

Run on: November 27, 2003, 02:00:45 ; Search time 6538.89 Seconds
(without alignments)
11430.368 Million cell updates/sec

Title: US-10-054-579-3

Perfect score: 1827

Sequence: 1 atgaagggtgagcggagat.....gaattatcccgaaaggttaa 1827

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:

- 1: gb_ba:*
- 2: gb_htg:*
- 3: gb_in:*
- 4: gb_om:*
- 5: gb_ov:*
- 6: gb_pat:*
- 7: gb_ph:*
- 8: gb_pl:*
- 9: gb_pr:*
- 10: gb_ro:*
- 11: gb_ste:*
- 12: gb_sy:*
- 13: gb_uni:*
- 14: gb_vi:*
- 15: em_ba:*
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- 27: em_ste:*
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- 32: em_htg_other:*
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- 36: em_htg_man:*
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- 39: em_htgo_hum:*
- 40: em_htgo_mus:*
- 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1827	100.0	1827	6	AX661193	Sequence
2	1827	100.0	2007	6	AX661191	Sequence
3	1825.4	99.9	2908	6	AR232170	Sequence
4	1825.4	99.9	3516	9	AY166857	Homo sapi
5	1813	99.2	3364	6	AR232171	Sequence
6	1759.6	96.3	2025	6	AX327995	Sequence
7	1759.6	96.3	2219	6	AX327993	Sequence
8	1727	94.5	1956	9	HSA6701	Homo sapi
9	1330.4	72.8	3156	9	AK074411	Homo sapi
10	851.4	46.6	2385	6	AX166526	Sequence
11	851.4	46.6	2576	9	AB058714	Homo sapi
12	851.4	46.6	2720	9	HSM805307	Homo sapi
13	851.4	46.6	2897	6	AX642966	Sequence
14	851.4	46.6	3007	9	AF479826	Homo sapi
15	851.4	46.6	3109	9	AF479827	Homo sapi
16	594	32.5	2333	9	AF020089	Homo sapi
17	583.2	31.9	1873	9	BC024291	Homo sapi
18	426	23.3	5609	3	AY060288	Homo sapi
19	391	21.4	2128	9	BC016681	Drosophil
20	355.4	19.5	3059	3	AF316542	Homo sapi
21	349.2	19.1	3933	3	AB014885	Caenorhab
22	340	18.6	2123	3	AB014885	Halocynth
23	255	14.0	1791	9	AK116009	Ciona int
24	233	12.8	2259	10	AY151083	Macaca fa
25	232.4	12.7	1594	6	AX056390	Mus muscu
26	229.8	12.6	3170	6	AX305103	Sequence
27	229.8	12.6	3250	6	AX305104	Sequence
28	225	12.3	1549	6	AX685979	Sequence
29	225	12.3	2462	6	AX399987	Sequence
30	225	12.3	2650	9	AY120867	Sequence
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32	225	12.3	2954	9	AK075272	Homo sapi
33	225	12.3	3226	9	AY057448	Homo sapi
34	225	12.3	3269	6	AX680149	Sequence
35	225	12.3	3312	6	AX305105	Sequence
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37	225	12.3	3529	9	AB088047	Homo sapi
38	225	12.3	3609	9	AB049127	Homo sapi
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40	224.6	12.3	2650	10	AB020480	Rattus no
41	224.6	12.3	4092	10	AF106937	Sequence
42	222.8	12.2	2352	6	AX262512	Sequence
43	222.8	12.2	2533	6	AX024729	Sequence
44	222.8	12.2	2632	6	AX024732	Sequence
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ALIGNMENTS

RESULT 1	AX661193	AX661193	1827 bp	DNA	linear	PAT 22-MAR-2003
LOCUS	Sequence 3 from Patent WO02059287.					
DEFINITION	Sequence 3 from Patent WO02059287.					
ACCESSION	AX661193					
VERSION	AX661193.1	GI:29162845				
KEYWORDS						
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE	1					
AUTHORS	Turner C.A. and Mathur B.					
TITLE	Novel human kinases and polynucleotides encoding the same					
JOURNAL	Patent: WO 02059287-A 3 01-AUG-2002;					

ORGANISM	Homo sapiens									
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.									
AUTHORS	Turner, C.A. and Mathur, B.									
TITLE	Novel human kinases and polynucleotides encoding the same									
JOURNAL	Patent: WO 02059287-A 1 01-AUG-2002;									
FEATURES	Lexicon Genetics Incorporated (US)									
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	Best Local Similarity 100.0%; Pred. No. 0;									
	Matches 1827; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
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QY	61	CTGACGACGCTTTATGAAAACAAATAATTTGTACCTGGTGTAGAACACGTTGCAGT	120							
Db	241	CTGACGACGCTTTATGAAAACAAATAATTTGTACCTGGTGTAGAACACGTTGCAGT	300							
QY	121	GGTGAGCTCTTCGACTACCTGGTGAAGGGGAGGCTGACGCTTAAGAGGCTCGAAG	180							
Db	301	GGTGAGCTCTTCGACTACCTGGTGAAGGGGAGGCTGACGCTTAAGAGGCTCGAAG	360							
QY	181	TTCTTCGGCAGATCATCTCTGGCTGGACTTCTGCCACAGCCACTCCATATGCCACAGG	240							
Db	361	TTCTTCGGCAGATCATCTCTGGCTGGACTTCTGCCACAGCCACTCCATATGCCACAGG	420							
QY	241	GATCTGAACCTGAAACCTCTCTGTGGACGAGTCTTGGAGACCAACATCGCATCGCAGACTTT	300							
Db	421	GATCTGAACCTGAAACCTCTCTGTGGACGAGTCTTGGAGACCAACATCGCATCGCAGACTTT	480							
QY	301	GGCATGGGGTCCCTCGAGTTGGGCGACAGCTGTGTGGAGACCAAGCTGTGGGTCCCCCAC	360							
Db	481	GGCATGGGGTCCCTCGAGTTGGGCGACAGCTGTGTGGAGACCAAGCTGTGGGTCCCCCAC	540							
QY	361	TACGCTGCCCGCAGGTGATCGGGGGGAGAAATGATGACGCGCGGAGGCGGACGTGTGG	420							
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QY	481	TTGCCACAGCTCTGGAGAAAGTGAACGGGGGCTGTTCCACATGCCGACTTTATCCCG	540							
Db	661	TTGCCACAGCTCTGGAGAAAGTGAACGGGGGCTGTTCCACATGCCGACTTTATCCCG	720							
QY	541	CCCGACTGCCAGGTCTGTACTCGGGGATGATCGAGGTGGACGCGCAGCGCCCTCACG	600							
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AR232170 AR232170 2908 bp DNA linear PAT 20-DEC-2002
LOCUS
DEFINITION Sequence 1 from patent US 6455292.
ACCESSION AR232170
VERSION AR232170.1 GI:27274061
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 2908)
AUTHORS Shu, Y., Fan, W., Kovacs, K.F., Zidanic, M. and Jay, G.
TITLE Full-length serine protein kinase in brain and pancreas
JOURNAL Patent: US 6455292-A 1 24-SEP-2002;
FEATURES
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BASE COUNT 603 a 948 c 879 g 478 t
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Best Local Similarity 99.9%; Pred. No. 0;
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DB 346 CTGACGAGCTTTATGAAACAAAATAATTTGTACCTGGTCTAGAACACAGTGTGAGGT 405
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DB 406 GGTGAGCTCTCGACTACCTGCTGAAGAGGAGGAGCTGAGCCCTAAGAGGCTCGGAAG 465
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DB 466 TTCTTCGCGAGATCATCTCTCGCTGGAATTTCTGCCACAGCACTTCCATATGCCACAGG 525
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DB 706 AGCTGGGGCTCATCTCTGCTGCTGCTGCTGGGGGCTCTGCCCTTCGACGATGACAA 765
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LOCUS AR232171 3364 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 3 from patent US 6455292.
ACCESSION AR232171
VERSION AR232171.1 GI:27274062
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3364)
AUTHORS Shu, Y., Fan, W., Kovacs, K.F., Zidanic, M. and Jay, G.
TITLE Full-length serine protein kinase in brain and pancreas
JOURNAL Patent: US 6455292-A 3 24-SEP-2002;
FEATURES
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BASE COUNT 639 a 1078 c 1069 g 578 t
ORIGIN

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RESULT 7
AX327993
LOCUS AX327993 2219 bp DNA linear PAT 07-JAN-2002
DEFINITION Sequence 1 from Patent WO0181588.
ACCESSION AX327993
VERSION AX327993.1 GI:18098146
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Meyers, R.
2246, protein kinase molecules and uses therefor
Patent: WO 0181588-A 1 01-NOV-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES
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DEFINITION Homo sapiens mRNA for putative serine/threonine protein kinase, partial.
ACCESSION AJ006701
VERSION AJ006701.1 GI:3217027
KEYWORDS putative; serine/threonine protein kinase.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Stanchi, F., Bertocco, E., Toppo, S., Dioguardi, R., Simonati, B., Cannata, N., Zimbellio, R., Lanfranchi, G. and Valie, G.
TITLE Characterization of 16 novel human genes showing high similarity to

JOURNAL MEDLINE	Yeast 18 (1), 69-80 (2001)	Yeast sequences
PUBMED	21064499	Yeast 18 (1), 69-80 (2001)
REFERENCE	11124703	2 (bases 1 to 1956)
AUTHORS	Stanchi, F.	Stanchi, F.
TITLE	Direct Submission	Submitted (02-JUN-1998)
JOURNAL	Universita' di Padova, Via G. Colombo 3, 35121 Padova, 35121, ITALY	Location/Qualifiers
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VERSION AK074411.1 GI:18677005
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SOURCE Homo sapiens (human)
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AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 Kawakami, T., Noguchi, S., Itoh, T., Shigeta, K., Senba, T.,
Matsumura, K., Nakajima, Y., Mizuno, T., Morinaga, M., Tanigami, A.,
Fujiwara, T., Ono, T., Yamada, K., Fujii, Y., Ozaki, K., Hira, M.,
Ohmori, Y., Ota, T., Suzuki, Y., Obayashi, M., Nishi, T., Shibahara, T.,
Tanaka, T., Nakamura, Y., Isogai, T. and Sugano, S.
NEDO human cDNA sequencing project
Unpublished
2 (bases 1 to 3156)
Sugano, S., Suzuki, Y., Ota, T., Obayashi, M., Nishi, T., Isogai, T.,
Shibahara, T., Tanaka, T. and Nakamura, Y.
Direct Submission
Submitted (14-FEB-2002) Sumio Sugano, Institute of Medical Science,
University of Tokyo, Laboratory of Genome Structure, Human Genome
Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan
(E-mail: cdna@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
Fax:81-3-5449-5416)
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing;
Research Association for Biotechnology; cDNA library construction,
5'- & 3'-end one pass sequencing; Department of Virology and Human
Genome Center, Institute of Medical Science, University of Tokyo
(partly supported by Science and Technology Agency).
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RESULT 10
AX166526
LOCUS AX166526 2385 bp DNA linear PAT*22-JUN-2001
DEFINITION Sequence 17 from Patent WO0138503.
ACCESSION AX166526
VERSION AX166526.1 GI:14546871
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Plowman,G.D., Whyte,D., Manning,G.S., Sudarsanam,S.S., Martinez,R.,
Flanagan,P. and Clary,D.S.
TITLE Novel human protein kinases and protein kinase-like enzymes
JOURNAL Patent: WO 0138503-A 17 31-MAY-2001;
Sugen, Inc. (US)
FEATURES
source
1. 2385
/organism="Homo sapiens"
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BASE COUNT 494 a 768 c 731 g 392 t
ORIGIN

Query Match 46.6%; Score 851.4; DB 6; Length 2385;
Best Local Similarity 68.9%; Pred. No. 2e-145;
Matches 1356; Conservative 0; Mismatches 416; Indels 195; Gaps 6;
Qy 1 ATGAAGTGGAGCGGAGATCGCGATCCTGAGCTCATTTGAGCACCCCGCAGCTCTTAAG 60
Db 274 ATGAAGTGGAGCGGAGATCGCGATCCTGAGCTCATTTGAGCACCCCGCAGCTCTTAAG 333
Qy 61 CTGACACGAGCTTTATGAAAACAAAAATATTTGACCTGTGTAGAACACGTTGTCAGGT 120
Db 334 CTGACACGAGCTTACGAGAACAGAAATATTTGACCTGTGTGAGACAGCTCTCGGG 393
Qy 121 GGTGAGCTTTTCGACTACCTGTTGAAGAAGGGAGGTGACGCTTAAGAGGCTCGGAAG 180
Db 394 GGTGAGCTTTTCGACTACCTGTTGAAGAAGGGAGAGCTGACGCTTAAGAGGCTCGGAAG 453
Qy 181 TTCTTCGGGAGATCATCTCGCGCTGGAATTCTGCCACAGCCCATTCATATGCCAGG 240
Db 454 TTCTTCGGGAGATTTGTCTCGCGCTGAGCTTTCTGCCACAGCTACTTCATCTGCCACAGA 513
Qy 241 GATCTGAAAACCTGAAAACCTCTCTGTCGACGAGAGAACACATCCGCTCGCAGACTTT 300
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Qy 301 GGCATGGCGTCCCTGCGAGTTGGCGACAGCGCTGTTGGAGACCGAGCTGTGGGTCCCCC 360

574 GGCATGCGCTCCCTGACGCTGGGGGACAGCTCTCTGGAGACCAAGCTGCGGGTCCCCCAT 633
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RESULT 11

AB058714
LOCUS AB058714
DEFINITION Homo sapiens mRNA for KIAA1811 protein, partial cds.
ACCESSION AB058714
VERSION AB058714.1 GI:14017838
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (sites)
AUTHORS Nagase,T., Nakayama,M., Nakajima,D., Kikuno,R. and Ohara,O.
TITLE Prediction of the coding sequences of unidentified human genes. XX.
The complete sequences of 100 new cDNA clones from brain which code
for large proteins in vitro
JOURNAL DNA Res. 8 (2), 85-95 (2001)
MEDLINE 21245130
PUBMED 11347906
REFERENCE 2 (bases 1 to 2576)
AUTHORS Ohara,O., Nagase,T. and Kikuno,R.
TITLE Direct Submission
JOURNAL Submitted (27-MAR-2001) Osamu Ohara, Kazusa DNA Research Institute,
Department of Human Gene Research, 1532-3, Yana, Kisarazu, Chiba
292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp,
URL:http://www.kazusa.or.jp/huge, Tel:81-438-52-3913,
Fax:81-438-52-3914)
FEATURES
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BASE COUNT 508 a 842 c 766 g 460 t
ORIGIN
Query Match 46.6%; Score 851.4; DB 9; Length 2576;
Best Local Similarity 68.9%; Pred. No. 2e-145;
Matches 1356; Conservative 0; Mismatches 416; Indels 195; Gaps 6;
QY 1 ATGAGGTGGAGGGAGATCCGATCTCTGAAGCTCATTTGAGCACCCCAAGTCTCTAAAG 60
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38 ATGAGGTGGAGGGAGATCCGATCTCTGAAGCTCATTCGAACACCCACATGCTCTCAAG 97
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98 CTCCAGAGCTCTACAGAACCAAGAAATAATTTGTACCTGGTCTGGAGCAGCTCTCGGG 157
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QY 121 GGTGAGCTTTCGACTTACCTGTGAAGAGGGAGGCTGACGCCCTAAGAGGCTCGGAAG 180
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158 GGTGAGCTATTCGACTTACCTGTGAAGAGGGAGAGCTGACGCCCAAGAGGCCCGAAG 217
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QY 181 TTCCTCCGCGACATCATCTCTCGCTGGACTTCTGCGACAGCACCTCCATATGCCACAGG 240
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218 TTCCTCCGCGACATTTGTCTCGCTGGACTTCTGCGACAGCTACTCCATCTGCCACAGA 277
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QY 241 GATCTGAACCTGAAACCTCTGCTGGACGAGAGAACAAACATCGCATCCGACTTT 300
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ACCESSION AX642966
VERSION AX642966.1 GI:28550113
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Yue,H., Lal,P., Bandman,O., Borowsky,M., Au-Young,J., Lu,Y.,
Gandhi,A.R., Tribouley,C.M., Walla,N., Yao,M.G., Lu,D.A.,
Greenwald,S.R., Rankumar,J., Griffin,J.A., Kearney,L., Burford,N.,
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JOURNAL Incyte Genomics, Inc. (US)
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Best local Similarity 68.9%; Pred. No. 2e-145;
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LOCUS Homo sapiens putative serine/threonine protein kinase mRNA,
DEFINITION complete cds.
ACCESSION AF479826
VERSION AF479826.1 GI:19401870
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3007)
AUTHORS She, X. Y., Guo, J. H. and Yu, L.
DIRECT SUBMISSION
SUBMITTED (02-FEB-2002) School of Life Sciences, Laboratory of
Human Genes Research, Institute of Genetics, Fudan University, 220
Handan Road, Shanghai 200433, P. R. China
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RESULT 15
AF479827

LOCUS 3109 bp mRNA linear PRI 12-MAR-2002
DEFINITION Homo sapiens protein kinase-like protein mRNA, complete cds.

ACCESSION AF479827
VERSION AF479827.1 GI:19401873

KEYWORDS
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 3109)
AUTHORS She,X.Y., Yu,L. and Guo,J.H.

Direct Submission
Submitted (02-FEB-2003) School of Life Sciences, Laboratory of
Human Genes Research, Institute of Genetics, Fudan University, 220
Handan Road, Shanghai 200433, P. R. China
Location/Qualifiers
1. 3109
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BASE COUNT 611 a 1033 c 957 g 508 t
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Best Local Similarity 68.9%; Pred. No. 2e-145;
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GenCore version 5.1.6
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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US-09-930-181-1

; Sequence 1, Application US/09930181

; Patent No. 6455292

; GENERAL INFORMATION:

; APPLICANT: Origene Technologies

; TITLE OF INVENTION: Full-Length Serine Protein Kinase in Brain and Pancreas

; FILE REFERENCE: 16U 101 V1

; CURRENT APPLICATION NUMBER: US/09/930,181

; NUMBER OF SEQ ID NOS: 18

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 1

; LENGTH: 2908

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (106)..(2112)

; US-09-930-181-1

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QY 1737 GCCTGGGCGCCAGCATTTGTGTCAGACCACTAACTGATGAAATGATGACGGGCGGCT 1796
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QY 1797 TTCCAAATGTGAATTAATCCGAAAAGTTAA 1827
Db 2209 TTCCAAATGTGAATTAATCCGAAAAGTTAA 2239

RESULT 3

US-08-557-006C-38
; Sequence 38, Application US/08557006C
; Patent No. 6258547
; GENERAL INFORMATION:
; APPLICANT: Beri, Rajindar K.
; APPLICANT: Carling, David
; APPLICANT: Forder, Robert A.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING AMP-ACTIVATED PROTEIN KINASE
; FILE REFERENCE: NGAP/PHM31588/UST
; CURRENT APPLICATION NUMBER: US/08/557,006C
; CURRENT FILING DATE: 1996-03-06
; PRIOR APPLICATION NUMBER: PCT/GB94/01093
; PRIOR FILING DATE: 1994-05-20
; PRIOR APPLICATION NUMBER: GB 9310489.1
; PRIOR FILING DATE: 1993-05-21
; PRIOR APPLICATION NUMBER: GB 9318010.7
; PRIOR FILING DATE: 1993-08-31
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
; LENGTH: 1742
; TYPE: DNA
; ORGANISM: Human AMP protein kinase
; US-08-557-006C-38

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Best Local Similarity 57.1%; Pred. No. 3.4e-36;
Matches 362; Conservative 0; Mismatches 272; Indels 0; Gaps 0;
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DB 561 GCAGCACCAGGTCATCTCAGGAGGCTGTATGCGGGTCTGAGGTGATATCTGGAGC 620
QY 424 TGGCGGCTCATCTGTTCGCTTGTGCTGTGGGGCTCTGCCCTTCGACGATGACAACTTG 483
DB 621 TGTGGTGTATCTGTATGCCCTTCTCTGTGCGACCCCTCCCGTTCGACGATGACGACGTG 680
QY 484 CGACAGCTGCTGAGAGGTGAAGCGGGCGGTGTTCCACATGCCCACTTTATCCGCCC 543
DB 681 CTTACGCTTTTAAAGAGATCCGAGGGGTGTCTCTACATCCCGAGTATCTCAACCGT 740
QY 544 GACTGCGCAGATCTGTACGCGGCATGATCGAGGTGGAGCGCGCAGCGCTCAGCTTA 603
DB 741 TCTATTGCCACTCTGCTGATGCACATGCTGCAGGTGGAGCCCTTGAAGCGGCACTATC 800
QY 604 GAGCATTTCAGAAACACATATGTTATATAGGG 637
DB 801 AAAGACATACGAGATGATGAATGTTTAAACAG 834

RESULT 6

US-09-101-146-44
; Sequence 44, Application US/09101146
; Patent No. 6124125
; GENERAL INFORMATION:
; APPLICANT: Dartmouth College, St. Vincent's Institute of
; APPLICANT: Medical Research, Kemp et al.
; TITLE OF INVENTION: No. 6124125el AMP Activated Protein Kinase
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jane Massey Licata, Esq.
; STREET: 66 B. Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: USA
; ZIP: 08053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: WORDPERFECT 6.0 FOR WINDOWS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/101,146
; FILING DATE: October 7, 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PN7450

; FILING DATE: 8 JAN 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: DC-0050
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (856) 810-1515
; TELEFAX: (856) 810-1454
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1647
; TYPE: Nucleic acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: No
; US-09-101-146-44

Query Match 9.9%; Score 181.2; DB 3; Length 1647;
Best Local Similarity 55.8%; Pred. No. 3.3e-32;
Matches 345; Conservative 0; Mismatches 273; Indels 0; Gaps 0;

QY 14 GGGAGATCGGATCCTGAAGCTCATTTGAGCACCACCCAGCTCTAAAGCTGCACGAGCTTT 73
DB 188 GAGAGATCCAGAACCTGAAGCTTTTCAGGCAACCTCATATAATCAAACTGTACCAGGTCA 247
QY 74 ATGAAACAAAAAATATTTGTACCTGTGTAGAACACGCTGTAGGTGAGGAGAGCTTTTC 133
DB 248 TCAGTACACCTCTGATATTTTCATGTGTATGGAATATGTCTCAGGAGGAGAGCTATT 307
QY 134 ACTACCTGTGTAAGAGGGGAGGCTGACGCTAAGGAGGCTCGAAGTTCTTCGCGCAGA 193
DB 308 ATTATATCTGTAAATATGGAAGTTTGGACGAAAAGGAGAGTCTGTTTCCAGCAGA 367
QY 194 TCATCTCGCCTGGACTTCTGCCACAGCCTCCATATGCCACAGGATCTGAAACCTG 253
DB 368 TCCTTTCTGGTGTGACTATTTGTACAGGCAATATGTTGGTGTCCACAGAGATTGAAACCTG 427
QY 254 AAAACCTCTCTCGACGAGAGAACACATCCGCTCGCAGACTTTTGGCATGGGTCCTCC 313
DB 428 AAAAGTCTCTGTATGTCACACATGATGCAAGATAGCCGACTTCGGTCTTTCAAACA 487
QY 314 TGCAGTTGGCGACAGCCTGTTGGAGACCACTGTGGGTCCCCCACTACGCTGCCCCG 373
DB 488 TGATGTCAAGATGTTGAATTTTAAAGACGAGCTGTGGCTCGCCCAATTTATGCTGCACCAG 547
QY 374 AGGTATCCGGGGGAGAGATATGACGCGCGGAGGAGGAGCTGTGGAGCTGCGGCTCA 433
DB 548 AAGTAATTTTCAGGAAGATTTCTACGACGCGCTGAAGTAGACATCTGGAGCAGCGGGTCA 607
QY 434 TCCTGTTCTGCTGTGGTGGGGCTCTGCCCTTCGACGATGACAACTTGGCAGAGCTGC 493
DB 608 TTCTATGCTTTGCTGTGTGGAACCTCTCCCTTTTGTATGATGACACGCTGCAACTCTTT 667
QY 494 TGGAGAGGTGAAGCGGGGCTGTTCACATGCGCACTTTTATCCGCGCCGAGCTGCCAGA 553
DB 668 TTAAGAAGATATGTGACGGGATATTTTATACCCCTCAGTATTTGAATCCCTCTGTAAATA 727
QY 554 GTCTGTACGGGGCATGATCGAGGTGGAGCGGCGGACCGGCTCAGCTAGAGCATTTC 613
DB 728 GCCTTTTGAACATATGCTGCAGGTAGATCTCTGAAGAGGGGCCACATAAAGATATCA 787
QY 614 AGAAACACATATGTTATA 631
DB 788 GGAACATGAATGTTTA 805

RESULT 7

US-09-984-890-1
; Sequence 1, Application US/09984890
; Patent No. 6492156
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

;; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;; FILE OF INVENTION: THEREOF
;; FILE REFERENCE: CL001306
;; CURRENT APPLICATION NUMBER: US/09/984,890
;; CURRENT FILING DATE: 2001-10-31
;; NUMBER OF SEQ ID NOS: 4
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 1
;; LENGTH: 2175
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-984-890-1

Query Match 9.7%; Score 177.4; DB 4; Length 2175;
Best Local Similarity 54.3%; Pred. No. 2.6e-31;
Matches 359; Conservative 0; Mismatches 301; Indels 0; Gaps 0;
QY 3 GAAGTGGAGCGGAGATCCGATCCTGAAGCTCATTTGACAGCCGCCAGTCTCAAGCT 62
DB 285 GAAACTATTCCGCGAAGTAAGAATAATGAAGGTTTGAATCATCCCAACATAGTTAAATT 344
QY 63 GCAGGAGTTTATCAAAACAAAATAATTTGTACCTGGTCTAGAACACAGTGTCAAGTGG 122
DB 345 ATTGAAGTGAATTGAGACTGAGAAAACGCTCTACTTGTCTATGAGTACGCTAGTGGCGG 404
QY 123 TGAGCTCTTCGACTACCTGCTGAAGAGGGAGGCTGACGCCCTAAGAGAGGCTCGGAAGTT 182
DB 405 AGAGGTATTTGATTACCTAGTGGCTCATGCGAGGATGAAGAAAAGAGGCTCGAGCCAA 464
QY 183 CTTCCGCGAGATCATCTCGGCTGGATCTTCTGCCAGAGCACTCCCATATGCCACAGGGA 242
DB 465 ATTCCGCGAGTGTGCTGCTGTCAGTACTGTCTACCCAGAGGTTTATTGTCATAGAGA 524
QY 243 TCTGAACTCTGAAACCTCTGCTGAGAGAGAGAAACATCCGATCCAGACTTTGG 302
DB 525 CTTAAGGCGAAGAACCTGCTCTTGGATGCTGATATGAACATCAAGATTGCGAGCTTTGG 584
QY 303 CATGGCTCCCTGCGAGGTGTGGCAGACAGCTTTTGGAGACAGCTGTGGTCCGCCCACTA 362
DB 585 CTTGAGCAATGAATACCTTTTGGGAACAGCTGGACACCTTCTGTGGCAGTCCCCCTTA 644
QY 363 CGCTGCCCCAGGTGATCCGGGGGGAGAGATGAGCGGGGAGAGCGGAGCGAGCTGTGGAG 422
DB 645 TGCTGCCGCCAGAACTTTCCAGGGCAAAAATAATGATGAGACCCGAGGTGATGTGGAG 704
QY 423 CTGCGGCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 482
DB 705 CCTAGGAGTTATCTCTATACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 764
QY 483 GCGACAGCTGCTGAGAGAGGTGAAGCGGGGCGTGTTCACATGCCGCACTTTATCCCGCC 542
DB 765 CAAGGAGTGGCGGAACGGGTACTGAGGGGAAATACCGTATTCATTCTACATGTCCAC 824
QY 543 CGACTGCCAGAGTCTGCTACGGGGGATGATCGAGGTGAGCCCGCAGCCGCTCAGCT 602
DB 825 GGAATGTGAAACCTGCTTAAGAAAATTTCTCATTTTAAATCCAGCAAGAGAGCACTTT 884
QY 603 AGAGCACATTGAGAAACATATGATATAGGGGCAAGATAGGCCGCAACAGAGC 661
DB 885 AGAGCAATCATGAAGATCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 943

RESULT 8
US-08-557-006C-44
; Sequence 44, Application US/08557006C
; Patent No. 625847
; GENERAL INFORMATION:
; APPLICANT: Beri, Rajindar K.
; APPLICANT: Carling, David
; APPLICANT: Forster, Robert A.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING AMP-ACTIVATED PROTEIN KINASE
; FILE REFERENCE: NGA/P/PM37588/UST
; CURRENT APPLICATION NUMBER: US/08/557,006C

;; CURRENT FILING DATE: 1996-03-06
;; PRIOR APPLICATION NUMBER: PCT/GB94/01093
;; PRIOR FILING DATE: 1994-05-20
;; PRIOR APPLICATION NUMBER: GB 9310489.1
;; PRIOR FILING DATE: 1993-05-21
;; PRIOR APPLICATION NUMBER: GB 9318010.7
;; PRIOR FILING DATE: 1993-08-31
;; NUMBER OF SEQ ID NOS: 44
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 44
;; LENGTH: 1747
;; TYPE: DNA
;; ORGANISM: Human
;; FEATURE:
;; LOCATION: (1) (1747)
;; OTHER INFORMATION: Full length cDNA sequence fragment of Human AMPK -
;; OTHER INFORMATION: fragment begins at nucleotide 24 and ends with
;; OTHER INFORMATION: nucleotide 1765
US-08-557-006C-44

Query Match 9.5%; Score 173.8; DB 3; Length 1747;
Best Local Similarity 56.7%; Pred. No. 1.6e-30;
Matches 362; Conservative 0; Mismatches 272; Indels 5; Gaps 2;
QY 4 AAGGTGGAGCGGAGATCCGATCCTGAAGCTCATTTGACAGCCGCCAGTCTCAAGCTG 63
DB 178 AAAATAAAACAGAGAAATTCAAAATCTTAAACTCTTTCGTATCCTCATATTATCAAACTC 237
QY 64 CACGAGCTTTATGAAAAAATAATTTGTACCTGGTCTAGAACACAGTGTCAAGTGT 123
DB 238 TACCAAGTGATCAGCACTTCAAACAGACTTTTATGGTAAATGGAATATGTGTCTGAGGT 297
QY 124 GAGCTCTTCGACTACTGCTGTAAGAGGGAGGCTGACGCCCTAAGAGGCTCGGAAGTTC 183
DB 298 GAATTGTTTCGACTACATCTGTATAACACGGAGGGTTGAAGAGTGAAGCTCGCGGCTC 357
QY 184 TTCCGCGAGATCATCTCTGCGCTGGACTTCTG - CCACAGCCACTCCATATGCCACAGGG 241
DB 358 TTCCAGCAGATTCTGTCTGCGCTGGACTACTGTCTCACAGGCACATGGTTGTCCACAGGG 417
QY 242 ATCTGAAACCTGAAACCTCTGCTGGAGAGAGAGAAACATCCGCATCGCAGACTTTG 301
DB 418 AACTGAAAGCCAGAGAACGTTGCTGGAGCCCGCAGATGAATGCTAAGATAGTGAATTCTCG 477
QY 302 GCATGCGCTCCCTGCGAGGTGGCGACAGCTGTGGAGACACAGCTGTGGTCCCGCACT 361
DB 478 GACTCTCTAATATGATGTCAGATGGTGAATTTCTACGAATAGTGTGGATCGCCAAAT 537
QY 362 AGCTTGTCCCGAGGTGATCCGGGGGAGAGTATGACCGCGGAGAGGCGGAGCTGTGGA 421
DB 538 ATGCAGCACCGGAGGTCACTCTCAGGAAGGCTGTATCGGGTCTCTGAGGTGATATCTGGA 597
QY 422 GCTGCGGCTCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 478
DB 598 GCTGTGCTGTATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 657
QY 479 ACTTGGCAGACAGTGTCTGAGAGAGGTGAAGCGGGGCGTGTTCACATCGCCGCACTTTATCC 538
DB 658 ACCTGCTACGCTCTTTAAGAGATCCGAGGGGGTGTGTCTTACATCCCGGAGTATCTCA 717
QY 539 CGCCCGACTGCCAGATCTGCTACGGGGGATGATCGAGGTGAGCGCCGACCGCCCTCA 598
DB 718 ACCGTCTATTGGCACTCTGCTGATGCATGCTGCAAGTGGAGGAGCCCTTTGAAGCGAGCA 777
QY 599 CGCTAGAGCATTTCAGAAACACATATGATATAGGG 637
DB 778 CTATCAAGACATACGAGAGCATGAATGGTTTAAACAGG 816

RESULT 9
US-09-359-161-4
; Sequence 4, Application US/09359161A

Patent No. 6342656
; GENERAL INFORMATION:
; APPLICANT: Bradford, Kent J.
; APPLICANT: Dahal, Peetambar
; APPLICANT: Yang, Hong
; APPLICANT: Cooley, Michael
; APPLICANT: Downie, Bruce
; APPLICANT: Gee, Oliver
; TITLE OF INVENTION: The Regents of the University of California
; TITLE OF INVENTION: Regulation of Source-Sink Relationships and Responses
; FILE REFERENCE: 021070-095900US
; CURRENT APPLICATION NUMBER: US/09/359,161A
; CURRENT FILING DATE: 1999-07-21
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1929
; TYPE: DNA
; ORGANISM: Lycopersicon esculentum
; FEATURE:
; OTHER INFORMATION: Lycopersicon esculentum plant homolog of yeast
; OTHER INFORMATION: SNF1 kinase subunit of protein kinase (LeSNF1)
US-09-359-161-4

Query Match 9.4%; Score 171.6; DB 4; Length 1929;
Best Local Similarity 54.6%; Pred. No. 5.3e-30;
Matches 342; Conservative 0; Mismatches 284; Indels 0; Gaps 0;
QY 3 GAAGTGGAGCGGAGATCGGATCCTGAAGCTCAATTGAGCACCCACCGCTCAAGCT 62
DB 218 GAAATCCGTAGAGAAATCAAAATATTGAGATTGTTCATGCTCCTATATTACGGCT 277
QY 63 GCACGACCTTTATGAAAAAATAATTTGTACCTGTGTGTAGAACACGCTGTCAGGTG 122
DB 278 TTATGAGTCTAGAGACACCATCAGATATATATGTTGTATGAGTATGAAATCTGG 337
QY 123 TGAGCTTTCGACTACCTGGTGAAGAGGGAGGCTGACCGCTTAAGGAGGCTCGGAAGTT 182
DB 338 CGAGTTATTTGATTACATTTGTAGAGGGCAGATTTCAGGAGGATGAAGCTCGTAACCT 397
QY 183 CTTCCGGCAGATCATCTCGCTGGACTTTGCCACAGCCACTCCATATGCCACAGGA 242
DB 398 TTTTCAGCAGATAATTTCTGTGTGGAGTACTGCCATAGAAACATGTTGGTTTCATAGAGA 457
QY 243 TCTGAAACCTGAAACCTCCTGCTGGAGAGAGAAACAAACATCCGCATCGCAGACTTTGG 302
DB 458 CTTTAAGCTGAAACCTCCTCTGGACTCCAAATGGAATGTGAAGATCGCAGATTTGG 517
QY 303 CATGCGCTCCCTGAGGTGGCGACAGCCTGTTGGAGACCAAGCTGTGGTCCCCCACTA 362
DB 518 TTTGAGCAATATCATGCGCATGGTCAATTTCTGAAGACAAAGTTGCGGAAGCCCAACTA 577
QY 363 CGCTCCCGGAGGTATCCGGGGGAGAGTATGACCGCGGAGGCGGAGCTGTGGAG 422
DB 578 TGCTGCCCCAGAGGTATATCAGGTAAATTTGATGCTGGCCCTGAGGTAGATGTGGAG 637
QY 423 CTGCGGCTCATCTCTGTCGCTGCTGGTGGGGCTCTGCGCTTCGACGATGACAACTT 482
DB 638 CTGTGTTGTTATCTTTATGCTCTCTCTGTGGCACCTTTCGGTTGACGATGAAACAT 697
QY 483 GCGACAGCTGTGGAGAGGTGAAGCGGGGCGGTGTTCCACATGCGCGCACTTTATCCCGCC 542
DB 698 ACCCAACTTTTTTAAGAAAAATAAGGGTGAATATAATACTCTGCCACCCATTTATCAGC 757
QY 543 CGACTGCCAGAGTCTGCTACGGGGATGATCGAGGTGGACCGCGCACCGCCCTCAGCT 602
DB 758 TGGTGGAGGAGTTGATTCGAGGATGCTTATAGTCGACCCAAATGAAGCGAATGACTAT 817
QY 603 AGAGCACATTTCAGAAACACATATGCT 628
DB 818 TCCTGAGATTGCTGACCCCTTGGT 843

RESULT 10
US-09-579-664B-4
; Sequence 4, Application US/09579664B
; Patent No. 6514719
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Bird, Timothy A.
; APPLICANT: Virca, G. Duke
; APPLICANT: Martin, Unja
; APPLICANT: Anderson, Dirk M.
; TITLE OF INVENTION: NOVEL MURINE AND HUMAN KINASES
; FILE REFERENCE: 2923-A
; CURRENT APPLICATION NUMBER: US/09/579,664B
; CURRENT FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 2902
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-579-664B-4

Query Match 9.2%; Score 168.4; DB 4; Length 2902;
Best Local Similarity 55.0%; Pred. No. 3.2e-29;
Matches 353; Conservative 0; Mismatches 286; Indels 3; Gaps 1;
QY 2 TGAAGTGGAGCGGAGATCGGATCCTGAAGCTCAATTGAGCACCCACCGCTCCTAAGC 61
DB 418 TGCATATACGAGGAGATTGAGATCATGTCTTCACTCAACCCCCACATCATTTGCCA 477
QY 62 TGACACGAGTTTATGAAAAAATAATTTGTACCTGTGTGTAGAACACGCTGTCAGGTG 121
DB 478 TCCATGAAGTTTGAATATAGCAGCAAGATTGTGATTGTTCATGAGTATGCCAGCGAG 537
QY 122 GTGAGCTTTCGACTACTCTGTTGAAGAGGGAGGCTGACCGCTTAAGAGGCTCGGAAGT 181
DB 538 GCGATCTGTATGATTATCATCAGTGAGCGGCCACCGCTGAGTGAGCGGAGCGCCAGGCA 597
QY 182 TCTTCGGCAGATCATCTCTGCGCTGGACTTTCGCCACAGCACTCCATATGCCACAGGG 241
DB 598 TCTTCGACAGATGCTGTCTGCTGCACTACTGCTGCACTACTGCTGCACTACTGCTGCACT 657
QY 242 ATCTGAAACCTGAAACCTCTCTGCTGCACTGCACTGCACTGCACTGCACTGCACTGCACT 301
DB 658 ATCTCAAGCTGGAACATCATCTTCTAGATGCAATGCAATGCAATGCAATGCAATGCAAT 717
QY 302 GCATGGCGTCCCTGAGGTTGGCGACAGCCTGTTGGAGACAGCTGTGGTGGTGGTGGTGGT 361
DB 718 GCCTCTCAACCTGTACCAAGGCAAGTTCTCTCCAGACGTTCTGTGGGAGCGCTCTCT 777
QY 362 ACGCTCCCGGAGGTGATCCGGGGGAGAAAGTATGACGCGGAGGAGCGGAGCGGTGGGA 421
DB 778 ACGCTCCCTGAGATGATCAACGGGAGCCCTATGTTGGGCGCCAGAGGTGGAAGTGGT 837
QY 422 GCTGCGCGCTCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 481
DB 838 CTCTGGCGGTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 897
QY 482 TGCGACAGCTGCTGGAGAGGTGAGCGGGGCGGTGTTCCACATGCTCCGCACTTTATCCGCG 541
DB 898 ATAAACACCTGGTGAAGCAAAATCAGTAAACGGGCTTACCGGTGAGCCGCCCC 954
QY 542 CCGACTCCAGAGTCTGCTACGGGGATGATCGAGGTGGAGCGCGCGCACCGCGCTCAGCG 601
DB 955 CCGATGCTGTGGCTGATCGGTGGCTGTTAATGTTGAACCCACCGCTCGGCGCACAC 1014
QY 602 TAGAGCACATTTCAGAAACACATATGTTATAGGGGGCAAGA 643
DB 1015 TGGAGGATGATAGCCAGTCAATTGGTGGTCAACTTGGGGTTTACA 1056

RESULT 11


```

US-08-557-006C-37
; Sequence 37, Application US/08557006C
; Patent No. 6259547
; GENERAL INFORMATION:
; APPLICANT: Beri, Rajindar K.
; APPLICANT: Carling, David
; APPLICANT: Forder, Robert A.
; TITLE OF INVENTION: NUCLEIC ACID EN
; FILE REFERENCE: NGAP/PM37588/UST
; CURRENT APPLICATION NUMBER: US/08/55
; CURRENT FILING DATE: 1996-03-06
; PRIOR APPLICATION NUMBER: PCT/GB94/
; PRIOR FILING DATE: 1994-05-20
; PRIOR APPLICATION NUMBER: GB 931048
; PRIOR FILING DATE: 1993-05-21
; PRIOR APPLICATION NUMBER: GB 931801
; PRIOR FILING DATE: 1993-08-31
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 37
; LENGTH: 1736
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of A
; OTHER INFORMATION: protein kinase
US-08-557-006C-37

```

Query Match	8.3%	Score 151.6	DB 3	Length 1736
Best Local Similarity	52.5%	Prod. No. 1.8e-25		
Matches 331	Conservative 0	Mismatches 299	Indels 0	Gaps 0
Qy	4	AAGGTGAGCGGGAGATCGCGATCTCTGAAGCTCATTGAGCACCCACCGCTCTAAAGCTG	63	
Db	178	AAATAAAACGAGAAATCAAAATCTAAACTCTTTGGTATCTCATATATCAAACTA	237	
Qy	64	CACGACGTTTATGAAAAAATAATTTGTACCTTGGTGTAGAACACGCTGTCAAGTGGT	123	
Db	238	TACCAGGTGATCAGCACTCCCAACAGATTTTTTATGGTAAATGGAATATGTCTCTGGAGT	297	
Qy	124	GAGCTCTTCGACTACCTGGTCAAGAGGGGAGGCTGACGCTCAAGGAGGCTCGGAAGTTC	183	
Db	298	GAATATTTGACTACATCTGTAGCATGCGACGGGTTGAAGAGATGGAAGCCAGCGGCTC	357	
Qy	184	TTCCGGCAGATCATCTCTGCGCTGGACTCTTGCCACAGCCACTCCATATGCCACAGGAT	243	
Db	358	TTTCAGCAGATTTCTGTCTGTGGATTACTGTCTATGGCATATGGTTGTTTCATCGAGAC	417	
Qy	244	CTGAAACTGAAACCTCTCTCTGGACGAGAGACACATCCGCATCGCAGACTTTGGC	303	
Db	418	CTGAAACGAGAGATGTCCTGTGGATGCAACATGAATGCCAAGATAGCCGATTTCCGA	477	
Qy	304	ATGGCGTCCCTGCAGGTTGGCGACAGCCCTGTTGGAGACCAGCTGTGGGTCCCGCCACTAC	363	
Db	478	TTATCTAATATGATGTCAGATGGTGAAATTTCTGAGAACTAGTTGGGATCTCCAAATAT	537	
Qy	364	GCCTGCCCCGAGGTGATCCGGGGGGGAGAAGTATGACGGCCGGAAGCGGAGCTGTGGAGC	423	
Db	538	GCAGCACCCTGAAGTCATCTCAGGCAGATTTGTATGCAGGTCTCTGAATTTGATATCTGGAGC	597	
Qy	424	TGGCGGTCATCTGTTTCGCTTGTCTGGTGGGGGCTCTGCCCTTCGACGATGACAACTTG	483	
Db	598	TGTGGTGTATCTGTATGTCTCTTTGTGGCACCCCTCCCAATTTGATGATGAGCATGTA	657	
Qy	484	CGACAGCTGTGGAGAAAGGTGAAGCGGGGGGTGTTTCCATGCGCGCATTTTATCCCGCCC	543	
Db	658	CCTACGTTATTTAAGAAAGATCCGAGGGGGTGTCTTTTATATCCCAGAAATATCTCAATCGT	717	
Qy	544	GACTGCCAGAGTCTGTACGGGGCATGATCCAGGTTGGACGGCGACGCCGCTCAACGCTA	603	
Db	718	TCTGTGCGCATCTCTCCTGATGATATGCTGCAGGTTTGACCACTGAGAAAGAGCAACTATC	777	
Qy	604	GAGCACATTTGAGAAACACATATGGTATATA	633	

Db 778 AAGACATAGAGCATGAATGTTAAA 807

RESULT 12
US-08-557-006C-36
; Sequence 36, Application US/08557006C
; Patent No. 6258547
; GENERAL INFORMATION:
; APPLICANT: Beri, Rajindar K.
; APPLICANT: Carling, David
; APPLICANT: Forder, Robert A.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING AM
; FILE REFERENCE: NGAP/PM37588/UST
; CURRENT APPLICATION NUMBER: US/08/557,006C
; CURRENT FILING DATE: 1996-03-06
; PRIOR APPLICATION NUMBER: PCT/GB94/01093
; PRIOR FILING DATE: 1994-05-20
; PRIOR APPLICATION NUMBER: GB 9310489.1
; PRIOR FILING DATE: 1993-05-21
; PRIOR APPLICATION NUMBER: GB 9318010.7
; PRIOR FILING DATE: 1993-08-31
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 36
; LENGTH: 1783
; TYPE: DNA
; ORGANISM: Human AMP protein kinase
US-08-557-006C-36

Query Match	8.3%;	Score 151.6;	DB 3;	Length 1783;
Best Local Similarity	52.5%;	Pred. No. 1.8e-25;		
Matches 331;	Conservative 0;	Mismatches 299;	Indels 0;	Gaps 0;
QY	4	AAGGTGAGCGGGAGATCGCGATCCTGAAGTCTATTGAGCACCCACCGTCTAAAGCTG	63	
DB	179	AAAATAAAACGAGAAATCTAAACTCTTTGGTATCTCATATTATCAAACTA	238	
QY	64	CAGCACGTTTATGAAAAACAAAAATATTTGTACTGTGGTGTAGAAACACGTTGAGGTGGT	123	
DB	239	TACCAGGTGATCAGCACTCCCAACAGATTTTTTTATGTGTAATGGAATATGTGTCGTGGAGGT	298	
QY	124	GAGCTCTTCGACTACCTGGTGAAGAGGGGAGGCTGACGCTCAAGGAGGCTCGGAAGTTC	183	
DB	299	GAATATTTGACTACACTGTGAACATGAGACGGTTGAAAGATGGAAGCAAGCGGGCTC	358	
QY	184	TTCCGGCAGATCATCTCTGCCTCGACTTCTGCCACGCCACTCCATATGCCACAGGAT	243	
DB	359	TTTCAGCAGATTCTGTCTGCTGTGGATTACTGTCTATAGGCATATGTTGTTTCATCGAGAC	418	
QY	244	CTGAAACCTGAAACCTCTCTCTGGAAGAGAAACAACATCCGGCATCGCAGACTTTGGC	303	
DB	419	CTGAAACCGAGAAATGTCCTCTTGGATGACACATGAATGCCAAGATAGCCGATTTCGGA	478	
QY	304	ATGCGCTCCCTGCAGTTGGCGGACAGCCTGTTGGAGACGAGTGTGGGTGCCCCCACTAC	363	
DB	479	TTATCTAATATGATGTCAAGTGTGAATTTCTCGAACTAGTTGGGATCTCCAATATAT	538	
QY	364	GCCTGCCCCGAGGTGATCCGGGGGAGAGATATGACGCCGGAAAGCCGAGCGTGTGAGC	423	
DB	539	GCAGCACCTGAAGTCATCTCAGGCAGATTGTATGCAGTCCCTGAAGTTGATATCTGAGC	598	
QY	424	TGCGGGCTCATCTGTTTCGCTTCTGTGGGGGGCTGCGCTTCGACGATGACAACTTG	483	
DB	599	TGTGGTGTTATCTTTGATGCTCTCTTTGTGGCACCCCTCCCACTTTGATGATGAGCATGTA	658	
QY	484	CGACAGCTGCTGGAGAAAGGTGAAGCGGGGCGGTGTTTCCATGCCCCGACCTTTATCCCGCC	543	
DB	659	CCTACGTTATTTAAGAGATCCGAGGGGGTGTCTTTTATATCCCAAGATATCTCAATGCT	718	
QY	544	GACTGCCAGATCTGTTACGGGGGCAATGATCGAGGTGAGCGGGCAAGCGGCTCTACGCTA	603	
DB	719	TCTGTGCGCACTCTCCTGATGCATATGCTGCAGGTTCGCCCATGTAACGAGCAACTATC	778	

Db 426 CCTGAAGCCGAGAAATCATCTGCTGGCAAGACGCGAGCCGCCGCAATTAAGCT 485
Qy 291 GGCAGACTTTGGCATGCGCTCCCTGCGAGTTGGCGACAGCTTTGGAGACAGCTGTGG 350
Db 486 CATCGACTTTGGCATGCGCGACAGGATCGAGGCTGGCAGCGATTCAAGAAACATCTTTGG 545
Qy 351 GTCCCCCACTAGCGCTGCCCCCGAGGTGATCCGGGGGGAAGATATGACGGCCGGAAGGC 410
Db 546 CACACCCGAGTTGTCCGCCCGA---GATCGTGAACATATGAGCCACTTTGGCTTGGAGGC 602
Qy 411 GGACGTGTGAGCTGCGCGCTCATCTGTTGCGCTTCTGCTGGGGGCTCTGCCCTTCGA 470
Db 603 TGACATGTGAGCATTTGGCGTTCATCACTACATCTCTCTGAGCGGAGCGTCCCATTCCT 662
Qy 471 CGATGACAACTTGGCAGCTGTGGAGAA 500
Db 663 GGGCGAGACCAAGCAGGAGCGCTGACGAA 692

RESULT 15

US-09-186-277-4

; Sequence 4, Application US/09186277

; Patent No. 6171841

; GENERAL INFORMATION:

; APPLICANT: AKIRA, SHIZUO

; APPLICANT: KAWAI, TARO

; TITLE OF INVENTION: DNA CODING FOR SERINE/THREONINE KINASE

; FILE REFERENCE: 081356/0128

; CURRENT APPLICATION NUMBER: US/09/186,277

; EARLIER FILING DATE: 1998-11-05

; EARLIER APPLICATION NUMBER: JP97/261589

; EARLIER FILING DATE: 1997-09-26

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 4

; LENGTH: 1429

; TYPE: DNA

; ORGANISM: Mus musculus

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (10)..(1353)

US-09-186-277-4

Query Match 7.4%; Score 135.2; DB 3; Length 1429;
Best Local Similarity 57.3%; Pred. No. 9.2e-22;
Matches 292; Conservative 0; Mismatches 203; Indels 15; Gaps 2;
Qy 3 GAAGTGGAGCGGAGATCGCGATCCTGGAAGCTCATTTGAGCACCCTCCCTAAAGCT 62
Db 186 GGAGATCGAACCGGAGGTGAGCATCTCGCGGAGATCGCCCAACATCAACACT 245
Qy 63 GCAGAGCTTTATGAACAAATAATTTCTACTGTGTAGAACACGTCTCAGGTGG 122
Db 246 GATGACGTGTTGGAACAAGACAGATGTGTGCTGATCTTGAGCTGHTCCGTTGG 305
Qy 123 TGAGCTTTTCGACTACCTGTTGAAGAGGAGGTGACGCTTAAGAGGCTCGGAAGTT 182
Db 306 CGAGCTTTTCGACTTCTCTGGCGGAGAGGAGTTCATTGACGGAGGATGAGGCCACGAGTT 365
Qy 183 CTTCCGGCAGATCATCTCTGGCTGGACTTTGCGACAGCCACTCCATATGCCACAGGGA 242
Db 366 CCTCAACAAATCCTAGACGGTGTCCACTCTGCACTCCAAAGCGCATCGCACACTTTGA 425
Qy 243 TCTGAACCTGAACCTCTCTGCGAGAGAAACAAACATCCGC-----AT 290
Db 426 CTTGAAGCCCGAAGACATCATGTTCTGGAACAGCAGCAGCCGCCCATTAAGCT 485
Qy 291 GCGAGACTTTGGCATGGCGTCCCTGCGAGTTGGGACAGCCTGTTGGAGACCACTGTGG 350
Db 486 CATCGACTTTGGCATCGCGCAGGATCGAGGCTGGCAGCGAGTTCAAGAAACATCTTTGG 545
Qy 351 GTCCCCCACTAGCGCTGCCCCCGAGGTGATCCGGGGGGAAGATATGACGGCCGGAAGGC 410

Db 546 CACACCCGAGTTTGTGCCCCCGA---GATCGTGAACATATGAGCCACTTTGGCTTGGAGGC 602
Qy 411 GGACGTGTGAGCTGCGCGCTCATCTGTTGCGCTTGTGTTGGGGGCTCTGCCCTTCGA 470
Db 603 TGACATGTGAGCATTTGGCGTTCATCACTACATCTCTCTGAGCGGAGGCTCCCATTCCT 562
Qy 471 CGATGACAACTTGGCAGCTGTGGAGAA 500
Db 663 GGGCGAGACCAAGCAGGAGCGCTGACGAA 692

Search completed: November 27, 2003, 11:09:42
Job time : 121.131 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 27, 2003, 04:08:07 ; Search time 3468.16 Seconds
(without alignments)
12803.430 Million cell updates/sec

Title: US-10-054-579-3

Perfect score: 1827

Sequence: 1 atgaagtggagcggagat.....gaattatcccgaaagtaa 1827

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rtd:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_ges1:*

29: gb_ges2:*

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	639.4	35.0	769	13	BQ442940
2	601.4	32.9	732	13	BQ443783
3	599	32.8	791	13	BU611869
4	595.2	32.6	1201	9	AL538014

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT 1

BQ442940

LOCUS

DEFINITION

IMAGE:5707609 5', mRNA sequence.

ACCSSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BQ442940 769 bp mRNA linear EST 29-MAY-2002

UI-M-EVO-bxf-o-02-0-UI.r1 NIH-BMAP_EVO Mus musculus CDNA clone

IMAGE:5707609 5', mRNA sequence.

ACCSSION BQ442940

VERSION BQ442940.1 GI:21246052

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 769)

AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

TITLE Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

JOURNAL NIH-MGC http://mgc.nci.nih.gov/

COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgabs-@email.nih.gov

Tissue Procurement: Dr. James Lin, University of Iowa

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

This clone was contributed by the Brain Molecular Anatomy Project

(BMAP)

5	593.4	32.5	723	14	CA315127	CA315127 UI-M-FW0-
6	588.2	32.2	733	13	BQ178695	BQ178695 UI-M-EVO-
7	584.8	32.0	733	10	BG395625	BG395625 602458251
8	583.8	32.0	1882	11	BC017182	BC017182 Homo sapi
9	574.2	31.4	712	13	BQ180079	BQ180079 UI-M-EWO-
10	562.2	30.8	740	10	BF222739	BF222739 7q32f02.x
11	559.8	30.6	563	10	BE251924	BE251924 601107590
12	548.2	30.0	693	13	BQ443644	BQ443644 UI-M-EWO-
13	515	28.2	589	10	BE259121	BE259121 601107773
14	496.8	27.2	699	14	CA319314	CA319314 UI-M-FW0-
15	495.2	27.1	727	12	BI825755	BI825755 603072158
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17	476.8	26.1	697	13	BQ392070	BQ392070 603802721
18	459	25.1	889	13	BQ434571	BQ434571 AGENCOURT
19	445.6	24.4	709	12	BI916891	BI916891 603177863
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21	445	24.4	937	10	BF527021	BF527021 602039908
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23	425.6	23.3	881	13	BQ717903	BQ717903 AGENCOURT
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25	413.8	22.6	1041	13	BQ882776	BQ882776 AGENCOURT
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27	406.2	22.2	701	10	BE256016	BE256016 601113531
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29	403.6	22.1	831	10	BF529743	BF529743 602044002
30	398	21.8	1177	12	BM466629	BM466629 AGENCOURT
31	393.6	21.5	639	10	BF342303	BF342303 602013084
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36	379	20.7	742	12	BM944329	BM944329 UI-M-EHOP
37	377	20.6	378	13	EX090836	EX090836 BX090836
38	362.8	19.9	728	13	BQ769984	BQ769984 UI-M-P10-
39	355.4	19.5	898	10	BF529174	BF529174 602042051
40	355.2	19.4	783	13	BU348106	BU348106 603524982
41	352	19.3	1073	12	BM475434	BM475434 AGENCOURT
42	339.8	18.6	730	13	BU613922	BU613922 UI-M-FRO-
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45	325.4	17.8	614	12	BM944236	BM944236 UI-M-EHOP

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Seq primer: pYX-5.
Location/Qualifiers
1. 769
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:5707609"
/tissue_type="whole brain"
/dev_stage="embryo 15.5 dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_EVO"
/notes="Organ: brain; Vector: pYX-Asc; Site 1: EcoR I; Site 2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured mRNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I, and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail, is GTGCGTGGAA. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institutes of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."
BASE COUNT 185 a 241 c 202 g 141 t
ORIGIN

Query Match 35.0%; Score 639.4; DB 13; Length 769;
Best Local Similarity 89.5%; Pred. No. 8.8e-131;
Matches 688; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

Qy 721 GACGTGTCGACAGATGCACTACTGCGTGTCTTCGAGACCCCAACAGACTGCTCCAG 780
Db 1 GATGTGTGGACAGATGCACTACTGCGTGTCTTCGAGACCCCAACAGACTGCTCCAG 60
Qy 781 GACGTGTCGACGAGGAGAAACAGAGAGATGATTACTTCCTCTCTCGACCGG 840
Db 61 GATCTGCTATCTGAGGAGGAGATCAGAAAGATGATTATTTCTCTCTCTGGATCGG 120
Qy 841 AAAGAAAGGTACCCGAGCAGGAGATGAGACCTGCCCTCCCGGACGAGATAGACCT 900
Db 121 AAAGAACGTTATCAAGCCATGAGATGAGACCTGCCCTCCCGGACGAGATAGACCT 180
Qy 901 CCCGGAAGCTGTGGACTCCCGATGCTGAACCGGACGCGCAGCGCGCCAGAACGC 960
Db 181 CCCGGAAGCTGTGGATTCCCGATGCTGAACCGGACGCGCAGCGCGCTGAGCGC 240
Qy 961 AAATCCATGAGGTGCTCAGCGTGACGACGCGCGCTCCCGGTGCTTCGCGCGCGGCC 1020
Db 241 AAGTCCATGGAAGTGTCTCAGTGTACAGATGTGTGCTCCCGAGTCTTCGCGGAGGCC 300
Qy 1021 ATTGAGATGGCCACGACGCGCAGAGGTCTCGGTCCATCAGCGTGTGCTCTCAGGCTT 1080
Db 301 ATTGAGATGGCCACGATGCGATGCGATGCTCGATCCATCAGTGTGTGCTCTCAGGCTT 360
Qy 1081 TCCACCGCCCACTCAGCAGCGCCCGGTGACCTTCACTCCCTCACCAGGGGAGTCCC 1140
Db 361 TCTACAAGTCCACTCAGCAGCTCTCGGTGACCTTCACTCCCTCACCAGGGGAGTCCC 420
Qy 1141 CTCGCCACCCCAAGGGAGACCTGTCCACACGCCCAAGAGAGAGCCCGGCTGGCAGCGCC 1200
Db 421 CTCCTACCTCCCAAGGAGCGCTGTCCACAGCCCAAGGAGAGCCAGCTGGCAGCACCC 480
Qy 1201 AACCCACGCCCCCGTCCAGCCCCAGCGTCCGAGGGGTGCCCTGAGGGCGCGCTCAAC 1260
Db 481 AACCCACACCAACCATCCAGCCCTAGTGTGGAGGAGTGCCTGCGGACGACGACTGAAC 540
Qy 1261 TCCATCAGAACAGCTTTCTGGGCTCACCCCGCTTCCACCGCCCGGAACTCAAGTTCCG 1320
Db 541 TCCATCAAGAACAGCTTTCTGGGCTCACCTGATTCACCCCGCGGAACTCAAGTTCCC 600

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Seq primer: pYX-5.
Location/Qualifiers
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/mol_type="mRNA"
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/db_xref="taxon:10090"
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/tissue_type="whole brain"
/dev_stage="embryo 15.5 dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_EVO"
/notes="Organ: brain; Vector: pYX-Asc; Site 1: EcoR I; Site 2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured mRNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I, and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail, is GTGCGTGGAA. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institutes of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

BASE COUNT 185 a 241 c 202 g 141 t
ORIGIN

Query Match 35.0%; Score 639.4; DB 13; Length 769;
Best Local Similarity 89.5%; Pred. No. 8.8e-131;
Matches 688; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

Qy 721 GACGTGTCGACAGATGCACTACTGCGTGTCTTCGAGACCCCAACAGACTGCTCCAG 780
Db 1 GATGTGTGGACAGATGCACTACTGCGTGTCTTCGAGACCCCAACAGACTGCTCCAG 60
Qy 781 GACGTGTCGACGAGGAGAAACAGAGAGATGATTACTTCCTCTCTCGACCGG 840
Db 61 GATCTGCTATCTGAGGAGGAGATCAGAAAGATGATTATTTCTCTCTCTGGATCGG 120
Qy 841 AAAGAAAGGTACCCGAGCAGGAGATGAGACCTGCCCTCCCGGACGAGATAGACCT 900
Db 121 AAAGAACGTTATCAAGCCATGAGATGAGACCTGCCCTCCCGGACGAGATAGACCT 180
Qy 901 CCCGGAAGCTGTGGACTCCCGATGCTGAACCGGACGCGCAGCGCGCCAGAACGC 960
Db 181 CCCGGAAGCTGTGGATTCCCGATGCTGAACCGGACGCGCAGCGCGCTGAGCGC 240
Qy 961 AAATCCATGAGGTGCTCAGCGTGACGACGCGCGCTCCCGGTGCTTCGCGCGGCC 1020
Db 241 AAGTCCATGGAAGTGTCTCAGTGTACAGATGTGTGCTCCCGAGTCTTCGCGGAGGCC 300
Qy 1021 ATTGAGATGGCCACGACGCGCAGAGGTCTCGGTCCATCAGCGTGTGCTCTCAGGCTT 1080
Db 301 ATTGAGATGGCCACGATGCGATGCGATGCTCGATCCATCAGTGTGTGCTCTCAGGCTT 360
Qy 1081 TCCACCGCCCACTCAGCAGCGCCCGGTGACCTTCACTCCCTCACCAGGGGAGTCCC 1140
Db 361 TCTACAAGTCCACTCAGCAGCTCTCGGTGACCTTCACTCCCTCACCAGGGGAGTCCC 420
Qy 1141 CTCGCCACCCCAAGGGAGACCTGTCCACACGCCCAAGAGAGAGCCCGGCTGGCAGCGCC 1200
Db 421 CTCCTACCTCCCAAGGAGCGCTGTCCACAGCCCAAGGAGAGCCAGCTGGCAGCACCC 480
Qy 1201 AACCCACGCCCCCGTCCAGCCCCAGCGTCCGAGGGGTGCCCTGAGGGCGCGCTCAAC 1260
Db 481 AACCCACACCAACCATCCAGCCCTAGTGTGGAGGAGTGCCTGCGGACGACGACTGAAC 540
Qy 1261 TCCATCAGAACAGCTTTCTGGGCTCACCCCGCTTCCACCGCCCGGAACTCAAGTTCCG 1320
Db 541 TCCATCAAGAACAGCTTTCTGGGCTCACCTGATTCACCCCGCGGAACTCAAGTTCCC 600

Qy 1321 ACGCGGAGGAGATGTCACACCTGACACGAGTGTCTCCAGAGCTGCGGAGAGTCC 1380
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Db 661 TGGTTTGGAACTTCATCAACCTCGAGAGGAGGAGAGATCTTTGTGTATCAAGGAC 720
Qy 1441 AAACCTCTGAGCTCCATCAGCTGACATCGTGACGCGCTTCCTCTCGA 1489
Db 721 AAGCCCTGAGCTCCATCAGGCTGACATCGTGATCGCTTCCTCTCGA 769

RESULT 2
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UI-M-EWO-bx1-e-03-0-UI-r1 NIH_BMAP_EWO Mus musculus cDNA clone
IMAGE:5708522 5', mRNA sequence.
BQ443783
BQ443783.1 GI:21246895
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue procurement: Dr. James Lin, University of Iowa
cDNA library preparation: Dr. M. Bento Soares, University of Iowa
cDNA library arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)

Seq primer: pYX-5.
Location/Qualifiers
1. 732
/organism="Mus musculus"
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/clone_lib="NIH_BMAP_EWO"
/notes="Organ: brain; Vector: pYX-Asc; Site 1: EcoR I; Site 2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured mRNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I, and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail, is GTGCGTGGAA. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institutes of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

BASE COUNT 178 a 240 c 188 g 125 t 1 others
ORIGIN

Query Match 32.9%; Score 601.4; DB 13; Length 732;
Best Local Similarity 88.8%; Pred. No. 2.2e-122;

Query Match	32.2%;	Score 588.2;	DB 13;	Length 733;
Best Local Similarity	88.4%;	Pred. No. 1.8e-119;		
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QY	285	CCGCATCGCAGACTTTGGCATGGCTCCCTGCGAGTTGGCGACAGCCTGTTGAGACCGAG	344	
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QY	345	CTGTGGTTCCTCCACATACGCTGCCCCGAGGTGATCCCGGGGGAGAGATGATACGCGCG	404	
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QY	405	GAAGCGGAGTGTGGAGCTGCGCGCTCATCTGTTGCGCTTCTGCTGGTGGGGCTTCGCC	464	
DB	121	CAAGCGAGATGTGGAGCTGTGTGTGATCTGCTGTTGCGCTTCTGCTGGTGGGGCTTCGCC	180	
QY	465	CTTCGACGATGACAACTTTCGACAGCTGCTGGAGAAGTGAAGCGGGCGCTGTTTCCACAT	524	
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QY	525	GCSCATTTTATCCCGCCGACTGCCAGAGTCTGCTACGGGGCATGATCGAGTGGACGC	584	
DB	241	GCCACACTTTATCCACCAGACTGCCAGAGTCTCTCGTGGCATGATTCAGGTGGATGC	300	
QY	585	CGCAGCGGCTCAGCTAGAGCACATTCGAAACACATATGTTATAGGGGCAAGAA	644	
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QY	645	TGAGCCGGAACGAGACGACCCATTCCTCGCAAGGTGCAGATCCGCTCGCTGCCAGCCT	704	
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DB	481	CAACAGCTGCTGAGGATCTGCTATCTGAGGAGGAGAAATCAGGAAGATGATTTATTT	540	
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QY	885	GAACGAGATAGACCTTCCCGGAGCGTGTGGATCTCCCGATGTGAAACCGGACGCA	944	
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QY	945	CGCGGGCCAGACGCAATCCATGGAGTCTCAGCGTGACGACGCGGCTCCCGGCT	1004	
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QY	1005	GC 1006		
DB	721	GC 722		

RESULT 7
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LOCUS
DEFINITION BG395625.1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:4580724 5',
733 bp mRNA linear EST 12-MAR-2001
RNA sequence.
ACCESSION BG395625
VERSION BG395625.1 GI:13289073
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 733)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM1300 row: e column: 13
High quality sequence stop: 719.
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Location/Qualifiers
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/note="Organ: eye; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
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adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC library."
BASE COUNT 162 a 238 c 214 g 119 t
ORIGIN

Query Match	32.0%;	Score 584.8;	DB 10;	Length 733;	
Best Local Similarity	99.7%;	Pred. No. 1e-118;	2;	Indels 0;	Gaps 0;
Matches 586;	Conservative 0;	Mismatches 2;			
QY	1179	GGAGAGCCCGGCTGGCACGCCCAACCCACGCCCCCGCTCCAGCCCCGAGGGGT	1238		
DB	2	GGAGAGCCCGGCTGGCACGCCCAACCCACGCCCCCGCTCCAGCCCCGAGGGGT	61		
QY	1239	GCCTTGGAGGGCGGCTCAACTCCATCAAGAAACAGCTTTCTGGGCTCACCCGGCTTCCA	1298		
DB	62	GCCTTGGAGGGCGGCTCAACTCCATCAAGAAACAGCTTTCTGGGCTCACCCGGCTTCCA	121		
QY	1299	CGCCCGGAAACTGCAAGTTCCGACGCGCGAGGAGATGTCCAACTCACACGAGTCTGTC	1358		
DB	122	CGCCCGGAAACTGCAAGTTCCGACGCGCGAGGAGATGTCCAACTCACACGAGTCTGTC	181		
QY	1359	CCCAGAGCTGGCGAAGAGTCTCTGGTTTGGGAACTTCATCAGCTCGGAGAAGGAGCA	1418		
DB	182	CCCAGAGCTGGCGAAGAGTCTCTGGTTTGGGAACTTCATCAGCTCGGAGAAGGAGCA	241		
QY	1419	GATCTTCTGGTTCATCAAGACAAACCTCTGAGCTCCATCAGGCTGACATCGTGACGC	1478		
DB	242	GATCTTCTGGTTCATCAAGACAAACCTCTGAGCTCCATCAGGCTGACATCGTGACGC	301		
QY	1479	CTTCTCTGTCGATTCCTCAGCCACAGCGTCACTCCCAAACGAGCTTCGGGCGCGA	1538		
DB	302	CTTCTCTGTCGATTCCTCAGCTCTAGCCACAGCGTCACTCCCAAACGAGCTTCGGGCGCGA	361		
QY	1539	GTACAAAGGCCACGGGGGGCGAGCCGTGTTTCCAGAACCGGTCAGTTCCAGTTGATAT	1598		
DB	362	GTACAAAGGCCACGGGGGGCGAGCCGTGTTTCCAGAACCGGTCAGTTCCAGTTGATAT	421		
QY	1599	CACCTACAGGAGGTGGGAGCGCGCAGAGGAGACGGCATCTACTCCGTCACTTTCAC	1658		
DB	422	CACCTACAGGAGGTGGGAGCGCGCAGAGGAGACGGCATCTACTCCGTCACTTTCAC	481		
QY	1659	CTGTCTCTCAGGCGCCAGCGCTCGCTTTCAGAGGGTGGAGACCATCCAGGCCAGCT	1718		
DB	482	CTGTCTCTCAGGCGCCAGCGCTCGCTTTCAGAGGGTGGAGACCATCCAGGCCAGCT	541		
QY	1719	GCTGAGCACACACGACCCCGCTCGGGCCCGACACTTGTGACAGACCAAC	1766		
DB	542	GCTGAGCACACACGACCCCGCTCGGGCCCGACACTTGTGAGAAACCCC	589		

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RESULT 8
BC017182
LOCUS
DEFINITION Homo sapiens, Similar to KIAA1811 protein, clone IMAGE:3343795,
            1882 bp mRNA linear HTC 09-NOV-2001
            mRNA.
ACCESSION BC017182
VERSION BC017182.1 GI:16877911
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Direct Submission
JOURNAL Submitted (05-NOV-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc.mgc@hgri.nih.gov
Shevchenko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M.,
Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S.,
Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R.,
Lim, M., Maduro, Q.L., Masiello, C., Mastrian, S.B., McCloskey, J.C.,
McDowell, J., Pearson, R., Snyder, B., Stantropop, S., Thomas, P.J.,
Tiongson, E.E., Touchman, J.W., Tsourgeon, C., Vogt, J.L., Walker, M.A.,
Zhang, L.-H. and Green, E.D.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 5 Row: J Column: 11
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 4103050
This clone has the following problem: frame shifted.
FEATURES
Location/Qualifiers
source 1..1882
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3343795"
/tissue_type="Eye, retinoblastoma"
/clone_lib="NIH_MGC_16"
/lab_host="DH10B-R"
/note="Vector: pOTB7"
BASE COUNT 352 a 609 c 572 g 349 t
ORIGIN
Query Match 32.0%; Score 583.8; DB 11; Length 1882;
Best Local Similarity 98.8%; Pred. No. 2.le-118;
Matches 588; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1172 CGCCAAAGAGAGCCGGCTGGCAGCGCCCAACCCACGCCCGCTCCAGCCCCAGCGTCG 1231
DB 3 CACGAGGGAGAGCCCGCTGGCAGCGCCCAACCCACGCCCGCTCCAGCCCCAGCGTCG 62
QY 1222 GAGGGTCCCTGGAGGCGCGGCTCAACTCATCAAGAACAGCTTTCTGGGCTCACCCC 1291
DB 63 GAGGGTCCCTGGAGGCGCGGCTCAACTCATCAAGAACAGCTTTCTGGGCTCACCCC 122
QY 1292 GCTTCCACCGCGGAACTGCAAGTTCCGAGCCGAGGAGATGCCACTGACACGAG 1351
|||||
123 GCTTCCACCGCGGAAACTGCAAGTTCCGAGCCGAGGAGATGTCACCACTGACACCAG 182
1352 AGTCGTCCTCCAGAGCTGGCGAAGAACTCTGTTGGGAACCTTCATCAGCTGGAGAGG 1411
183 AGTCGTCCTCCAGAGCTGGCGAAGAACTCTGTTGGGAACCTTCATCAGCTGGAGAGG 242
1412 AGGAGCAGATCTTCTGTTGGTTCATCAAAAGACAAACCTCTGAGCTCCATCAGGCTGACATCG 1471
243 AGGAGCAGATCTTCTGTTGGTTCATCAAAAGACAAACCTCTGAGCTCCATCAGGCTGACATCG 302
1472 TGACAGCTCTCTGTTGGTTCATCCAGTCTCAGCCACACGCTCATCTCCCAACAGGCTTCC 1531
303 TGACAGCTCTCTGTTGGTTCATCCAGTCTCAGCCACACGCTCATCTCCCAACAGGCTTCC 362
1532 GGGCCGAGTACAAAGGCGACGCGGGGGCCAGCGCTGTTCCAGAAAGCGGTCGAAGTTCCAGG 1591
363 GGGCCGAGTACAAAGGCGACGCGGGGGCCAGCGCTGTTCCAGAAAGCGGTCGAAGTTCCAGG 422
1592 TTGATATACCTACACGAGGAGGTGGGGAGCGCGAGAAAGGAGAACGGCATCTACTCCGTCA 1651
423 TTGATATACCTACACGAGGAGGTGGGGAGCGCGAGAAAGGAGAACGGCATCTACTCCGTCA 482
1652 CTTTACCTCTCTCTCAGGCCCGCCAGCGCTGCTTCAAGAGGTTGGTGGAGACCATCCAGG 1711
483 CTTTACCTCTCTCTCAGGCCCGCCAGCGCTGCTTCAAGAGGTTGGTGGAGACCATCCAGG 542
1712 CCCAGCTGTGTAGCACACACGACCGCCCGCTGGCGCCAGCACTTGTGAGACACACAC 1766
543 CCCAGCTGTGTAGCACACACGACCGCCCGCTGGCGCCAGCACTTGTGAGACACACCC 597

RESULT 9
BC180079
LOCUS
DEFINITION UI-M-EWO-bmw-d-22-0-UI.r1 NIH_BMAP_EWO Mus musculus cDNA clone
            IMAGE:5703909 5', mRNA sequence.
ACCESSION BC180079
VERSION BC180079.1 GI:20355571
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE NIH-MGC http://mgc.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. James Lin, University of Iowa
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
Seq primer: pyX-5.
Location/Qualifiers
source 1..712
/mol_type="mRNA"
/organism="Mus musculus"
/strains="C57BL/6"
/db_xref="taxon:10090"
/tissue_type="whole brain"
/dev stage="embryo 15.5 dpc"
/lab_host="DH10B (r1 phage resistant)"
/clone_lib="NIH_BMAP_EWO"
/note="Organ: brain; Vector: pyX-Abs; Site 1: EcoR I;
Site 2: Not I; The library was constructed according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,

```

1996. Denatured mRNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, and ligated with EcoR I adaptor, digested with Not I, and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is GTGGGTGAA. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP). Gene Discovery in the Developing Mouse Nervous System, supported by National Institutes of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

BASE COUNT 167 a 211 c 193 g 139 t 2 others
ORIGIN
Query Match 31.4%; Score 574.2; DB 13; Length 712;
Best Local Similarity 88.6%; Pred. No. 2.2e-116;
Matches 632; Conservative 0; Mismatches 80; Indels 1; Gaps 1;
QY 463 CCCTTCGACGATGACAACTTTCGACAGCTGCTCGAGAGGTGAAGCGGGCGTGTTCAC 522
DB 1 CTTTGTGATGATGACAACTTTCGCGAGTGTCTGGAGAGGTCAAGCGTGTGTTCAC 60
QY 523 ATGCGGACATTTATCCGCGCCGACTGCGAGAGTCTGCTACGGGGCATGATCGAGGTGAC 582
DB 61 ATGCCACACTTTATCCACAGACTGCCAGAGTCTCTGGTGGCATGATTGAGTGGAT 120
QY 583 GCCGACGCGCCCTCAGCTAGAGCATTTCAGAAACATATGTTATATAGGGGCAAG 642
DB 121 GCAGCTCGGCGCTCAGCTAGAGCATTTCAGAAACATATGTTATATAGTGGCAAG 180
QY 643 AATGAGCCGAAACAGAGCAGCCATTCCTCGAAGGTGCAGATCCGCTCGTCCCGAGC 702
DB 181 AATGAGCCGAGCCGAGAGCCATCCAGCGAGGTGCAGATCCGCTCACTACCCAGC 240
QY 703 CTGAGGAGATTCGACCCGAGCTGTGGAAGATGACATCTCATGGGTGCTTCCGAGAC 762
DB 241 TTGGAAGACATTTGACCTGTGTTGGAGAGCATGCACTCACTGGGCTGCTTCCGAGAC 300
QY 763 CGCAACAGCTGTGCGAGGACCTGCTGTCGAGGAGGAGAACAGAGAGATGATTAC 822
DB 301 CGCAACAGCTGTGCGAGGATCTCTGATCTGAGGAGGAGATCAGGAAAGATGATTAT 360
QY 823 TTCTCTCTCTGGAACGGAAGAGTATCCGAGCCAGGAGGATGAGGACCTGCCCGCC 882
DB 361 TTCTCTCTCTGATCGGAAGACGTATCCAGCCATGAGGATGAGGACCTGCCCGCC 420
QY 883 CGGAACGAGATAGACCTTCCCGGAAGCGGTGTGAGTCTCCCGATGCTGAACCGGCGAGC 942
DB 421 AGGAATGAGATAGACCTTCCCGGAAGCGGTGTGAGTCTCCCGATGCTGAACCGGCGATG 480
QY 943 AAGCGGCGCCAGAACCAATCCATGAGGTGCTCAGCGTGAGGAGCGGCGCTCCCG 1002
DB 481 AAGCGGCGACTGAGCGCAAGTCCATGAAAGTGTCTAGTGTGAGATGTGGTGTCTCCCA 540
QY 1003 GTGCTCGCGCGCGGCAATGAGATGCCAGCAGCGCCAGAGGTCTCGGTTCATCAGC 1062
DB 541 GTGCTCGACGAGAGCCATTGAGATGGCCAGCATGCGCAGAGATCTCGATCCATCAGT 600
QY 1063 GGTGCTCTCAGGCGCTTTCACAGGCCACTACAGAGCGCCCGGGTGACCCCTCACCCC 1122
DB 601 GGTGCTCTCAGGCGCTTTCACAGGCCACTACAGAGTCTCTCGGGTGACCCCTCACCCC 660
QY 1123 TCACCAAGGGGCGCTTCCCTCCACCCCAAGGGGACCTGTCCACAGCC 1175
DB 661 TCACCAAGGGGCGTGT-CCCTTCTTACCCCAAGGGGAGCGCTGTCCACAGCC 712

RESULT 10
BF222739/c
LOCUS
DEFINITION

7q32f02.x1 NCI CGAP GC6 Homo sapiens cDNA clone IMAGE:369987 3',
similar to TR:O60843 O60843 PUTATIVE SERINE/THREONINE PROTEIN

KINASE i, mRNA sequence.
BF222739
BF222739.1 GI:11129830
EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eukarya; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eukarya; Primates; Carnivora; Hominidae; Homo.
REFERENCE 1 (bases 1 to 740)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNL, send email to:
info@image.llnl.gov
High quality sequence stop: 492.
FEATURES
Location/Qualifiers
1..740
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:369987"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/clone_lib="NCI CGAP GC6"
/note="Vector: pRT3D-Pac (Pharmacia) with a modified
polylinker; Site: 1: Not 1; Site 2: Eco RI; Plasmid DNA
from the normalized library NCI CGAP GC4 was prepared, and
ss circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (cloneIDs
1257096-1259631, 1469064-1470983, and 1475592-1476743).
Subtraction by Bento Soares and M. Fatima Bonaldo."
BASE COUNT 125 a 206 c 241 g 163 t 5 others
ORIGIN
Query Match 30.8%; Score 562.2; DB 10; Length 740;
Best Local Similarity 97.8%; Pred. No. 9.9e-114;
Matches 578; Conservative 0; Mismatches 12; Indels 1; Gaps 1;
QY 1221 CCCACGCTCGGA-GGGGTGCGCTGGAGGGCGCGCTCAACTCCATCAAGAACAGCTTTC 1279
DB 721 CCCACGCTCGNAGGGGTGCGCTGGAGGGCGCGCTCAACTCCATCAAGAACAGCTTTC 662
QY 1280 TGGGCTCACCCGCTTCCACCGCGGAAACTGCAAGTTCGAGCGCGGAGGAGATGCCA 1339
DB 661 TGGGCTCACCCGCTTCCACCGCGGAAACTGCAAGTTCGAGCGCGGAGGAGATGCCA 602
QY 1340 ACCTGACACAGAGTCTGCCAGAGCTGGCAAGAGTCTGTTGGGAACTTCATCA 1399
DB 601 ACCTGACACAGAGTCTGCCAGAGCTGGCAAGAGTCTGTTGGGAACTTCATCA 542
QY 1400 GCTGAGAGAGGAGGAGAGATCTTCTGTTGTCATCAAGACAAACCTCTGAGCTCCATCA 1459
DB 541 GCTGAGAGAGGAGGAGAGATCTTCTGTTGTCATCAAGACAAACCTCTGAGCTCCATCA 482
QY 1460 AGGCTGACATGCTGACAGCGCTTCTGTTGTCATCAAGAGTCTGAGCTCATCTCC 1519
DB 481 AGGCTGACATGCTGACAGCGCTTCTGTTGTCATCAAGAGTCTGAGCTCATCTCC 422
QY 1520 AAACGAGCTTCCGGGCGGAGTACAGGCCACCGGGGGCGGCGCTGTTCCAGAGCCGG 1579
DB 421 AAACGAGCTTCCGGGCGGAGTACAGGCCACCGGGGGCGGCGCTGTTCCAGAGCCGG 362

Qy	1580	TCAAGTTCCAGGTTGATATCACTACACGAGGGTGGGAGCGCGAAGAGGAACGGCA	1639
Db	361	TCAGTTCCAGGTTGATATCACTACACGAGGGTGGGAGCGCGAAGAGGAACGGCA	302
Qy	1640	TCCTACTCCGTCACCTTCACCCCTGCTCTCAGGCCCCAGCCGTCGCTTCAAGAGGGTGGTGG	1699
Db	301	TCCTACTCCGTCACCTTCACCCCTGCTCTCAGGCCCCAGCCGTCGCTTCAAGAGGGTGGTGG	242
Qy	1700	AGACCATTCCAGGCCACGCTGCTAGCACACACACCCGCTCGGGGCCACGACTTGTTCAG	1759
Db	241	AGACCATTCCAGGCCACGCTGCTAGCACACACACCCGCTCGGGGCCACGACTTGTTCAG	182
Qy	1760	ACACCACTAACTGATATGAAATGATACGGGGCGGGCTTCCAAATGTGGAA	1810
Db	181	ACACCACTAACTGATATGAAATGATACGGGGCGGGCTTCCAAATGTGGCA	131

RESULT 11
BE251924
LOCUS
DEFINITION
601107590f1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343822 5',
mRNA sequence.
ACCSSION
VERSION BE251924
KEYWORDS BE251924.1 GI:9122058
SOURCE EST.
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae, Homo.
REFERENCE
AUTHORS 1 (bases 1 to 563)
TITLE NIH-MGC <http://mgc.nci.nih.gov/>.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished
Contact: Robert Strausberg, Ph.D.

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BASE COUNT      122 a   190 c   158 g
ORIGIN
      Note: this is a NIH_MGC Library.
Query Match      30.6%; Score 559.8; DB 10; Length 563;
Best Local Similarity 99.6%; Pred. No. 3.1e-113;
Matches 561; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1198 CCCAACCCACGCCCGCTCCAGCCCGCGAGGGGTGCCCTGGAGGGCGCGGCTC 1257
      1 CCCAACCCACGCCCGCTCCAGCCCGCGAGGGGTGCCCTGGAGGGCGCGGCTC 60
Db
QY 1258 AACTCCATCAAGAACAGCTTTCTTGGGCTCACCCCGCGGAAATGCAAGTT 1317

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Db	61	AACTCCATCAAGAAACAGCTTTC	TGGGCTCACCCCGCTCCACCGCGGAAAATCTC	AGTT	120
Qy	1318	CCGACGCGGAGAGAGATGTC	AACTTGACACAGAGTCTGT	CCCCAGAGCTGGCGGAAGAAG	1377
Db	121	CCGACGCGGAGAGAGATGTC	AACTTGACACAGAGTCTGT	CCCCAGAGCTGGCGGAAGAAG	180
Qy	1378	TCTGTGTTGGGAACTTCAT	CAGCCTGGGAAGAGGAGGAGAGATCTT	CGTGTGTCATCAAA	1437
Db	181	TCTGTGTTGGGAACTTCAT	CAGCCTGGGAAGAGGAGGAGAGATCTT	CGTGTGTCATCAAA	240
Qy	1438	GACAAACCTCTGAGCTCCAT	CAAGGCTGACATCGTGCACG	CTTCTGTGATTCCAGT	1497
Db	241	GACAAACCTCTGAGCTCCAT	CAAGGCTGACATCGTGCACG	CTTCTGTGATTCCAGT	300
Qy	1498	CTCAGCCACAGCGTCATCT	CCAAACAGAGTTCCGGGCGGAGTAC	AAAGCCACGGGGGGG	1557
Db	301	CTCAGCCACAGCGTCATCT	CCAAACAGAGTTCCGGGCGGAGTAC	AAAGCCACGGGGGGG	360
Qy	1558	CCAGCGTGTTCAGAAAGCGG	TCAAGTTCCAGTTTGATATCACCT	TACACGAGGGTGGG	1617
Db	361	CCAGCGTGTTCAGAAAGCGG	TCAAGTTCCAGTTTGATATCACCT	TACACGAGGGTGGG	420
Qy	1618	GAGCGGAGAGGAGAACGG	CATCTACTCGGTCACTTCA	CGCTGTCTTAGGCCCCAGC	1677
Db	421	GAGCGGAGAGGAGAACGG	CATCTACTCGGTCACTTCA	CGCTGTCTTAGGCCCCAGC	480
Qy	1678	CGTCTGCTTCAAGAGGGTGG	TGAGACCATCCAGGCC	CCAGCTGTCTGAGCACACACGACCCG	1737
Db	481	CGTCTGCTTCAAGAGGGTGG	TGAGACCATCCAGGCC	CCAGCTGTCTGAGCACACACGACCCG	540
Qy	1738	CTTGGGCGCCAGCACTTG	TCAGA	1760	
Db	541	CTTGGCTGCCAGCACTTG	CAGA	563	

RESULT 12	ACCESSION	REFERENCE
BQ443644	VERSION	AUTHORS
LOCUS	KEYWORDS	TITLE
DEFINITION	SOURCE	JOURNAL
	ORGANISM	COMMENT

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FEATURES
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Location/Qualifiers
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/mol_type="mRNA"
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/lab_host="DH10B (T1 phage resistant)"
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/note="Organ: brain; Vector: pYX-Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured mRNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was size selected according to mRNA size fraction,
ligated with EcoR I adaptor, digested with Not I, and then
cloned directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
, is GTGGCTGGA. This library was created for the
University of Iowa Mouse Brain Molecular Anatomy Project
(BMAP): 'Gene Discovery in the Developing Mouse Nervous
System', supported by National Institutes of Mental Health
(NIMH), Hemin Chin, Ph.D., program coordinator."

BASE COUNT 168 a 179 c 198 g 147 t 1 others

Query Match 30.0%; Score 548.2; DB 13; Length 693;

Best Local Similarity 87.8%; Pred. No. 1.2e-110;

Matches 609; Conservative 0; Mismatches 84; Indels 1; Gaps 1;

207 GGACTTCTGCCACAGCAGCTCCATATGCCACAGGATCTGAAACCTGAAACCTCTGCT 266

Db 1 GGACTTCTGCCACAGCAGCTCCATATGCCATAGAGACTTGAAGCCAGAGAACCTGCTGCT 60

267 GGACGAGAGAACACATCCGATCGCAGACTTTGGCATGGCTCCTCGAGGTTGGCA 326

Db 61 AGATGAGAGAAC-ACATCCGATTTGCAGACTTTGGCATGGCATCCCTCGAGTGGGAGA 119

327 CAGCCTGTTGGAGACAGCTGTGGTCCCCCACTACGCTCGCCCGAGGTGATCCGGGG 386

Db 120 CAGCCTGTTGGAGACAGCTGTGGATCTCCACATATGCTGTCCGGAAGTATTCGGGG 179

387 GGAGAGATATGACGGCCGGAAGCGGAGCTGTGGAGCTGCGGCGTATCTGTTCGCTT 446

Db 180 CGAGAGATATGATGGCCGCAAGGCAGATGTGTGGAGCTGTGTGATCTGTTCGCTT 239

447 GCTGGTGGGGCTGTGCTTCCAGATGACACTTGCAGACGCTCTGGAGAGGTGAA 506

Db 240 GCTGGTGGGGCTGTGCTTTCATGATGACACCTTCGCGCAGTGTCTGGAGAGGTCAA 299

507 GCGGGGCGTGTTCACATGCGCAGCTTTATCCGCGCCGACTGCGCAGATCTGCTACGGGG 566

Db 300 GCGTGGTGTGTTCACATGCGCAGCTTTATCCACACAGACTGCGCAGATCTCTCGGTGG 359

567 CATGATCGAGGTGACCGCGCAGCGCCCTCAGCTAGAGCAATTCAGAAAACATATG 626

Db 360 CATGATCGAGGTGATGATGAGCTGCGGCGCTCAGCTAGAGCAATTCAGAAAACATATG 419

627 GTATATAGGGGGCAAGATGAGCCGACAGAGCAGCGCCATTCCTCGCAAGGTGAGAT 686

Db 420 GTATATAGGGTGGCAAGAAATGAGCCAGAGCGCCGAAACAGCCCATCCCAAGGTGAGAT 479

687 CCGTCTGCTGCCAGCTCGAGAGACATCGACCCCGAGCTGTGGAGCATGCACTCACT 746

Db 480 CCGTCTACTACCCAGCTTGGAGACATGACCTGTGTTGGACAGCATGCACTCACT 539

747 GGGTGTCTCCGAGACCGCAACAAAGTGTGTGGAGACCTGCTGTCCGAGAGAGAACCA 806

Db 540 GGGTGTCTCCGAGACCGCAACAAAGTGTGTGGAGACCTGCTGTCCGAGAGAGAACCA 599

807 GGAGAGATGATTTACTTCTCTCTGAGCCGGAAGAGGTACCCGAGCCAGGAGGA 866

Db 600 GGAAAGATGATTTACTTCTCTCTGAGCCGGAAGAGGTACCCGAGCCAGGAGGA 659

867 TGAGGACCTGCCCCCGGGAACGAGATAGACCTT 900

Db 660 TGAGGACCTGCCCCCGGGAATGAGATAGACCTT 693

RESULT 13

BE259121

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BE259121 589 bp mRNA linear EST 13-JUL-2000

601107773F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343795 5',

mRNA sequence.

BE259121 GI:9129619

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

Plate: LLCM129 row: b column: 20.

Location/Qualifiers

1..589

/organism="Homo sapiens"

/mol_type="mRNA"

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/clone="IMAGE:3343795"

/tissue_type="retinoblastoma"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH MGC 16"

/note="Organ: eye; Vector: pOTB7; Site 1: XhoI; Site 2:

EcoRI; cDNA made by oligo-dT priming. Directionally

cloned into EcoRI/XhoI sites using the following 5'

adaptor: GGCACGAG(G). Library constructed by Ling Hong

in the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies).

Note: this is a NIH_MGC Library."

BASE COUNT 125 a 190 c 177 g 97 t

ORIGIN

Query Match 28.2%; Score 515; DB 10; Length 589;

Best Local Similarity 99.0%; Pred. No. 2.5e-103;

Matches 518; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

1174 CCAAGAGAGAGCCCGCTGGCACGCGCCCAACCCACGCCCCCTCCAGCCCGCTCGGA 1233

Db 31 CGAGGGGAGAGCCCGCTGGCACGCGCCCAACCCACGCCCCCTCCAGCCCGCTCGGA 90

1234 GGGGTGCTCTGGAGGGCGGCTCAACTCCATCAAGACAGCTTTCTGGGCTCACCCCGC 1293

Db 91 GGGGTGCTCTGGAGGGCGGCTCAAGCCATCAAGAACAGCTTTCTGGGCTCACCCCGC 150

1294 TTTCACCGCGGAAACTGCAAGTTCGACGCGCGGAGGAGATGCCAACCTGACACAGAG 1353

Db 151 TTTCACCGCGGAAACTGCAAGTTCGACGCGCGGAGGAGATGCCAACCTGACACAGAG 210

1354 TCGTCCCCAGAGCTGGCGAAGTTCCTGGTTTGGGAATTCATCAGCCTGAGAGGAG 1413

Db 211 TCGTCCCCAGAGCTGGCGAAGTTCCTGGTTTGGGAATTCATCAGCCTGAGAGGAG 270

1414 GAGCAGATCTTCTGGTTCATCAAGACAACTCTGAGCTCCATCAAGCTCAGATCGTG 1473

Db 271 GAGCAGATCTTCTGGTTCATCAAGACAACTCTGAGCTCCATCAAGCTCAGATCGTG 330

1474 CAGCGCTTCTCTGTCGATTCCTCCAGTCTCAGCCACAGCGTCTATCCCAAACGAGCTTCGG 1533

Db 331 CAGCGCTTCTCTGTCGATTCCTCCAGTCTCAGCCACAGCGTCTATCCCAAACGAGCTTCGG 390

Qy	1534	GCCAGTACAAAGGCCACGGGGGGGCCAGCGGTGTTCAGAAAGCGGTCAAGTTCCAGGTT	1593
Db	391	GCCAGGTACAAAGGCCACGGGGGGGCCAGCGGTGTTCAGAAAGCGGTCAAGTTCCAGGTT	450
Qy	1594	GATATCACCTACACGAGGGTGGGGAGCGCCAGAGGAGAACGGCATCTACTCGGTCAAC	1653
Db	451	GATATCACCTACACGAGGGTGGGGAGCGCCAGAGGAGAACGGCATCTACTCGGTCAAC	510
Qy	1654	TTCAACCTGCTCTCAGGCCCCAGCGCTCGCTTCAAGAGGGTGG	1696
Db	511	TTCAACCTGCTCTCAGGCCCCAGCGCTCGCTTCAAGAGGGTGG	553

RESULT	14
CA319314	
LOCUS	CA319314
DEFINITION	UT-M-FW0-cbz-i-20-0-UI.r1 NIH BMAP_FW0 Mus musculus linear EST 26-NOV-2002
ACCESSION	CA319314
VERSION	CA319314.1
KEYWORDS	GI:24537438
SOURCE	EST.
ORGANISM	Mus musculus (house mouse)
REFERENCE	Mus musculus
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
JOURNAL	1. (bases 1 to 699)
COMMENT	NTH-MGC http://mgc.nci.nih.gov/ . National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Dr. Jim Lin, University of Iowa cDNA Library preparation: Dr. M. Bento Soares, University of Iowa cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov This clone was contributed by the Brain Molecular Anatomy Project (BMAP) Seq primer: pYX-5.

BASE COUNT	169 a	237 c	182 g	108 t	3 others
ORIGIN					
Query Match	27.2%; Score 496.8; DB 14; Length 699;				
Best Local Similarity	86.9%; Pred. No. 2.7e-99;				
Matches 546; Conservative	0; Mismatches 82; Indels 0; Gaps 0;				

RESULT 15	BI825755	603072158FI NTH_MGC_119	727 bp	mRNA	linear	EST 04-OCT-2001
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DEFINITION	BI825755	603072158FI NTH_MGC_119	727 bp	mRNA	linear	EST 04-OCT-2001
ACCESSION	BI825755	603072158FI NTH_MGC_119	727 bp	mRNA	linear	EST 04-OCT-2001
VERSION	BI825755.1	GI:15937305				
KEYWORDS	EST.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
TITLE	1 (bases 1 to 727)					
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/ .					
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)					
	Unpublished					
	Contact: Robert Strausberg, Ph.D.					
	Email: cgapbs-r@mail.nih.gov					
	Tissue Procurement: Life Technologies, Inc.					
	cDNA Library Preparation: Life Technologies, Inc.					
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)					
	DNA Sequencing by: Incyte Genomics, Inc.					
	Clone distribution: MGC clone distribution information can be					
	found through the I.M.A.G.E. Consortium/LLNL at:					
	http://image.llnl.gov					
	Plate: LLAM11407 row: d column: 16					
	High quality sequence stop: 727.					

FEATURES
source

Location/Qualifiers

1. .727
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:516399"
/tissue_type="medulla"
/lab_host="DH10B"
/clone_lib="NIH_MGC_119"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: EcoRV (destroyed); RNA source normal medulla from
anonymous male age 27. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.3 kb, insert size range
0.9-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 013. Note:
this is a NIH MGC Library."
161 a 238 c 204 g 124 t

BASE COUNT
ORIGIN

Query Match 27.1%; Score 495.2; DB 12; Length 727;
Best Local Similarity 98.9%; Pred. No. 6.2e-99;
Matches 530; Conservative 0; Mismatches 3; Indels 3; Gaps 3;

QY 1234 GGGGTGCCCTGGAGGGCGGCGC-TCAACTCCATCAAGACAGCTTTCTGGGCTCACCCCG 1292
DB 1 GGGGTGCCCTGGAGGGCGGCGCTCACTCCATCAAGACAGCTTTCTGGGCTCACCCCG 60

QY 1293 CTTCCACCGCCGGAACCTGCAA-GTTCCGACCGGAGGAGATGTCCAACTGACACACAG 1351
DB 61 CTTCCACCGCCGGAACCTGCAAGGTTCCGACCGGAGGAGATGTCCAACTGACACACAG 120

QY 1352 AGTCGTCCCGAGAGCTGGCGAAGTCTCTGGTTCGGAACTTCATCAGCTGGAGAGG 1411
DB 121 AGTCGTCCCGAGAGCTGGCGAAGTCTCTGGTTCGGAACTTCATCAGCTGGAGAGG 180

QY 1412 AGGAGCAGATCTTCGTGGTTCATCAAGACAAACCTCTGAGCTCCATCAAGGCTGACATCG 1471
DB 181 AGGAGCAGATCTTCGTGGTTCATCAAGACAAACCTCTGAGCTCCATCAAGGCTGACATCG 240

QY 1472 TGCAAGCTTTCCTGTGTAATTCACAGTCTCAGCCACAGCGTCATCTCCCAAACGAGCTTCC 1531
DB 241 TGCAAGCTTTCCTGTGTAATTCACAGTCTCAGCCACAGCGTCATCTCCCAAACGAGCTTCC 300

QY 1532 GGGCCGAGTACAGGCCACAGGGGGCCAGCCGTTTCCAGAGCCGTCAGTTCAGG 1591
DB 301 GGGCCGAGTACAGGCCACAGGGGGCCAGCCGTTTCCAGAGCCGTCAGTTCAGG 360

QY 1592 TTGATATCACCTACACCG-AGGGTGGGAGGCGCAGAGGAGAACGGCATCTACTCCGTC 1650
DB 361 TTGATATCACCTACACCGTAGGTGGGAGGCGCAGAGGAGAACGGCATCTACTCCGTC 420

QY 1651 ACCTTACCTCTCTCAGGCCCGAGCGCTGCTTCAAGAGGGTGGTGGAGACATCCAG 1710
DB 421 ACCTTACCTCTCTCAGGCCCGAGCGCTGCTTCAAGAGGGTGGTGGAGACATCCAG 480

QY 1711 GCCCAGTGTGAGCACACAGCCCGCTGCGCCCGAGCACTTGTTCAGACACACAC 1766
DB 481 GCCCAGTGTGAGCACACAGCCCGCTGCGCCCGAGCACTTGTTCAGACACACAC 536

Search completed: November 27, 2003, 11:05:17
Job time : 3469.16 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 27, 2003, 09:04:30 ; Search time 1060.75 Seconds
(without alignments)
5674.682 Million cell updates/sec

Title: US-10-054-579-3
Perfect score: 1827
Sequence: 1 atgaagtgaggcggagat.....gaattatcccgaaagtaa 1827

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2190069 seqs, 1647345023 residues
Total number of hits satisfying chosen parameters: 4380138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
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- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
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- 16: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1827	100.0	1827	13	US-10-054-579-3 Sequence 3, Appli
2	1827	100.0	2007	13	US-10-054-579-1 Sequence 1, Appli
3	1827	100.0	2647	12	US-10-288-798-42 Sequence 42, Appli
4	1825.4	99.9	2908	14	US-10-195-072-1 Sequence 1, Appli
5	1825.4	99.9	2908	14	US-10-195-071-1 Sequence 1, Appli
6	1813	99.2	3364	14	US-10-195-072-3 Sequence 3, Appli
7	1813	99.2	3364	14	US-10-195-071-3 Sequence 3, Appli
8	1761.2	96.4	2025	14	US-10-283-247-1 Sequence 1, Appli
9	1759.6	96.3	2025	10	US-09-842-582-3 Sequence 3, Appli
10	1759.6	96.3	2219	10	US-09-842-582-1 Sequence 1, Appli
11	1685.2	92.2	1911	14	US-10-283-247-4 Sequence 4, Appli
12	851.4	46.6	2112	12	US-10-116-326-5 Sequence 5, Appli
13	851.4	46.6	2137	12	US-10-116-326-1 Sequence 1, Appli
14	851.4	46.6	2980	12	US-10-354-358-91 Sequence 91, Appli
15	777.2	42.5	2289	12	US-10-116-326-3 Sequence 3, Appli
16	594	32.5	2173	12	US-10-102-558-1 Sequence 1, Appli

17	594	32.5	2173	14	US-10-102-558-1	Sequence 1, Appli
18	291.6	16.0	512	10	US-09-960-253-87	Sequence 87, Appli
19	232.4	12.7	1594	14	US-10-284-060-1	Sequence 1, Appli
20	232.4	12.7	1594	14	US-10-284-060-3	Sequence 3, Appli
21	225	12.3	2085	12	US-10-161-565-20	Sequence 20, Appli
22	225	12.3	2278	12	US-10-161-565-21	Sequence 21, Appli
23	225	12.3	3226	10	US-10-161-565-23	Sequence 23, Appli
24	225	12.3	3270	10	US-09-835-081-1	Sequence 1, Appli
25	225	12.3	3609	12	US-10-161-565-19	Sequence 19, Appli
26	225	12.3	4917	12	US-10-161-565-22	Sequence 22, Appli
27	222.8	12.2	2352	9	US-09-815-915-3	Sequence 3, Appli
28	222.8	12.2	2352	12	US-10-393-316-3	Sequence 3, Appli
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31	214.2	11.7	26729	14	US-10-283-247-6	Sequence 6, Appli
32	214.2	11.7	70383	14	US-10-283-247-3	Sequence 3, Appli
33	193.8	10.6	2349	11	US-09-823-187-25	Sequence 25, Appli
34	192.4	10.5	3154	10	US-09-919-585-19	Sequence 19, Appli
35	187.6	10.3	1539	10	US-09-938-842A-2657	Sequence 2657, Ap
36	182.6	10.0	3609	9	US-09-799-875-6	Sequence 6, Appli
37	182.6	10.0	4381	12	US-10-288-798-31	Sequence 31, Appli
38	182.6	10.0	5983	9	US-09-799-875-4	Sequence 4, Appli
39	179	9.8	2086	12	US-10-161-565-4	Sequence 4, Appli
40	179	9.8	2112	10	US-09-919-585-4	Sequence 4, Appli
41	179	9.8	2112	12	US-10-161-565-7	Sequence 7, Appli
42	179	9.8	2222	10	US-09-919-585-7	Sequence 7, Appli
43	179	9.8	2248	12	US-10-161-565-5	Sequence 5, Appli
44	179	9.8	2701	12	US-10-161-565-6	Sequence 6, Appli
45	179	9.8	2784	12	US-10-161-565-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-10-054-579-3
; Sequence 3, Application US/10054579
; Publication No. US20020137913A1
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathuz, Brian
; TITLE OF INVENTION: No. US20020137913A1 Human Kinases and Polynucleotides Encoding t
; FILE REFERENCE: LEX-0300-USA
; CURRENT APPLICATION NUMBER: US/10/054,579
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/263,378
; PRIOR FILING DATE: 2001-01-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1827
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-054-579-3

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Matches 1827;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;
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Db	1	ATGAAGTGGAGCGGAGATCGCGATCCTGAAGCTATTGAGCACCCTCCTAAAG	60	
Qy	61	CTGCACGACGTTTATGAAAACAAAATATTGTACCTGGTGTAGAACACGTCAGGT	120	
Db	61	CTGCACGACGTTTATGAAAACAAAATATTGTACCTGGTGTAGAACACGTCAGGT	120	
Qy	121	GGTGAGCTTTCGACTACCTGGTGAAGAGGGAGGCTGACGCCCTAAGAGGCTCGGAAG	180	
Db	121	GGTGAGCTTTCGACTACCTGGTGAAGAGGGAGGCTGACGCCCTAAGAGGCTCGGAAG	180	
Qy	181	TTCTTCGGGAGATCATCTCTGGCTGGACTTTCGCACAGCCACTCATATGCCACAGG	240	
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241 Db GATCTGAACCTGAAACCTCTCTGCGAGAGAGAACAACTCCGATCGAGACTTT 300
301 Qy GGATGGCGTCCCTGCGAGGTTGGCGACAGCCTGTTGGAGACCAGCTGTGGGTCCCCCAC 360
301 Db GGATGGCGTCCCTGCGAGGTTGGCGACAGCCTGTTGGAGACCAGCTGTGGGTCCCCCAC 360
361 Qy TACGCTGCCCGGAGGTGATTCGGGGGGAGAGATGACGGCGGGAAGGCGGAGCTGTGG 420
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421 Qy AGCTGGCGGTCATCTCTGCTGCTGCTGGGGGCTCTGCGCTTCGACGATGACAAC 480
421 Db AGCTGGCGGTCATCTCTGCTGCTGCTGGGGGCTCTGCGCTTCGACGATGACAAC 480
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541 Qy CCGACTGCCAGAGTCTGCTACGGGGGCAATGATGAGGTGGAGCGCGGCGCTCAAG 600
541 Db CCGACTGCCAGAGTCTGCTACGGGGGCAATGATGAGGTGGAGCGCGGCGCTCAAG 600
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601 Db CTAGAGCACATTCAGAACACATATGTTATAGGGGCAAGATGAGCCCGAACACAGAG 660
661 Qy CAGCCCATTCCTGCAAGGTGAGATCGCTGCTGCTGCGGCGGAGGAGATCGACCCC 720
661 Db CAGCCCATTCCTGCAAGGTGAGATCGCTGCTGCTGCGGCGGAGGAGATCGACCCC 720
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781 Qy GACCTGCTGCTCGAGGAGAGAACACAGAGAGAGATGATTTACTTCTCTCTCTCGACCGG 840
781 Db GACCTGCTGCTCGAGGAGAGAACACAGAGAGAGATGATTTACTTCTCTCTCTCGACCGG 840
841 Qy AAAGAAAGGTACCCGAGCAGAGAGATGAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
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961 Qy AAATCCATGGAGGTGCTCAGCGTGACGAGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
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1201 Qy AACCCCAAGCCCGCTGACGCGGCGAGCGTGGAGGGGTGCTGAGGGGCGGCTGCAAC 1260
1201 Db AACCCCAAGCCCGCTGACGCGGCGAGCGTGGAGGGGTGCTGAGGGGCGGCTGCAAC 1260
1261 Qy TCCATCAAGAACAGCTTTCTGCGGCTCACCCCGCTTCCACCGCGGAACTGCAAGTTCCG 1320
1261 Db TCCATCAAGAACAGCTTTCTGCGGCTCACCCCGCTTCCACCGCGGAACTGCAAGTTCCG 1320

1321 Qy AGCCGAGAGAGATGTCCAACTGACACAGAGTGTCTCCAGAGCTGGCGAAGAGTCC 1380
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1381 Qy TGGTTGGAACTTTCATCAGCCTGAGAGAGGAGAGATCTTCTGTGTCTATCAAGAC 1440
1381 Db TGGTTGGAACTTTCATCAGCCTGAGAGAGGAGAGATCTTCTGTGTCTATCAAGAC 1440
1441 Qy AAACCTCTCAGCTCCATCAAGGCTGACATCGGTGACGCGCTTCTGTGATTCACGCTC 1500
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1501 Qy AGCCACAGCGTCTCTCCCAAGAGCTTCCGGGCGGAGTACAAAGCCACGGGGGGCCCA 1560
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1561 Qy GCGTGTTCAGAGAGCGGTCAAGTTCAGGTTCCAGGTTGATATCACCTACAGGAGGTGGGAG 1620
1561 Db GCGTGTTCAGAGAGCGGTCAAGTTCAGGTTCCAGGTTGATATCACCTACAGGAGGTGGGAG 1620
1621 Qy GCGCAGAGAGAGAGCGCATCTACTCCGTCACTTCACTTCACTTCACTTCACTTCACTT 1680
1621 Db GCGCAGAGAGAGAGCGCATCTACTCCGTCACTTCACTTCACTTCACTTCACTTCACTT 1680
1681 Qy CGCTTCAAGAGAGGTGGAGACCATCCAGGCGGAGTGTGTGAGCACACACGACCGCCT 1740
1681 Db CGCTTCAAGAGAGGTGGAGACCATCCAGGCGGAGTGTGTGAGCACACACGACCGCCT 1740
1741 Qy GCGGCGGAGCTTGTGACACACCATCTTATGTAATGATGAGGCGGCGCTTCC 1800
1741 Db GCGGCGGAGCTTGTGACACACCATCTTATGTAATGATGAGGCGGCGCTTCC 1800
1801 Qy AAATGTGGAATATCCCGAAAGTTAA 1827
1801 Db AAATGTGGAATATCCCGAAAGTTAA 1827

RESULT 2

US-10-054-579-1
; Sequence 1, Application US/10054579
; Publication No. US20020137913A1
; GENERAL INFORMATION:
; APPLICANT: Mathur, Brian
; TITLE OF INVENTION: No. US20020137913A1el Human Kinases and Polynucleotides Encoding t
; FILE REFERENCE: LEX-0300-USA
; CURRENT APPLICATION NUMBER: US/10/054,579
; PRIOR FILING DATE: 2002-01-22
; PRIOR FILING DATE: 2001-01-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-054-579-1

Query Match 100.0%; Score 1827; DB 13; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1827; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAAGTGGAGGGGAGATCGGATCTCTGAAGCTCATTTAGCACCCCCACGCTCTAAAG 60
Db 181 ATGAAGTGGAGGGGAGATCGGATCTCTGAAGCTCATTTAGCACCCCCACGCTCTAAAG 240
Qy 61 CTGACACGCTTTATGAAAACAAAATATTTGTACTGTGTGTAGAACACGTTGAGGT 120
Db 241 CTGACACGCTTTATGAAAACAAAATATTTGTACTGTGTGTAGAACACGTTGAGGT 300
Qy 121 GGTGAGCTCTTCGACTACCTGCTGAGAGGGGAGGCTGACGCTAAGGAGGCTCGAAG 180

Db 301 GGTGAGCTTTTCGACTACCTGGTGAAGAGGGAGGCTGACGCCCTAAGGAGGCTCGGAAG 360
Qy 181 TTCTTCGGGAGATCATCTCTGGCGTGGACTTTCGCCACAGCCACTCATATGCCACAG 240
Db 361 TTCTTCGGGAGATCATCTCTGGCGTGGACTTTCGCCACAGCCACTCATATGCCACAG 420
Qy 241 GATCTGAACCTGAAACCTCTCTCTGGAGAGAGAAACAACATCCGCATCGCAGACTTT 300
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Qy 301 GGCATGGGCTCCCTGCGAGTGGCGAGCAGCTTGTGGAGACAGCTGTGGTCCCCCAG 360
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Qy 361 TACGCTGCCCGGAGGTGATCCGGGGGAGAAATGATGACGCGCGGAAAGCGAGCTGTGG 420
Db 541 TACGCTGCCCGGAGGTGATCCGGGGGAGAAATGATGACGCGCGGAAAGCGAGCTGTGG 600
Qy 421 AGCTGCGGCGTCACTCTCTCTCTGGTGGGGGCTCTGCCCTTCGACGATGACAAC 480
Db 601 AGCTGCGGCGTCACTCTCTCTCTGGTGGGGGCTCTGCCCTTCGACGATGACAAC 660
Qy 481 TTGCGACAGCTGCTGGAGAGGTGAAGCGGGGCTGTTCACATGCCGCACTTTATCCCG 540
Db 661 TTGCGACAGCTGCTGGAGAGGTGAAGCGGGGCTGTTCACATGCCGCACTTTATCCCG 720
Qy 541 CCCGACTGCCAGAGTGTCTACGGGGGATGATCGAGGTGGAGCGCGCGGCTCACG 600
Db 721 CCCGACTGCCAGAGTGTCTACGGGGGATGATCGAGGTGGAGCGCGCGGCTCACG 780
Qy 601 CTAGAGCACATTCAGAAACACATATGTTATATAGGGGGGAGAAATGAGCCCGAACAGAG 660
Db 781 CTAGAGCACATTCAGAAACACATATGTTATATAGGGGGGAGAAATGAGCCCGAACAGAG 840
Qy 661 CAGCCCATCTCTCGAGAGTGCAGATCGCTGCTGCCAGCTGGAGAGCATGCAACCC 720
Db 841 CAGCCCATCTCTCGAGAGTGCAGATCGCTGCTGCCAGCTGGAGAGCATGCAACCC 900
Qy 721 GAGTGTGGAGACATGCTCACTCTGGCTGCTTCGAGAGCGCAACAAGCTGCTCGAG 780
Db 901 GAGTGTGGAGACATGCTCACTCTGGCTGCTTCGAGAGCGCAACAAGCTGCTCGAG 960
Qy 781 GACTGTCTCTCGAGAGGAGAACACAGAGAAATGATTTACTTCTCTCTCTCGACCGG 840
Db 961 GACTGTCTCTCGAGAGGAGAACACAGAGAAATGATTTACTTCTCTCTCTCGACCGG 1020
Qy 841 AAAGAAAGGTACCCGAGCAGAGGATGAGACCTGCCCGGCGGAGCAGATAGACCT 900
Db 1021 AAAGAAAGGTACCCGAGCAGAGGATGAGACCTGCCCGGCGGAGCAGATAGACCT 1080
Qy 901 CCCCAGGAGGTGTGGACTCCCGATGCTGAACCGGACGCGGAGCGGCGGCGGCGG 960
Db 1081 CCCCAGGAGGTGTGGACTCCCGATGCTGAACCGGACGCGGAGCGGCGGCGGCGG 1140
Qy 961 AAATCCATGAGGTGCTCAGCGTGACGAGCGGCGGCTCCCGGCTGCTGCGCGGCGG 1020
Db 1141 AAATCCATGAGGTGCTCAGCGTGACGAGCGGCGGCTCCCGGCTGCTGCGCGGCGG 1200
Qy 1021 ATTGAGATGGCCAGCAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
Db 1201 ATTGAGATGGCCAGCAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
Qy 1081 TCCACAGCCACTCAGCAGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
Db 1261 TCCACAGCCACTCAGCAGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
Qy 1141 CTCCCGACCCCGGAGGACACTGTTCACACGCGCAAGAGAGCGCGGCTGGCAGCGCC 1200
Db 1321 CTCCCGACCCCGGAGGAGACACTGTTCACACGCGCAAGAGAGCGCGGCTGGCAGCGCC 1380
Qy 1201 AACCCAGCGGCGGCTGAGCGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTCAAC 1260
Db 1381 AACCCAGCGGCGGCTGAGCGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTCAAC 1440

Qy 1261 TCCATCAAGAACAGCTTTCTGGGCTCACCCGCTTCCACCGCGGAAACTGCAAGTTCCG 1320
Db 1441 TCCATCAAGAACAGCTTTCTGGGCTCACCCGCTTCCACCGCGGAAACTGCAAGTTCCG 1500
Qy 1321 AGCCCGGAGGAGATGTCCAACTGACACACAGAGTCTGCTCCAGAGCTGGCGAAGAGTCC 1380
Db 1501 AGCCCGGAGGAGATGTCCAACTGACACACAGAGTCTGCTCCAGAGCTGGCGAAGAGTCC 1560
Qy 1381 TGGTTTGGGAACTTTCATCATGCTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1440
Db 1561 TGGTTTGGGAACTTTCATCATGCTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1620
Qy 1441 AAACCTCTGAGCTCCATCAAGCTGACATGCTGACGCGCTTCTGCTGCTGCTGCTGCTGCT 1500
Db 1621 AAACCTCTGAGCTCCATCAAGCTGACATGCTGACGCGCTTCTGCTGCTGCTGCTGCTGCT 1680
Qy 1501 AGCCACAGCGTCACTTCCAAACGAGCTTCCGCGGCGAGGTACAAGGCCACGCGGGGGCCA 1560
Db 1681 AGCCACAGCGTCACTTCCAAACGAGCTTCCGCGGCGAGGTACAAGGCCACGCGGGGGCCA 1740
Qy 1561 GCGTGTTCAGAGAGCGGTCAAGTTCAGGTTCCAGGTTGATATCACTACAGCGAGGTTGGGAG 1620
Db 1741 GCGTGTTCAGAGAGCGGTCAAGTTCAGGTTCCAGGTTGATATCACTACAGCGAGGTTGGGAG 1800
Qy 1621 GCGCAGAGGAGAGCGCATCTACTCCGCTCACTTCCAGCTTCACTCAGCGCCCGAGCGCT 1680
Db 1801 GCGCAGAGGAGAGAGCGCATCTACTCCGCTCACTTCCAGCTTCACTCAGCGCCCGAGCGCT 1860
Qy 1681 CGTTTCAAGAGGTTGGTGGAGACCATCCAGGCGGAGCTGCTGAGGAGCAGACGAGCGGCT 1740
Db 1861 CGTTTCAAGAGGTTGGTGGAGACCATCCAGGCGGAGCTGCTGAGGAGCAGACGAGCGGCT 1920
Qy 1741 GCGGCGGAGCTTGCAGACACCATCACTTATGTAATGATGAGGAGGAGGAGGAGGAGGAG 1800
Db 1921 GCGGCGGAGCTTGCAGACACCATCACTTATGTAATGATGAGGAGGAGGAGGAGGAGGAG 1980
Qy 1801 AAATGTGGAATTTATCCCGAAAGTTAA 1827
Db 1981 AAATGTGGAATTTATCCCGAAAGTTAA 2007

RESULT 3

US-10-288-798-42
; Sequence 42, Application US/10288798
; Publication No. US20030207299A1
; GENERAL INFORMATION:
; APPLICANT: BANDMAN, Olga; NGUYEN, Dannie B.;
; APPLICANT: WALIA, Narinder K.; HAFALIA, April J.A.;
; APPLICANT: YAO, Monique G.; GANDHI, Ameena R.;
; APPLICANT: GURURAJAN, Rajagopal; DING, Li;
; APPLICANT: PATTERSON, Chandra; YUE, Henry;
; APPLICANT: BAUGHN, Mariah R.; TRIBOULEY, Catherine M.;
; APPLICANT: THORNTON, Michael; ELLIOTT, Vicki S.;
; APPLICANT: LU, Yan; ISON, Craig H.;
; APPLICANT: AU-YOUNG, Janice; TANG, Y. Tom;
; APPLICANT: AZIMZAI, Yalda; BURRILL, John D.;
; APPLICANT: MARCUS, Gregory A.; ZINGLER, Kurt A.;
; APPLICANT: LU, Dying Aina M.; LAL, Freeti G.;
; APPLICANT: RAMKUMAR, Jayalaxmi; WARREN, Bridget A.;
; APPLICANT: KEARNEY, Liam; POLICKY, Jennifer L.;
; APPLICANT: THANGAVELU, Kavitha; BURFORD, Neil
; TITLE OF INVENTION: HUMAN KINASES
; FILE REFERENCE: PI-0209 USA
; CURRENT APPLICATION NUMBER: US/10/288,798
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: PCT/US01/27219
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/240,542
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: US 60/238,389
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 60/236,499

;; PRIOR FILING DATE: 2000-09-29
;; PRIOR APPLICATION NUMBER: US 60/234,902
;; PRIOR FILING DATE: 2000-09-22
;; PRIOR APPLICATION NUMBER: US 60/232,654
;; PRIOR FILING DATE: 2000-09-14
;; PRIOR APPLICATION NUMBER: US 60/231,357
;; PRIOR FILING DATE: 2000-09-08
;; PRIOR APPLICATION NUMBER: US 60/229,873
;; PRIOR FILING DATE: 2000-08-31
;; NUMBER OF SEQ ID NOS: 48
;; SOFTWARE: PERL Program
;; SEQ ID NO 42
;; LENGTH: 2647
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc_feature
;; OTHER INFORMATION: Incyte ID No. US20030207299A1 4022651CB1
US-10-288-798-42

Query Match 100.0%; Score 1827; DB 12; Length 2647;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1827; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAGGTGGAGCGGAGATCGCGATCCTGAAGCTCATTTGAGCACCCGCCACGTCCTAAAG 60
DB 169 ATGAAGGTGGAGCGGAGATCGCGATCCTGAAGCTCATTTGAGCACCCGCCACGTCCTAAAG 228

QY 61 CTGACGACGTTTATGAAAAAATAATTTGACTCTGTGTGTAGAACACGTTGTACGGT 120
DB 229 CTGACGACGTTTATGAAAAAATAATTTGACTCTGTGTGTAGAACACGTTGTACGGT 288

QY 121 GGTGAGCTCTTCGACTCTGCTGAGAGGAGGAGGCTGAGCCCTAAGAGGCTCGGAAG 180
DB 289 GGTGAGCTCTTCGACTCTGCTGAGAGGAGGAGGCTGAGCCCTAAGAGGCTCGGAAG 348

QY 181 TTCTCCGGCAGATCATCTCTGCGCTGAGACTTCTGCCACAGCCACTCCATATGCCACAGG 240
DB 349 TTCTCCGGCAGATCATCTCTGCGCTGAGACTTCTGCCACAGCCACTCCATATGCCACAGG 408

QY 241 GATCTGAACCTGAAACCTCTCTGCTGAGAGAGAAACAAACATCCGGATCGAGACTTT 300
DB 409 GATCTGAACCTGAAACCTCTCTGCTGAGAGAGAAACAAACATCCGGATCGAGACTTT 468

QY 301 GGCAATGGCGTCCCTGCGAGTTGGCAGACGCTGTTGGAGACCACTGTGGGTCCCCCCAC 360
DB 469 GGCAATGGCGTCCCTGCGAGTTGGCAGACGCTGTTGGAGACCACTGTGGGTCCCCCCAC 528

QY 361 TACGCTGCCCCCGAGGTGATCCGGGGGAGAGATGACGCGCGGAAAGCGGAGCGTGTGG 420
DB 529 TACGCTGCCCCCGAGGTGATCCGGGGGAGAGATGACGCGCGGAAAGCGGAGCGTGTGG 588

QY 421 AGCTGGCGGTTCATCTCTGCTGCTGCTGGGGGCTCTGCCCTTCGAGATGACAAAC 480
DB 589 AGCTGGCGGTTCATCTCTGCTGCTGCTGGGGGCTCTGCCCTTCGAGATGACAAAC 648

QY 481 TTGGCAGACGCTGCTGGAGAGGTGAAGCGGGCGGTGTTCCACATGCGCGCACTTTATCCCG 540
DB 649 TTGGCAGACGCTGCTGGAGAGGTGAAGCGGGCGGTGTTCCACATGCGCGCACTTTATCCCG 708

QY 541 CCCGACTGCCAGAGTCTGCTACGCGGCGATGATCGAGGTGAGCGCGCACGCGGCTCACG 600
DB 709 CCCGACTGCCAGAGTCTGCTACGCGGCGATGATCGAGGTGAGCGCGCACGCGGCTCACG 768

QY 601 CTAGAGCATTTCAGAAACATATGTTATATAGGGGCGAGATGAGCCCGAACCCAGAG 660
DB 769 CTAGAGCATTTCAGAAACATATGTTATATAGGGGCGAGATGAGCCCGAACCCAGAG 828

QY 661 CAGCCCATCTCTCGCAAGGTGAGATCCGCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
DB 829 CAGCCCATCTCTCGCAAGGTGAGATCCGCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 888

QY 721 GACGTGCTGAGCAGCATGCACTCACTGGGCTGCTTCCGAGACCGCAACAGCTGCTGAG 780

DB 889 GACGTGCTGAGCAGCATGCACTCACTGGGCTGCTTCCGAGACCGCAACAGCTGCTGCAG 948
QY 781 GACCTGCTGCTCGAGGAGAGAACCGAGAGATGATTACTTCTCTCTCTCTCTCTCTCTCTCT 840
DB 949 GACCTGCTGCTCGAGGAGAGAACCGAGAGATGATTACTTCTCTCTCTCTCTCTCTCTCTCT 1008
QY 841 AAAGAAAGGTACCCGAGCCAGGAGATGAGGACTCTCCCGGAGGAGGAGGAGGAGGAGGAGG 900
DB 1009 AAAGAAAGGTACCCGAGCCAGGAGATGAGGACTCTCCCGGAGGAGGAGGAGGAGGAGGAGG 1068
QY 901 CCCGGAAGCGTGTGCACTCCCGATGCTGAACCGGACCGGACCGGAGGAGGAGGAGGAGGAGG 960
DB 1069 CCCGGAAGCGTGTGCACTCCCGATGCTGAACCGGACCGGAGGAGGAGGAGGAGGAGGAGG 1128
QY 961 AATCCATGAGGTGCTCAGCGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1020
DB 1129 AATCCATGAGGTGCTCAGCGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1188
QY 1021 ATTGAGATGGCCAGCAGCAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1080
DB 1189 ATTGAGATGGCCAGCAGCAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1248
QY 1081 TCCACAGCCCACTCAGCAGCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1140
DB 1249 TCCACAGCCCACTCAGCAGCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1308
QY 1141 CTCCCAACCCCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1200
DB 1309 CTCCCAACCCCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1368
QY 1201 AACCCCAACCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1260
DB 1369 AACCCCAACCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1428
QY 1261 TCCATCAAGAAACAGCTTTCTGGGCTCAACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1320
DB 1429 TCCATCAAGAAACAGCTTTCTGGGCTCAACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1488
QY 1321 ACCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1380
DB 1489 ACCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1548
QY 1381 TGGTTTGGGAACTTTCATCAGCCTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1440
DB 1549 TGGTTTGGGAACTTTCATCAGCCTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1608
QY 1441 AAACCTTGAGCTTCCATCAAGGCTGATCGGTGACGCTTCTCTGCTGCTGCTGCTGCTGCTC 1500
DB 1609 AAACCTTGAGCTTCCATCAAGGCTGATCGGTGACGCTTCTCTGCTGCTGCTGCTGCTGCTC 1668
QY 1501 AGCCACAGGCTCATCTCCAAACGAGCTTCCGGGCGGAGTACAAAGGCGCACGGGGGGGCCA 1560
DB 1669 AGCCACAGGCTCATCTCCAAACGAGCTTCCGGGCGGAGTACAAAGGCGCACGGGGGGGCCA 1728
QY 1561 GCGGTGTTCCAGAAAGCGGCTCAAGTTCCAGTTGATATCACTTACACGAGGAGGAGGAGGAG 1620
DB 1729 GCGGTGTTCCAGAAAGCGGCTCAAGTTCCAGTTGATATCACTTACACGAGGAGGAGGAGGAG 1788
QY 1621 GCGCAGAGGAGAAAGGCTATCTACTCGGTCACTTCACTTCACTTCACTTCACTTCACTTCACT 1680
DB 1789 GCGCAGAGGAGAAAGGCTATCTACTCGGTCACTTCACTTCACTTCACTTCACTTCACTTCACT 1848
QY 1681 CGCTTCAAGAGGAGTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1740
DB 1849 CGCTTCAAGAGGAGTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1808
QY 1741 GCGGCCCGAGCACTTGTGAGACCACTTAACTGTATGAAATGATGAGGAGGAGGAGGAGGAGGAG 1800
DB 1909 GCGGCCCGAGCACTTGTGAGACCACTTAACTGTATGAAATGATGAGGAGGAGGAGGAGGAGGAG 1968
QY 1801 AATGTGAAATTTATCCCGAAAAAGTTAA 1827

Db 1969 AAATGTGAATTATCCCGAAAGTTAA 1995

RESULT 4
US-10-195-072-1
; Sequence 1, Application US/10195072
; Publication No. US20030092036A1
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies
; TITLE OF INVENTION: Full-length Serine Protein Kinase in Brain and Pancreas
; FILE REFERENCE: 16U 101 C2
; CURRENT APPLICATION NUMBER: US/10/195,072
; PENDING FILING DATE: 2002-07-15
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2908
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (106)..(2112)
; OTHER INFORMATION:
US-10-195-072-1

Query Match 99.9%; Score 1825.4; DB 14; Length 2908;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1826; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGAAGTGGAGCGGAGATCGCATCTCTGAAGCTCATTTAGACACCCCGCAGTCTCTAAAG 60
Db 286 ATGAAGTGGAGCGGAGATCGCATCTCTGAAGCTCATTTAGACACCCCGCAGTCTCTAAAG 345

Qy 51 CTGCACGACGTTTATGAACAAATAATTTGACCTGGTGTCTAGAACACGTTGTCAGGT 120
Db 346 CTGCACGACGTTTATGAACAAATAATTTGACCTGGTGTCTAGAACACGTTGTCAGGT 405

Qy 121 GGTGAGCTCTTCGACTACTCTGTGAAGAGGGAGGCTGACGCTTAAGAGGCTCGGAAG 180
Db 406 GGTGAGCTCTTCGACTACTCTGTGAAGAGGGAGGCTGACGCTTAAGAGGCTCGGAAG 465

Qy 181 TTCTCCCGCAGATCATCTCTGCGTGGACTTTCTGCCACAGCACTCCATATGCCACAGG 240
Db 466 TTCTCCCGCAGATCATCTCTGCGTGGACTTTCTGCCACAGCACTCCATATGCCACAGG 525

Qy 241 GATCTGAACCTGAACCTCTCTGTCGACGAGAGAAACAACATCCGATCGCAGACTTT 300
Db 526 GATCTGAACCTGAACCTCTCTGTCGACGAGAGAAACAACATCCGATCGCAGACTTT 585

Qy 301 GGCATGGCGTCCCTGACGTTGGCAGACAGCTTTGGAGACACAGCTGGGTGCGCCAC 360
Db 586 GGCATGGCGTCCCTGACGTTGGCAGACAGCTTTGGAGACACAGCTGGGTGCGCCAC 645

Qy 361 TACGCTCCCGCAGGTTGATCCGGGGGAGAGTATGACGCGGAGAGCGGAGCGTGTGG 420
Db 646 TACGCTCCCGCAGGTTGATCCGGGGGAGAGTATGACGCGGAGAGCGGAGCGTGTGG 705

Qy 421 AGCTCGCGGCTCATCTGTCCTGCTGCTGTTGGGGGCTCTGGGCTTCGACGATGACAC 480
Db 706 AGCTCGCGGCTCATCTGTCCTGCTGCTGTTGGGGGCTCTGGGCTTCGACGATGACAC 765

Qy 481 TTGCGACAGCTGCTGAGAGAGTGAAGCGGGCGTGTTCACATCCGCACTTTATCCCG 540
Db 766 TTGCGACAGCTGCTGAGAGAGTGAAGCGGGCGTGTTCACATCCGCACTTTATCCCG 825

Qy 541 CCGCATCCCGCAGGTTCTCTACGGGGCAGTATCGAGGTGAGCGCGCAGCGCGCTCACG 600
Db 826 CCGCATCCCGCAGGTTCTCTACGGGGCAGTATCGAGGTGAGCGCGCAGCGCGCTCACG 885

Qy 601 CTAGAGCACATTGAGAAACATATGTTATATAGGGGGCAAGATGAGCCCGAACCAGAG 660

Db 886 CTAGAGCACATTGAGAAACACATATGTTATATAGGGGGCAAGATGAGCCCGAACCAGAG 945

Qy 661 CAGCCCATTCCTCGCAGGTGAGATCCGCTCGCTGCCAGCCTGGAGGACATCGACCCC 720
Db 946 CAGCCCATTCCTCGCAGGTGAGATCCGCTCGCTGCCAGCCTGGAGGACATCGACCCC 1005

Qy 721 GAGCTGCTGGACAGCATGCACTCACTGGGGTGTCTTCGAGACCGCAACAAGTGTCTGAG 780
Db 1006 GAGCTGCTGGACAGCATGCACTCACTGGGGTGTCTTCGAGACCGCAACAAGTGTCTGAG 1065

Qy 781 GACCTGCTGTCGAGAGGAGAACCCAGGAGAAAGATGATTTACTTCTCTCTGAGACGG 840
Db 1066 GACCTGCTGTCGAGAGGAGAACCCAGGAGAAAGATGATTTACTTCTCTCTGAGACGG 1125

Qy 841 AAAGAAAGGTACCCGAGCAGGAGGATGAGACCTGCCCGCCCGGAAACGAGATAGACCT 900
Db 1126 AAAGAAAGGTACCCGAGCAGGAGGATGAGACCTGCCCGCCCGGAAACGAGATAGACCT 1185

Qy 901 CCCCGGAAGCGTGTGGACTCTCCCGATGCTGAACCGGCACGCGCAAGCGCGGCCAGAACGC 960
Db 1186 CCCCGGAAGCGTGTGGACTCTCCCGATGCTGAACCGGCACGCGCAAGCGCGGCCAGAACGC 1245

Qy 961 AATTCATGAGAGTGTCTACGCTGACGAGCGGGCTCTCCCGGTGCTTCGCGCGCGGGCC 1020
Db 1246 AAGTTCATGAGAGTGTCTACGCTGACGAGCGGGCTCTCCCGGTGCTTCGCGCGCGGGCC 1305

Qy 1021 ATTGAGATGCCCGACGACGCGCAGAGGTCTCGGTCCATCAGCGGTGCTCTCTCAGGGCTT 1080
Db 1306 ATTGAGATGCCCGACGACGCGCAGAGGTCTCGGTCCATCAGCGGTGCTCTCTCAGGGCTT 1365

Qy 1081 TCCACACGCCCACTCAGCAGCCCCCGGGTGACCCCTCACCCCTCACCAAGGGGAGTCCC 1140
Db 1366 TCCACACGCCCACTCAGCAGCCCCCGGGTGACCCCTCACCCCTCACCAAGGGGAGTCCC 1425

Qy 1141 CTCCCAACCCCAAGGGGACACCTGTCTCAACGCGCAAGAGAGCCCGGTGCGACGCC 1200
Db 1426 CTCCCAACCCCAAGGGGACACCTGTCTCAACGCGCAAGAGAGCCCGGTGCGACGCC 1485

Qy 1201 AACCCACGCCCGCTCCAGCCCGCAGCGTGGAGGGTCCCTGGAGGGCGCGCTCAAC 1260
Db 1486 AACCCACGCCCGCTCCAGCCCGCAGCGTGGAGGGTCCCTGGAGGGCGCGCTCAAC 1545

Qy 1261 TCCATCAAGAACAGCTTTCTGGGCTCACCCCGCTTCCACCGCGGAACTGCAAGTTCCG 1320
Db 1546 TCCATCAAGAACAGCTTTCTGGGCTCACCCCGCTTCCACCGCGGAACTGCAAGTTCCG 1605

Qy 1321 AGCGCGAGAGATGTCAAACCTGACACAGAGTGTCTCCCGCAGAGCTGGCGAAGTCC 1380
Db 1606 AGCGCGAGAGATGTCAAACCTGACACAGAGTGTCTCCCGCAGAGCTGGCGAAGTCC 1665

Qy 1381 TGGTTTGGGAACTTCATCAGCCTGGAGAGGAGGAGATCTTCGTTGGTTCATCAAGAG 1440
Db 1666 TGGTTTGGGAACTTCATCAGCCTGGAGAGGAGGAGATCTTCGTTGGTTCATCAAGAG 1725

Qy 1441 AAACCTCTGAGCTCCATCAAGGCTGACATCGTCAGCGCTTCTCTGTCGATTCCAGTCTC 1500
Db 1726 AAACCTCTGAGCTCCATCAAGGCTGACATCGTCAGCGCTTCTCTGTCGATTCCAGTCTC 1785

Qy 1501 AGCCACAGCTCATCTCCCAACGAGCTTCGGGGCGAGTACAAAGCCACGGGGGGGCCA 1560
Db 1786 AGCCACAGCTCATCTCCCAACGAGCTTCGGGGCGAGTACAAAGCCACGGGGGGGCCA 1845

Qy 1561 GCGTGTTCAGAAAGCGGTCAGGTTTCAGGTTTCAGTTGATATCACTTACCGAGGGTGGGGAG 1620
Db 1846 GCGTGTTCAGAAAGCGGTCAGGTTTCAGGTTTCAGTTGATATCACTTACCGAGGGTGGGGAG 1905

Qy 1621 GCGCAGAGGAGAACGGCATCTACTCCGTCACTTCACTTCACTTCTCAGGCCCCCAGCCGT 1680
Db 1906 GCGCAGAGGAGAACGGCATCTACTCCGTCACTTCACTTCACTTCTCAGGCCCCCAGCCGT 1965

Qy 1681 CGCTTCAAGAGGTTGTGAGACCATTCAGGCCCCAGTGTCTGAGCACACAGACCCGCT 1740
Db 1966 CGCTTCAAGAGGTTGTGAGACCATTCAGGCCCCAGTGTCTGAGCACACAGACCCGCT 2025

QY 1741 GCGGCCAGCACTTGTGAGACACCACTAACTGTATGGAATGATGACGGGGCGCTTTCC 1800
Db 2026 GCGGCCAGCACTTGTGAGACACCACTAACTGTATGGAATGATGACGGGGCGCTTTCC 2085
QY 1801 AAATGTGGAATTATCCCGAAAGTTAA 1827
Db 2086 AAATGTGGAATTATCCCGAAAGTTAA 2112

RESULT 5
US-10-195-071-1
; Sequence 1, Application US/10195071
; Publication No. US20030096271A1
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies
; TITLE OF INVENTION: Full-Length Serine Protein Kinase in Brain and Pancreas
; FILE REFERENCE: 160 101 Cl
; CURRENT APPLICATION NUMBER: US/10/195,071
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: US 09/930,181
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2908
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (106)..(2112)
; OTHER INFORMATION:
US-10-195-071-1

Query Match 99.9%; Score 1825.4; DB 14; Length 2908;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1826; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGAAGGTGGAGCGGAGATCGCATCTCTGAAGCTCAATTGAGCACCCGCCAGCTCTCTAAAG 60
Db 286 ATGAAGGTGGAGCGGAGATCGCATCTCTGAAGCTCAATTGAGCACCCGCCAGCTCTCTAAAG 345
QY 61 CTGACGACGTTTATGAAAAAATAATTTGTACCTGTGTGTAGAACACGTTCTCAGGT 120
Db 346 CTGACGACGTTTATGAAAAAATAATTTGTACCTGTGTGTAGAACACGTTCTCAGGT 405
QY 121 GGTGAGCTCTTCGACTACTCTGTGAGAGGGAGGCTGACGCTTAAGAGGCTCGGAAG 180
Db 406 GGTGAGCTCTTCGACTACTCTGTGAGAGGGAGGCTGACGCTTAAGAGGCTCGGAAG 465
QY 181 TTCTTCCGGCAGATCATCTCTGCGCTGGACTTTCTGCCACAGCCACTCCATATGCCACAGG 240
Db 466 TTCTTCCGGCAGATCATCTCTGCGCTGGACTTTCTGCCACAGCCACTCCATATGCCACAGG 525
QY 241 GATCTGAAACCTGAAACCTCTCTGTGAGAGAGAAACAACATCCGATCGCAGACTTT 300
Db 526 GATCTGAAACCTGAAACCTCTCTGTGAGAGAGAAACAACATCCGATCGCAGACTTT 585
QY 301 GGCATGGCGTCCCTGACGTTGGCCACAGCCTGTGTGAGACACAGCTGTGGTCCGCCAC 360
Db 586 GGCATGGCGTCCCTGACGTTGGCCACAGCCTGTGTGAGACACAGCTGTGGTCCGCCAC 645
QY 361 TACGCTTCCCGAGGATGATCCGGGGGAGAGTATGACGCGCGGAGGCGGAGCGTGTGG 420
Db 646 TACGCTTCCCGAGGATGATCCGGGGGAGAGTATGACGCGCGGAGGCGGAGCGTGTGG 705
QY 421 AGCTCGGGGTCATCTGTTGCCCTTGTGTGGGGGCTCTGCCCTTCGACGATGACAAAC 480
Db 706 AGCTCGGGGTCATCTGTTGCCCTTGTGTGGGGGCTCTGCCCTTCGACGATGACAAAC 765
QY 481 TTGCGACAGCTCTCTGAGAGGTGAAGCGGGCGGTTCACATCCGCACTTTATCCCG 540
Db 766 TTGCGACAGCTCTCTGAGAGGTGAAGCGGGCGGTTCACATCCGCACTTTATCCCG 825

QY 541 CCCGACTGCCAGTCTGTACGGGECATGATCGAGGTGGACGCCGCAACGCCGCTCAGC 600
Db 826 CCCGACTGCCAGTCTGTACGGGECATGATCGAGGTGGACGCCGCAACGCCGCTCAGC 885
QY 601 CTAGAGCACAATTCAGAAACACATATGTGTATATAGGGGGCAGAAATGAGCCCCGAAACAGAG 660
Db 886 CTAGAGCACAATTCAGAAACACATATGTGTATATAGGGGGCAGAAATGAGCCCCGAAACAGAG 945
QY 661 CAGCCCATTTCTCGCAAGGTGCAGATCGCTCGCTGCGCCAGCTCGAGGACATCGACCCC 720
Db 946 CAGCCCATTTCTCGCAAGGTGCAGATCGCTCGCTGCGCCAGCTCGAGGACATCGACCCC 1005
QY 721 GACGTGCTGGACAGCATGCACTCACTGGGCTGCTTCCGAGACCGCAACAAAGTGTGCGAG 780
Db 1006 GACGTGCTGGACAGCATGCACTCACTGGGCTGCTTCCGAGACCGCAACAAAGTGTGCGAG 1065
QY 781 GACCTGCTGTCGAGGAGGAGAACACAGGAGAGATGATTTACTTCTCTCTCTGGACCGG 840
Db 1066 GACCTGCTGTCGAGGAGGAGAACACAGGAGAGATGATTTACTTCTCTCTCTGGACCGG 1125
QY 841 AAAGAAAGGTACCCGAGCCAGGAGATGAGGACCTGCCCCCGGAAACGAGATAGACCTT 900
Db 1126 AAAGAAAGGTACCCGAGCCAGGAGATGAGGACCTGCCCCCGGAAACGAGATAGACCTT 1185
QY 901 CCCCGGAAGCTGTGGACTTCCCGATGCTTGAACCGGACCGCAAGCGGCGGCGCAACGC 960
Db 1186 CCCCGGAAGCTGTGGACTTCCCGATGCTTGAACCGGACCGCAAGCGGCGGCGCAACGC 1245
QY 961 AATTCATCGAGGTGCTCAGCGTGACGAGCGGGCTCCCGGTGCTCGGCGGGCGG 1020
Db 1246 AAGTCCATGGAGTGTCTCAGCGTGACGAGCGGGCTCCCGGTGCTCGGCGGGCGG 1305
QY 1021 ATTGAGATGGCCAGCACGCGCCAGAGGTCTCGGTCCATCAGCGGTGCTCTCAGGCGCTT 1080
Db 1306 ATTGAGATGGCCAGCACGCGCCAGAGGTCTCGGTCCATCAGCGGTGCTCTCAGGCGCTT 1365
QY 1081 TCACACAGCCCACTCAGCAGCCCCCGGGTGACCCCTTACCCCTTCAACAGGGGCGAGTCCC 1140
Db 1366 TCACACAGCCCACTCAGCAGCCCCCGGGTGACCCCTTACCCCTTCAACAGGGGCGAGTCCC 1425
QY 1141 CTCGCCACCCCAAGGGGACACCTGTCCACACGCGCAAGAGAGAGCCGGTGGCAGGCC 1200
Db 1426 CTCGCCACCCCAAGGGGACACCTGTCCACACGCGCAAGAGAGAGCCGGTGGCAGGCC 1485
QY 1201 AACCCACGCCCCCGCTCCAGCCCCAGCGGCGGAGGGTGCCTTGGAGGGCGCGGCTCAAC 1260
Db 1486 AACCCACGCCCCCGCTCCAGCCCCAGCGGCGGAGGGTGCCTTGGAGGGCGCGGCTCAAC 1545
QY 1261 TCATCAAGAACAGCTTTCTGGGCTCACCCCGTTCACCGCCGGAAACTGTCAAGTTCCG 1320
Db 1546 TCATCAAGAACAGCTTTCTGGGCTCACCCCGTTCACCGCCGGAAACTGTCAAGTTCCG 1605
QY 1321 ACCCGGAGGAGATGTCACACCTGACACAGAGTCCGTCACAGAGTCCCGCAGAGTGGCGAGAGTCC 1380
Db 1606 ACCCGGAGGAGATGTCACACCTGACACAGAGTCCGTCACAGAGTGGCGAGAGAGTCC 1665
QY 1381 TGGTTTGGGAACCTTCATCAGCTTGGAGAGGAGGAGCAGATCTTCGTGTGTCATCAAGAG 1440
Db 1666 TGGTTTGGGAACCTTCATCAGCTTGGAGAGGAGGAGCAGATCTTCGTGTGTCATCAAGAG 1725
QY 1441 AAACCTCTGAGCTCCATCAAGGCTGACATCGTGCAAGCTTCTGTGATCCAGTCTC 1500
Db 1726 AAACCTCTGAGCTCCATCAAGGCTGACATCGTGCAAGCTTCTGTGATCCAGTCTC 1785
QY 1501 AGCCACAGCTCATCTCCCAACAGCTTCCGGCGCGAGTACAAGGCCACGCGGGGGCCA 1560
Db 1786 AGCCACAGCTCATCTCCCAACAGCTTCCGGCGCGAGTACAAGGCCACGCGGGGGCCA 1845
QY 1561 GCGGTGTTCCAGAGCGGTCAGGTTTCCAGGTTTATATACCTTACACGAGGGGTGGGGAG 1620
Db 1846 GCGGTGTTCCAGAGCGGTCAGGTTTCCAGGTTTATATACCTTACACGAGGGGTGGGGAG 1905

Db 1909 TCTCAGCCACAGCGTCTATCTCCCAAACGAGCTTCGCGGCCGAGTACAAAGCCACGCGGGG 1968
Qy 1557 GCGAGCGGTGTCAGAAAGCGGTCAGATGTCAGGTTGATATCACTACAGGAGGGTGG 1616
Db 1969 GCCAGCGGTGTCAGAAAGCGGTCAGATGTCAGGTTGATATCACTACAGGAGGGTGG 2028
Qy 1617 GGAGCGCAGAGGAGAGCGCATCTACTCGTCGTCACCTTCAACCTGCTCTCAGGCCCCAG 1676
Db 2029 GGAGCGCAGAGGAGAGCGCATCTACTCGTCGTCACCTTCAACCTGCTCTCAGGCCCCAG 2088
Qy 1677 CCGTCGCTTCAAGAGGGTGGTGGAGACCATTCAGGCCCCAGTGTGTGAGCACACAGCC 1736
Db 2089 CCGTCGCTTCAAGAGGGTGGTGGAGACCATTCAGGCCCCAGTGTGTGAGCACACAGCC 2148
Qy 1737 GCCTGCGGCCCCAGCAGTGTGTGAGCACACCACTAATGTGTAATGATGAGCGGGCGCT 1796
Db 2149 GCCTGCGGCCCCAGCAGTGTGTGAGCACACCACTAATGTGTAATGATGAGCGGGCGCT 2208
Qy 1797 TTCCAAATGTGGAATTTATCCCGAAAAGTTAA 1827
Db 2209 TTCCAAATGTGGAATTTATCCCGAAAAGTTAA 2239

RESULT 7
US-10-195-071-3
; Sequence 3, Application US/10195071
; Publication No. US2003096271A1
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies
; TITLE OF INVENTION: Full-Length Serine Protein Kinase in Brain and Pancreas
; FILE REFERENCE: 16U 101 C1
; CURRENT APPLICATION NUMBER: US/10/195,071
; PRIORITY FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: US 09/930,181
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 3364
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (482)..(2239)
; OTHER INFORMATION:
US-10-195-071-3

Query Match 99.2%; Score 1813; DB 14; Length 3364;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1827; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

Qy 1 ATGAAGTGGAGCGGAGATCGGATCTGAACTCATTTGAGCACCCCGCAGTCTCTAAAG 60
Db 409 ATGAAGTGGAGCGGAGATCGGATCTGAACTCATTTGAGCACCCCGCAGTCTCTAAAG 468
Qy 61 CTGACGACGCTTTATGAAAAAATAATTTT---GTACCTGCTGTAGAAACAGTGTG 116
Db 469 CTGACGACGCTTTATGAAAAAATAATTTTGTAGTACCTGCTGTAGAAACAGTGTG 528
Qy 117 AGGTGGTGAAGCTCTTCGATACCTGCTGTAAGAGGAGGCTGACGCTTAAGAGGCTCG 176
Db 529 AGGTGGTGAAGCTCTTCGATACCTGCTGTAAGAGGAGGCTGACGCTTAAGAGGCTCG 588
Qy 177 GAAGTTCTTCGGGAGATCATCTCGGCTGAGCTTCTGCGCACGCCACTTCATATGCCA 236
Db 589 GAAGTTCTTCGGGAGATCATCTCGGCTGAGCTTCTGCGCACGCCACTTCATATGCCA 648
Qy 237 CAGGATCTGAAACCTGAAACCTCTCTGTCGAGAGAAACAACTCCGCATCGCAGA 296
Db 649 CAGGATCTGAAACCTGAAACCTCTCTGTCGAGAGAAACAACTCCGCATCGCAGA 708
Qy 297 CTTTGGCATGGCGTCCCTGCGAGTGGCGACAGCCCTGTTGGAGACCAAGCTGTGGTCCCC 356

Db 709 CTTTGGCATGGCGTCCCTGCGAGTTTGGCGACAGCTGTTGGAGACAGCTGTGGTCCCC 768
Qy 357 CCACTACGCTCCCGGAGGTGATCCGGGGGAGAAATGATGACGGCCGGAAGCGGAGCT 416
Db 769 CCACTACGCTCCCGGAGGTGATCCGGGGGAGAAATGATGACGGCCGGAAGCGGAGCT 828
Qy 417 GTGGAGCTCGCGGCTCATCTGCTTGGCTTGGTGGGGGCTCTGCCCTTCGACGATGA 476
Db 829 GTGGAGCTCGCGGCTCATCTGCTTGGCTTGGTGGGGGCTCTGCCCTTCGACGATGA 888
Qy 477 CAACTTGGCAGAGCTGCTGAGAAAGTGAAGCGGGCGTGTTCACATATCCCGCATTTAT 536
Db 889 CAACTTGGCAGAGCTGCTGAGAAAGTGAAGCGGGCGTGTTCACATATCCCGCATTTAT 948
Qy 537 CCGGCCGAGTCCGAGAGTCTGTAAGGGGATGATCGAGGTGGAGCGCGCAGCCGCT 596
Db 949 CCGGCCGAGTCCGAGAGTCTGTAAGGGGATGATCGAGGTGGAGCGCGCAGCCGCT 1008
Qy 597 CACGCTAGAGCACATTCAGAAAACATATGTTATAGGGGGCAAGAAATGAGCCCGAAC 656
Db 1009 CACGCTAGAGCACATTCAGAAAACATATGTTATAGGGGGCAAGAAATGAGCCCGAAC 1068
Qy 657 AGAGCAGCCCATTCCTGCAAGGTGCAGATCCGCTGCTGCCAGCTTGAGAGACATCGA 716
Db 1069 AGAGCAGCCCATTCCTGCAAGGTGCAGATCCGCTGCTGCCAGCTTGAGAGACATCGA 1128
Qy 717 CCGCGAGCTGTCGAGCAGCATGCTCACTGGGCTGCTTCGAGAGCCGCAACAGCTGCT 776
Db 1129 CCGCGAGCTGTCGAGCAGCATGCTCACTGGGCTGCTTCGAGAGCCGCAACAGCTGCT 1188
Qy 777 GCAGGACCTGCTGTCGAGGAGAGAACAGAGAGAGATGATTTACTTCTCTCTCTGGA 836
Db 1189 GCAGGACCTGCTGTCGAGGAGAGAACAGAGAGAGATGATTTACTTCTCTCTCTGGA 1248
Qy 837 CCGGAAAGAAAGTACCCGAGCAGAGGATGAGAGCTGCCCCCCCCCGGAAACAGATAGA 896
Db 1249 CCGGAAAGAAAGTACCCGAGCAGAGGATGAGAGCTGCCCCCCCCCGGAAACAGATAGA 1308
Qy 897 CCTCTCCCGGAGCGTGTGAGCTCCCGGATGCTGAACCGGCGAGCAAGCGGGCGCAGA 956
Db 1309 CCTCTCCCGGAGCGTGTGAGCTCCCGGATGCTGAACCGGCGAGCAAGCGGGCGCAGA 1368
Qy 957 ACGCAATCCATGAGGTGCTCAGCGTGCAGCGCGCTCCCGGCTGCTGCGCGGCG 1016
Db 1369 ACGCAATCCATGAGGTGCTCAGCGTGCAGCGCGCTCCCGGCTGCTGCGCGGCG 1428
Qy 1017 GGCATTTGATGAGTGGCCAGCAGCGCCAGAGGTCTCGGTTCATCAGCGGTGCTCTCAGG 1076
Db 1429 GGCATTTGATGAGTGGCCAGCAGCGCCAGAGGTCTCGGTTCATCAGCGGTGCTCTCAGG 1488
Qy 1077 CTTTTCACCGCCACTCAGCAGCCCCCGGGGTGACCCCTCACCCCTCACCAAGGGGCGAG 1136
Db 1489 CTTTTCACCGCCACTCAGCAGCCCCCGGGGTGACCCCTCACCCCTCACCAAGGGGCGAG 1548
Qy 1137 TCCCTCTCCCGACCCCAAGGGGACACTGTGCCACGCCAAAGAGAGCCCGGCTGGCAC 1196
Db 1549 TCCCTCTCCCGACCCCAAGGGGACACTGTGCCACGCCAAAGAGAGCCCGGCTGGCAC 1608
Qy 1197 GCCAAACCCACCGCCCCGTCAGCCCCAGCGTTCGAGGGGTGCCCTTGAGGGCGCGGCT 1256
Db 1609 GCCAAACCCACCGCCCCGTCAGCCCCAGCGTTCGAGGGGTGCCCTTGAGGGCGCGGCT 1668
Qy 1257 CAACTCCATCAAGAACAGCTTTCTGGGCTCACCCCGCTTCACCGCGGAAACTGCAAGT 1316
Db 1669 CAACTCCATCAAGAACAGCTTTCTGGGCTCACCCCGCTTCACCGCGGAAACTGCAAGT 1728
Qy 1317 TCCGAGCGCGGAGGATGTCCAACTGACACAGAGTGTCTCCCGAGAGTGTGCGAAGAA 1376
Db 1729 TCCGAGCGCGGAGGATGTCCAACTGACACAGAGTGTCTCCCGAGAGTGTGCGAAGAA 1788
Qy 1377 GTCTGTGGTGGAACTTATCAGCCCTGGAGAGGAGGAGATCTTGTGTGTATCAA 1436

Db	1789	GTCTGTTGGGAACTTTCATCAAGCCTGGAGAGAGGAGCGAGTCTTCGTGTCATCAA	1848
Qy	1437	AGACAAACCTCTGAGCTCCATCAAGGCTGACATCGTGACGCCTTCCTGTGATTCGCCAG	1496
Db	1849	AGACAAACCTCTGAGCTCCATCAAGGCTGACATCGTGACGCCTTCCTGTGATTCGCCAG	1908
Qy	1497	TCTCAGCCACACGTCATCTCCCAACGAGCTTCCGGGCCGAGTACNAGGCCACGGGGGG	1556
Db	1909	TCTCAGCCACAGGTCATCTCCCAACGAGCTTCCGGGCCGAGTACNAGGCCACGGGGGG	1968
Qy	1557	GCCAGCGCTGTTCCAGAAGCGGTCAAGTTCACAGTTGATATCACCTTACACGAGGGTGG	1616
Db	1969	GCCAGCGGTTTCCAGNAGCGGTCAAGTTCACAGTTGATATCACCTTACACGAGGGTGG	2028
Qy	1617	GGAGGCGCAGAGGAGAAACGGCATCTACTCCGTCACTTCAACCTGCTCTCAGGCCCCAG	1676
Db	2029	GGAGGCGCAGAGGAGAAACGGCATCTACTCCGTCACTTCAACCTGCTCTCAGGCCCCAG	2088
Qy	1677	CCGTGCGTTCAAGAGGGTGTGGAGACCATCCAGGCCCCAGCTGCTGAGCACACGACCC	1736
Db	2089	CCGTGCGTTTCAAGAGGGTGTGGAGACCATCCAGGCCCCAGCTGCTGAGCACACGACCC	2148
Qy	1737	GCCTGGGGCCACGACCTTGTTCAGACACCACTTAATGTATGGAATGATGACGGGGGGCT	1796
Db	2149	GCCTGGGGCCACGACCTTGTTCAGACACCACTTAATGTATGGAATGATGACGGGGGGCT	2208
Qy	1797	TTCCAATGTGGAATTATCCGAAAAGTTAA	1827
Db	2209	TTCCAATGTGGAATTATCCGAAAAGTTAA	2239

RESULT 8

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US-10-283-247-1
; Sequence 1, Application US/10283247
; Publication No. US20030119037A1
; GENERAL INFORMATION:
; APPLICANT: NEELAM, Beena et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001304
; CURRENT APPLICATION NUMBER: US/10/283,247
; CURRENT FILING DATE: 2002-10-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2025
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-283-247-1

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Query Match	96.4%	Score 1761.2	DB 14	Length 2025
Best Local Similarity	99.8%	Pred. No. 0		
Matches 1763	Conservative 0	Mismatches 3	Indels 0	Gaps 0
Qy	1	ATGAAGTGTGAGCGGGAGATCGCGATCCTGAAAGCTCATTTGAGCAGCCACCCACGTCCTTAAG	60	
Db	181	ATGAAGTGTGAGCGGGAGATCGCGATCCTGAAAGCTCATTTGAGCAGCCACCCACGTCCTTAAG	240	
Qy	61	CTGCACGACGTTTATGAAAAAATAATTTGTACCTGTGCTAGAACACGTCGTCAAGT	120	
Db	241	CTGCACGACGTTTATGAAAAAATAATTTGTACCTGTGCTAGAACACGTCGTCAAGT	300	
Qy	121	GGTGAGCTCTTCGACTACCTGGTGAAGAGGGGAGGCTGACGCCCTAAGGAGGCTCGAAG	180	
Db	301	GGTGAGCTCTTCGACTACCTGGTGAAGAGGGGAGGCTGACGCCCTAAGGAGGCTCGAAG	360	
Qy	181	TTCTTTCGGGAGATCATCTCTGCGCTGGACTTTCTGCCACAGCCACTCCATATGCCACAGG	240	
Db	361	TTCTTTCGGGAGATCATCTCTGCGCTGGACTTTCTGCCACAGCCACTCCATATGCCACAGG	420	
Qy	241	GATCTGAAAACCTGAAAACCTCTCCTCGGACGAGAAGAAACAATCCGCATCGCAGACTTT	300	


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Db 1493 TCCATCAAGAACAGCTTTCTGGGCTCACCCGCTTCCACCGCGGAACCTGCAAGTTCCG 1552
Qy 1321 AGCCGGAGGAGATGTCCAACTGACACGAGATGCTGCCAGAGCTGGGGAAGAAGTCC 1380
Db 1553 AGCCGGAGGAGATGTCCAACTGACACGAGATGCTGCCAGAGCTGGGGAAGAAGTCC 1612
Qy 1381 TGGTTTGGGAACCTTTCATCAGCGCTGGAGAAGGAGAGAGATCTTCTGTTGTTTCATCAAAGAC 1440
Db 1613 TGGTTTGGGAACCTTTCATCAGCGCTGGAGAAGGAGAGAGATCTTCTGTTGTTTCATCAAAGAC 1672
Qy 1441 AAACCTCTGAGCTCCATCAAGGCTGACATCGTGCAACGCTTCTGTCGATTTCCAGTCTC 1500
Db 1673 AAACCTCTGAGCTCCATCAAGGCTGACATCGTGCAACGCTTCTGTCGATTTCCAGTCTC 1732
Qy 1501 AGCCACAGCTCATCTCCAAACGAGCTTCCGGGCGAGTACAGGCGACCGGGGGGCCA 1560
Db 1733 AGCCACAGCTCATCTCCAAACGAGCTTCCGGGCGAGTACAGGCGACCGGGGGGCCA 1792
Qy 1561 GCGGTGTTCCAGAACCGGTCAAGTTCCAGGTTGATATCACCTACACGAGGGGTGGGGAG 1620
Db 1793 GCGGTGTTCCAGAACCGGTCAAGTTCCAGGTTGATATCACCTACACGAGGGGTGGGGAG 1852
Qy 1621 GCGCAGAGGAGAACGGCATCTACTTCGTCACCTTACCTGCTCAGGCCCCCAGCGT 1680
Db 1853 GCGCAGAGGAGAACGGCATCTACTTCGTCACCTTACCTGCTCAGGCCCCCAGCGT 1912
Qy 1681 CGCTTCAGAGGGGTGGAGAACCATCCAGGCCAGCTGCTGAGCACACACGACCCGCT 1740
Db 1913 CGCTTCAGAGGGGTGGAGAACCATCCAGGCCAGCTGCTGAGCACACACGACCCGCT 1972
Qy 1741 GCGGCCACGACCTTGTGACAGACACCA 1766
Db 1973 GCGGCCACGACCTTGTGAGAACCCCC 1998

RESULT 11
US-10-283-247-4
; Sequence 4, Application US/10283247
; Publication No. US20030119037A1
; GENERAL INFORMATION:
; APPLICANT: NEELAM, Beena et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001304
; CURRENT APPLICATION NUMBER: US/10/283,247
; CURRENT FILING DATE: 2002-10-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1911
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-283-247-4

Query Match 92.2%; Score 1685.2; DB 14; Length 1911;
Best Local Similarity 96.2%; Pred. No. 0;
Matches 1763; Conservative 0; Mismatches 3; Indels 56; Gaps 1;

Qy 1 ATGAAGGTGGAGCGGAGATCCGATCTCTGAAGCTCATGTGACACCCCAAGTCTCTAAAG 60
Db 1 ATGAAGGTGGAGCGGAGATCCGATCTCTGAAGCTCATGTGACACCCCAAGTCTCTAAAG 60
Qy 61 CTGACAGGCTTTATGAACAAATAATTTGTACCTGCTGTAGACACGCTGTGAGGT 120
Db 61 CTGACAGGCTTTATGAACAAATAATTTGTACCTGCTGTAGACACGCTGTGAGGT 120
Qy 121 GGTGAGCTTTCGATCTACCTGCTGAAGAGGGGAGGCTGACGCTTAAGGAGGCTCGGAAG 180
Db 121 GGTGAGCTTTCGATCTACCTGCTGAAGAGGGGAGGCTGACGCTTAAGGAGGCTCGGAAG 180
Qy 181 TTCCTCCGAGATCATCTCTCGCTGGAATTTCTGCCACAGCACTCCATATGCCACAGG 240
Db 181 TTCCTCCGAGATCATCTCTCGCTGGAATTTCTGCCACAGCACTCCATATGCCACAGG 240
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Db 181 TTCTTCCGCGAGATCATCTCTGGCTGGACTTCTGCCACAGCACTCCATATGCCACAGG 240
Qy 241 GATCTGAAAACCTGAAAACCTCTCTGCTGGAGCAGAGAAACAAATCCGCACTGGAGACTTT 300
Db 241 GATCTGAAAACCTGAAAACCTCTCTGCTGGAGCAGAGAAACAAATCCGCACTGGAGACTTT 300
Qy 301 GGCATCGGCTGCTCTGAGGTTGGCGACAGCTTGTGAGACACAGCTGTGGTCTCCCCCAC 360
Db 301 GGCATCGGCTGCTCTGAGGTTGGCGACAGCTTGTGAGACACAGCTGTGGTCTCCCCCAC 360
Qy 361 TACGCTTCCGCGAGTGATTCGCGGGGAGAAATGATGACGCGCGGAAAGCGAGCTGTGG 420
Db 361 TACGCTTCCGCGAGTGATTCGCGGGGAGAAATGATGACGCGCGGAAAGCGAGCTGTGG 420
Qy 421 AGCTGCGGGCTCATCTGTTTGGCTTGTGGTGGGGCTCTGCCCTTCGACGATGACAAAC 480
Db 421 AGCTGCGGGCTCATCTGTTTGGCTTGTGGTGGGGCTCTGCCCTTCGACGATGACAAAC 480
Qy 481 TTCCGACAGCTGCTGGAGAAAGTGAAGCGGGGCTGTTCACATGCGGCACTTTATCCCG 540
Db 481 TTCCGACAGCTGCTGGAGAAAGTGAAGCGGGGCTGTTCACATGCGGCACTTTATCCCG 540
Qy 541 CCCGACTGCGAGAGTCTGTACGCGGGGATGATCGAGGTGAGACCGCGGACGCGCCCTCACG 600
Db 541 CCCGACTGCGAGAGTCTGTACGCGGGGATGATCGAGGTGAGACCGCGGACGCGCCCTCACG 600
Qy 601 CTAGAGCACATTCAGAAAACACATATGATATAGGGGGGCAAGAAATGAGCCCGAACACAGAG 660
Db 601 CTAGAGCACATTCAGAAAACACATATGATATAGGGGGGCAAGAAATGAGCCCGAACACAGAG 660
Qy 661 CAGCCCAATTCCTCGCAAGGTGACATCCGCTCGCTGCCAGCCTGGAGGACATCGACCCC 720
Db 661 CAGCCCAATTCCTCGCAAGGTGACATCCGCTCGCTGCCAGCCTGGAGGACATCGACCCC 720
Qy 721 GACGTGCTGACAGATGCACTCACTGGGGTGTCTCCGAGACCGCAACAAAGCTGTGTCAG 780
Db 721 GACGTGCTGACAGATGCACTCACTGGGGTGTCTCCGAGACCGCAACAAAGCTGTGTCAG 780
Qy 781 GACCTGCTGTCGAGGAGGAGAACACAGGAGAAATGATTTTACCTCTCTCTGGACCGG 840
Db 781 GACCTGCTGTCGAGGAGGAGAACACAGGAGAAATGATTTTACCTCTCTCTGGACCGG 840
Qy 841 AAAGAAAGGTACCCGAGCAGGAGGATGAGGACCTGCCCCCGGAAACGAGATAGACCT 900
Db 841 AAAGAAAGGTACCCGAGCAGGAGGATGAGGACCTGCCCCCGGAAACGAGATAGACCT 900
Qy 901 CCGCGAAGCGTGTGAGTCTCCGATGCTGAAACCGGACCGGCAAGCGCGCGGACAGACGC 960
Db 901 CCGCGAAGCGTGTGAGTCTCCGATGCTGAAACCGGACCGGCAAGCGCGCGGACAGACGC 960
Qy 961 AAATCCATGAGGTGCTCAGCGTGAACGCGGCTGCCCGGTGCCCTGCGCGCGGGGCC 1020
Db 961 AAATCCATGAGGTGCTCAGCGTGAACGCGGCTGCCCGGTGCCCTGCGCGCGGGGCC 1020
Qy 1021 ATTGAGATGCGCCAGCACGCGCCAG- 1044
Db 1021 ATTGAGATGCGCCAGCACGCGCCAGAGTAAAGCAATGTTTCAAGTAAAGCCTTGGATATCGCT 1080
Qy 1045 -----AGTCTCGGTCCATCAGCGGTGCTCTCTCA 1074
Db 1081 GAGGCCCATCCCCAATTCAGCAAGAAAGACAGAGTCTCGGTCCATCAGCGGTGCTCTCTCA 1140
Qy 1075 GGCCTTTCCACACGACCCACTCAGCAGCCCCGGGTGACCCCTCACCCCTCACCAAGGGGC 1134
Db 1141 GGCCTTTCCACACGACCCACTCAGCAGCCCCGGGTGACCCCTCACCCCTCACCAAGGGGC 1200
Qy 1135 AGTCCCTTCCCAACCCCAAGGGGACACCTGTCCACACGCCAAAGGAGAGCCCGGTGGC 1194
Db 1201 AGTCCCTTCCCAACCCCAAGGGGACACCTGTCCACACGCCAAAGGAGAGCCCGGTGGC 1260
Qy 1195 ACGCCCAACCCCAAGGGGACACCTGTCCAGCCCCAGCGTCCGAGGGGTGCCCTGGAGGGCGGG 1254
Db 1261 ACGCCCAACCCCAAGGGGACACCTGTCCAGCCCCAGCGTCCGAGGGGTGCCCTGGAGGGCGGG 1320
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QY 1255 CTCAACTCCATCAAGAACAGCTTTCTGGGCTCAACCCGCTTCCACCGCGGAACCTGCAA 1314
Db 1321 CTCAACTCCATCAAGAACAGCTTTCTGGGCTCAACCCGCTTCCACCGCGGAACCTGCAA 1380
QY 1315 GTTCCGACGCGGAGAGATGCTCAACCTGACACACAGAGTGTGCTCCCAAGAGTGGCGAAG 1374
Db 1381 GTTCCGACGCGGAGAGATGCTCAACCTGACACACAGAGTGTGCTCCCAAGAGTGGCGAAG 1440
QY 1375 AAGTCTCTGTTGGGAACTTCATCAGCTGAGAGAGGAGGAGAGATCTTCTGCTGCTATC 1434
Db 1441 AAGTCTCTGTTGGGAACTTCATCAGCTGAGAGAGGAGGAGAGATCTTCTGCTGCTATC 1500
QY 1435 AAAGACAAACCTCTGAGCTCCATCAAGGCTGACATCGTGCACGCTTCTCTGCTGATTTCCC 1494
Db 1501 AAAGACAAACCTCTGAGCTCCATCAAGGCTGACATCGTGCACGCTTCTCTGCTGATTTCCC 1560
QY 1495 AGTCTCAGCCACAGCGTGTATCTCCAAACAGAGCTTCGCGGCGGAGTACAAGGCCACAGGG 1554
Db 1561 AGTCTCAGCCACAGCGTGTATCTCCAAACAGAGCTTCGCGGCGGAGTACAAGGCCACAGGG 1620
QY 1555 GGGGAGCGGCTGCTCCAGAGCGGCTCAAGTTCAGAGTTGATATCACCTACACGAGGGT 1614
Db 1621 GGGGAGCGGCTGCTCCAGAGCGGCTCAAGTTCAGAGTTGATATCACCTACACGAGGGT 1680
QY 1615 GGGGAGCGGCTGAGAGAGAAAGGCTACTCTCCGTCACCTTCCAGCTGCTCTCAGGCGCCC 1674
Db 1681 GGGGAGCGGCTGAGAGAGAAAGGCTACTCTCCGTCACCTTCCAGCTGCTCTCAGGCGCCC 1740
QY 1675 AGCGTCTGCTCAAGAGGCTGTGAGACCATCCAGGCTCCAGGCTGCTGAGACACACGAC 1734
Db 1741 AGCGTCTGCTCAAGAGGCTGTGAGACCATCCAGGCTCCAGGCTGCTGAGACACACGAC 1800
QY 1735 CGCGCTGGGCGGCGAGCTTTCAGACACAC 1766
Db 1801 CGCGCTGGGCGGCGAGCTTGTGACAAACCCC 1832

RESULT 12
US-10-116-326-5
; Sequence 5, Application US/10116326
; Publication No. US20030166889A1
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Brian
; APPLICANT: Fridele, Carl Johan
; TITLE OF INVENTION: No. US20030166889A1 Human Kinases and Polynucleotides Encoding
; FILE REFERENCE: LEX-0332-USA
; CURRENT APPLICATION NUMBER: US/10/116,326
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,036
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 2112
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-116-326-5

Query Match 46.6%; Score 851.4; DB 12; Length 2112;
Best Local Similarity 68.9%; Pred. No. 5e-224;
Matches 1356; Conservative 0; Mismatches 416; Indels 195; Gaps 6;

QY 1 ATGAAGGTGAGCGGAGATCCGATCTCGAGCTCATTTGACACCCCAAGCTCTCTAAAG 60
Db 1 ATGAAGGTGAGCGGAGATCCGATCTCGAGCTCATTCGAACACCCCAAGCTCTCTCAAG 60
QY 61 CTGACGAGCTTTATGAAACAAATAATTTGTACTGCTGCTAGAACACCTGTGCTGAGT 120
Db 61 CTCCACGAGCTTACGAGAACAAATAATTTGTACTGCTGCTGAGAACACCTGTGCTGAGT 120
QY 121 GGTGAGCTCTTCGACTACTGTTGTAAGAGAGGAGGCTGACGCTTAAGAGGCTCGGAAG 180
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Db 121 GGTGAGCTATTTCGACTACTTGGTAAAGAGGGAGACTGAGCGCCCAAGAGGCGCCGGAAG 180
QY 181 TTCTTTCGGGAGATCATCTCTGGCTGAGACTTCTGCGCACAGGCACTCATATGACCAAG 240
Db 181 TTCTTTCGGGAGATGTTGTTCTGGCTGAGACTTCTGCGCACAGGCACTCATATGACCAAG 240
QY 241 GATCTGAAACCTGAAACCTCTCTGCTGAGAGAGAAACAACATCCGATTCGAGACTTTT 300
Db 241 GACCTAAAGCCGAGAACCTCTCTTGTGATGAGAAACAACATCCGATTCGAGACTTTT 300
QY 301 GGCATGCGCTCTCTGAGGTTGGCAGCAGCTTGTGGAGACCAAGCTGTGGGTCCCCCACC 360
Db 301 GGCATGCGCTCTCTGAGGTTGGGGAAGCAGCTCTCTGAGACCAAGCTGTGGGTCCCCCACC 360
QY 361 TACGCTCTCCCGAGGTTGATCCGCGGAGAGATATCACCGCGGAGAGGCGGAGCTGTGG 420
Db 361 TATGCTGTCTCAGAGGTTGATTAAGGGGGAATAATATGATGCGCGCGGAGAGATGTGG 420
QY 421 AGCTGCGGCTCATCTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
Db 421 AGCTGCTGAGTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
QY 481 TTGCGACAGCTGCTGAGAGAGGTTGAAGCGGGGCTGTTTCCACATGCGCGCACTTTATCCCG 540
Db 481 CTGCGCAGCTGCTGAGAGAGGTTGAAGCGGGGCTGTTTCCACATGCGCGCACTTTATCCCT 540
QY 541 CCCGACTGCCAGATCTGCTACGGGGCATGATCGAGGTGAGCGGCGGACCGCGCTCAGC 600
Db 541 CCAGATTGCCAGAGCTCTCTGAGGGGAATGATGAAGTGGAGCGCGGAAAGAGCTCAGT 600
QY 601 CTAGAGCACATTCAGAAACACATATGTTATAGGGGCAAGATGAGCCCGAACC----- 656
Db 601 CTGAGACAAATTCAGAAACACATCTTGTGTA CTTAGCGGGAAACACAGACCGACCGCTGC 660
QY 657 --AGAGCAGGCCATTCCTGCAAGTGCAGATCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 714
Db 661 CTGAGCAGCGCCCTGCGCGGCTAGCCATCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
QY 715 GACCCGACGCTGCTGAGACAGATCATCTACTGGGCTGCTTCCGAGACCGGCAACAGCTG 774
Db 721 GACCCGACGCTCTAGAGAGCATGCGCATCTCTGGGCTGCTTCCGAGACCGGAGGCTG 780
QY 775 CTGAGGACCTGCTGCTCGAGGAGAGAAACAGGAGAGATGATTTACTTCTCTCTCTGCT 834
Db 781 CATCGGAGCTGCTGAGTGGAGAGAGAAACAGAGAGAGATGATATATATCTGCTTTTG 840
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QY 895 GACCTCTCCCGAGCGTGTGAGTCTCCGATGCTGAAACCGGCGAGCGGACGAGCGGCGCA 954
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QY 955 GAAGCAAAATCCATGAGGCTGCTCAGCGTGCAGG-----CGGCGGCTCCCGGCTG 1005
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QY 1006 CCTGCGGCGGCGCATTTGAGATGCGCCAGCA CGGCGAGAGGTCTCGGTTCATCAGCGGT 1065
Db 1021 CCCACCGGAGCGGCTTGGAGATGCGCGAGCACAGCGAGATCCCGGTAGCGTCAAGTGA 1080
QY 1066 GCTTCTCTCAGGCTTTTCCACGAGCGCATCTCAGGAGCGGCGGCGGCGGCGGCGGCGG 1108
Db 1081 GCCTTCCAGGCTCTGCTCTCTCAGCGCTTAAAGCAGCCCAAGGAGTCCGCTTCTTTTCTCTTT 1140
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Db 1201 CAGAGCTGCTTCTCGGGGCCCCCAGGGGTGGGGGCGCGGGAGAGAGCCCCCGCCCCC 1260
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Db 1261 AGTCCCGCTCCACACCCCTGCGGGGCCCCCAGGCTCCCGCGCTCTCTGCGGGAGC 1320
Qy 1150 CCCAAGGGGACACCTGTCCACACGCCAAAGAGAGCGCGGTGCGACGCCCAACCCACG 1209
Db 1321 CCCTTGACTCGCTCTGCAACGCCCGCGGCGAGTCCACCGGAGCCCCGGGGAACA 1380
Qy 1210 CCCCCGTCAGCCCC-----AGCGTCGAGGGGTGCCCTGAGGGCGCGCTCAACTCC 1263
Db 1381 CCAACCCCGAGCCCGGGGCGGTGCGGGGAGCGCGCTGAGGAGTCTCAACTCC 1440
Qy 1264 ATCAAGACAGCTTCTGCGGTCTACCCCGCTTCCACGCGGGAACCTGCAAGTTCGAGC 1323
Db 1441 ATCCGCAACAGCTTCTGCGGTCTCCCTCGCTTCCACGCGCAAGATGCAAGTCCCTACC 1500
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Qy 1444 CCTCTGAGCTCCATCAAGCTGACATCGTCAAGCTTCTGTCGATTCCTCAGTCTCAGC 1503
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Qy 1666 TCAGGCCCCAGCGCTCGCTTCAAGAGGGTGGTGGAGACCATCCAGGCCAGCTGCTGAGC 1725
Db 1861 TCGGGTCCCGAGCGTCTGTTCAAGCGAGTGGTGGAGACCATCCAGSCACAGCTCTGAGC 1920
Qy 1726 ACACAGAGCCCGCTGCGGCCAGCAGCTTGTGAGACACCACTAACTG 1772
Db 1921 ACTCATGACAGCCCTCGTGGAGGCGCTGGCAGACGAGAGAGAGAGAGAGAGAGAG 1967

RESULT 13

US-10-116-326-1
; Sequence 1, Application US/10116326
; Publication No. US2003016689A1
; GENERAL INFORMATION:
; APPLICANT: Mathur, C. Alexander Jr.
; APPLICANT: Friddle, Brian
; TITLE OF INVENTION: No. US2003016689A1el Human Kinases and Polynucleotides Encoding
; FILE REFERENCE: LEX-0332-USA
; CURRENT APPLICATION NUMBER: US/10/116,326
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,036
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2337
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-116-326-1

Query Match 46.6%; Score 851.4; DB 12; Length 2337;
Best Local Similarity 68.9%; Pred. No. 5.2e-224;
Matches 1356; Conservative 0; Mismatches 416; Indels 195; Gaps 6;
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Db 226 ATGAAGGTGGAGCGGAGATCGCATCTCTGAAGCTCATCGAAACACCCACATGTCTCTCAAG 285
Qy 61 CTGCACAGCTTTATGAACAACAATAATTTGTACTCTGTTGCTAGAACACGTTGTCAGGT 120
Db 286 CTCACAGAGCTCTACAGAAACAAGAAATATTTGTACTCTGTTGCTGAGCACGTCCTCGGG 345
Qy 121 GGTGAGCTCTTTCGACTACCTGTGTGAAGAGGGGAGGCTGACGCTTAAGGAGGCTCGGAAG 180
Db 346 GGTGAGCTATTTCGACTACCTGTGTGAAGAGGGGAGAGTGCAGCCCAAGGAGGCCCGAAG 405
Qy 181 TTCTTCCGGGAGATCATCTCTGCGCTGGACTTCTGCGACAGCCACTTCCATATGCCACAGG 240
Db 406 TTCTTCCGGGAGATTTGTCTGCGCTGGACTTCTGCGACAGCTTACTTCCATCTGCCACAGA 465
Qy 241 GATCTGAAACCTGAAACCTCTCTGCTGGAGAGAGAAACAACATCCGCTATCGCAGACTTT 300
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Db 586 TATGCGGTGTCCAGAGGTGATTAAGGGGGAAAAATATGATGGCGCGCGGGGAGACATGTGG 645
Qy 421 AGCTTGGCGCTCATCTCTGCTGCTGGTGGTGGCGCTCTGCTTCCAGCTATGACAAAC 480
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Qy 481 TTGCGACAGCTGTGGAGAGAGTGAAGCGGGGCGTGTTCACATGCGCGCATTTATCCCG 540
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Qy 541 CCGAGCTGCCAGAGTCTGCTACGGGGCATGATCAGGTGAGACGCGCGCGCTCAGC 600
Db 766 CCAGATTGCCAGAGCTCTCTGAGGGGAAATGATCGAAGTGGAGCCCGGAAAAAGAGCTCAGT 825
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Db 826 CTGAGCAAAATTCAGAAACATCTTGTGTACTGAGCGGGAAACACAGAGCCAGACCCGTGC 885
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Db 886 CTGGAGCCAGCCCTGCGCGCGGGTAGCCATGCGGAGCCTGCCATCCAAACGGAGAGCTG 945
Qy 715 GACCCGACGTGTGGACAGCATGCACTCACTGGGTGCTTCCGAGACCGCAACAGCTG 774
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Qy 775 CTGCAAGACCTGCTGTCGAGGAGGAGAAACAGGAGAGATGATTTACTTCTCTCTCTG 834
Db 1006 CATCGAGCTGCGCAGTGGAGGAGAGAACAGAAAGATGATATATATCTGCTTTG 1065
Qy 835 GACCGAAGAAAGGTACCCGAGCAGGAGGATGAGACCTGCCCCCGGAAACGAGATA 894
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Db 1246 CCCACCCGAGCGGCTTGGAGATGCCCCAGCAGCAGCAGATCCGTAGGTCAAGTGA 1305
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Db 1306 GCTCTCAGGCTTCTGCTCCAGCCCTCTAAGCAGCCCAAGGAGTCCGGTCTTTTCTTT 1365
Qy 1109 ----- 1108
Db 1366 TCACCGGAGCCGGGCTGGAGATGAGGCTCAGCGGGGGGCTCCCGACTTCGAAACG 1425
Qy 1109 -----TGACCCCTCACCCC 1122
Db 1426 CAGACGCTGCTTCTCGGGGCCCCAGGGGTGGGGGCGCGGGGAGCAGCCCCCGCCCC 1485
Qy 1123 TCACCAAGGGGAGTCCCTCTCC-----ACC 1149
Db 1486 AGTGCCCGTCCACACCCCTGCCCCGCCCCCAGGCTCCCGCGTCTCTTGGGGGAGCC 1545
Qy 1150 CCCAAGGGGACACCTGTCTCACACGCCCAAGGAGAGCCCGGCTGGCAGCCCAACCCACG 1209
Db 1546 CCTTGCATCGCTCTGACAGCCCGCGGCGAGTCCACCGGACCCCGGGGACAACA 1605
Qy 1210 CCCCCTCAGCCCC-----AGGCTGGAGGGGTGCCCTGGAGGGCGCGCTCAACTCC 1263
Db 1606 CCACCCCGCAGCCCGGGGTGGCGTGGGGGAGCGCGCTGGAGGAGTGGTCTCAACTCC 1665
Qy 1264 ATCAGAGACAGCTTCTGGGCTCACCCGCTTCCACCGCGGAACTCGAGTCCGAG 1323
Db 1666 ATCCGCAACAGCTTCTGGGCTCCCTCGCTTTCACCGGCGCAAGATGAGGTCCCTACC 1725
Qy 1324 CGGAGGAGATGCCAACCAGCAGAGTGGTCCCGCAGAGCTGGCGAAGAGTCTGG 1383
Db 1726 GCTGAGGAGATGCTCAGCTTGAGCCAGAGTCTTCCCGGAGCTGGCAAAAGCTCTTG 1785
Qy 1384 TTGGAAGTTCATCAGCTTGAGAGGAGGAGAGTCTTGGTGGTTCATCAAGACAA 1443
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Db 1846 CTTCTCAGAGATCAAGAGCAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1905
Qy 1504 CACAGCTCATCTCCCAACAGCTTCCGGGCGGAGTACAGGCCACCGGGGGCGCAGCC 1563
Db 1906 CACAGTGTCTCAGACAGCAGCTTACGGGCGGAGTACAGGCCAGTGGCGGCCCTCC 1965
Qy 1584 GTGTTCCAGAGCCGGTCAAGTTCAGGTTGATATCACTTACAGGAGGT----- 1614
Db 1966 GTCTTCCAAAGCCGCTCCGCTTCCAGGTGGACATCAGTCTCTTGAGGGTCCAGAGCC 2025
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Db 2026 TCCCGCAGGAGCAGCAGCGGAGGTGGTGGATCTACTCTGCTCAGCTTCACTCTCATC 2085
Qy 1666 TCAGGCCCGAGCGCTCGCTTCAAGAGGGTGGTGGAGACCATCCAGGCCAGCTGCTGAGC 1725
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RESULT 14

US-10-354-358-91

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; Publication NO. US20030157082A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc
; APPLICANT: Hunter, John Joseph
; APPLICANT: Macbeth, Kyle J.
; APPLICANT: Tsai, Fong-Ying
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; APPLICANT: Lesoon, Andrea
; APPLICANT: Lightcap, Eric S.
; APPLICANT: Williamson, Mark
; APPLICANT: Rudolph-Owen, Laura A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: CANCER USING 140, 1470, 1686, 2089, 2427, 3702, 5891, 6428,
; TITLE OF INVENTION: 7181, 7660, 25641, 69583, 49863, 8897, 1682, 17667, 9235,
; TITLE OF INVENTION: 3703, 14171, 10359, 1660, 1450, 18894, 2088, 32427, 2160,
; TITLE OF INVENTION: 9252, 9389, 1542, 85269, 10297, 1584, 9525, 14124, 4469,
; TITLE OF INVENTION: 8990, 2100, 9288, 64698, 10480, 20893, 33230, 1386, 9943,
; TITLE OF INVENTION: 16334, 68862, 9011, 14031, 6178, 21225, 1420, 32236, 2099,
; TITLE OF INVENTION: 2150, 26583, 2784, 8941, 9811, 27444, 50566 OR 66428 MOLECULES
; FILE REFERENCE: MPI02-020P1RNMNMIM
; CURRENT APPLICATION NUMBER: US/10/354,358
; PRIOR FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US 60/353,600
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 60/364,517
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/371,075
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: US 60/371,507
; PRIOR FILING DATE: 2002-04-10
; PRIOR APPLICATION NUMBER: US 60/372,984
; PRIOR FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: US 60/374,194
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/382,995
; PRIOR FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: US 60/385,023
; PRIOR FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: US 60/389,853
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: US 60/389,395
; PRIOR FILING DATE: 2002-06-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 91
; LENGTH: 2980
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (86) ... (2422)
; US-10-354-358-91

Query Match 46.6%; Score 851.4; DB 12; Length 2980;
Best Local Similarity 68.9%; Pred. No. 5.5e-224;
Matches 1356; Conservative 0; Mismatches 416; Indels 195; Gaps 6;

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Db 311 ATGAAGCTGGAGCGGAGATCGGATCCTGAAGCTCATTGAGCACCCCGCTTAAG 370
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Db 371 CTCAACGCTCTACGAGACAGAAATATTGTACCTGGTGTCTGGAGCAGCTCTCGGG 430
Qy 121 GGTGAGCTCTTCGACTACCTGGTGAAGAGGGGAGGTGACGCTTAAGAGGCTCGGAAG 180
Db 431 GGTGAGCTATTTCGACTACCTGGTAAAGAGGGGAGACTGACGCCCAAGAGGCGCGGAAG 490
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Qy 241 GATCTGAAACCTGAAACCTCCTCTGCGAGAGAGAACCAACATCCGCTATCGCAGACTTT 300
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Db 445 GATGAGAAACAACTCCGATTCGAGACTTCGGCATGGCTCCCTGCGAGTTGGGGGAC 504
Qy 328 AGCTGTGGAGACCACTGTGGTTCCTCCCACTACGCTGCTGCCCGGAGGTGATCCGGGG 387
Db 505 AGCTCTCTGGAGACCACTGGCTGGCTCCCTCATTTATGCTGTCCAGAGGTGATTAAGGG 564
Qy 388 GAGAAGTATGAGCGCGGAGCGGACGTGTGAGCTGCGCGCTCATCTGTTCGCCTTG 447
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Db 685 CGGGCGGTCTTCCATGCTCCCACTGCCCACTTCACTCTCCAGATTGCCAGAGCTCTGAGGGGA 744
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Qy 1531 CGGGCGAGTACAAAGCCACGCGGGGCGAGCGGTGTTCCAGAAAGCGGTCAAGTTCCAG 1590
Db 1885 AGGCGCGAGTACAAAGCCAGTGGCGGCCCTCTCCGAGAGCTCCAGAGCGGAGGT 1944
Qy 1591 GTTGATATCACTTACACGAGGT-----GGGAGGCGCAGAAAGGAG 1632
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Qy 1633 AAGGATCTACTCTCGTCACTTCACTGCTCTCAGGCGCGAGCGGTTCAGAGG 1692
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Db 2125 CTGGCAGACGAGAAGAACGG 2144

Search completed: November 27, 2003, 15:02:51
Job time : 1072.75 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 27, 2003, 01:57:44 ; Search time 501.488 Seconds
(without alignments)
10803.388 Million cell updates/sec

Title: US-10-054-579-1

Perfect score: 2007

Sequence: 1 atgacatcgacgggaagga.....gaattatcccgaaagtaa 2007

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1993	99.3	3364	25	ABX13584 Human cDNA encodin
4	1966	98.0	2647	24	AAAD34315 Human PKIN-18 cDNA
5	1939.6	96.6	2025	24	ABA02995 Human protein kina
6	1939.6	96.6	2217	24	ABA02994 Human protein kina
7	1827	91.0	1827	24	ABQ77626 Human kinase NHP #
8	1017.8	50.7	2799	25	AAL51889 Human cell cycle-r

9	965	48.1	2337	25	ABV74557 Human kinase #1 co
10	964.4	48.1	2385	22	AAS06717 Polynucleotide seq
11	964.4	48.1	2897	24	AAAD26464 Human kinase PKIN-
12	851.4	42.4	2112	25	ABV74559 Human kinase #3 co
13	777.2	38.7	2289	25	ABV74558 Human kinase #2 co
14	588.8	29.3	1797	25	ABX70994 Novel human cDNA s
15	539.8	26.9	2720	23	ABU10489 Drosophila melanog
16	449.2	22.4	906	22	ABA08296 Human HrPK-1 hom
17	291.6	14.5	512	24	ABK70216 Human lung cancer
18	265.8	13.2	3609	25	AAAD51408 Human microtubule
19	265	13.2	1594	22	AAFA4655 Novel protein kina
20	264.2	13.2	1549	24	ABSE64386 Human serine/threo
21	264.2	13.2	2085	25	AAAD51409 Human microtubule
22	264.2	13.2	2278	25	AAAD51410 Human cDNA SEQ ID
23	264.2	13.2	2462	24	ABQ93445 Human full-length
24	264.2	13.2	2954	22	AAK94923 Human microtubule
25	264.2	13.2	3226	25	AAAD51412 Human kinase (PKIN
26	264.2	13.2	3269	22	AAAD18831 Human neuronal ser
27	264.2	13.2	3312	24	ABA05739 Human neuronal ser
28	264.2	13.2	3392	24	ABA05740 Human microtubule
29	264.2	13.2	4917	25	AAAD51411 Human MARK cDNA.
30	262.6	13.1	3270	25	ABQ77242 Murine neuronal se
31	262.4	13.1	3170	24	ABA05737 Drosophila melanog
32	262.4	13.1	3250	24	ABA05738 Human protein kina
33	261.4	13.0	2663	23	ABU05573 Human protein kina
34	252.4	12.6	2352	22	AAI66823 Human kinase PKIN-
35	252.4	12.6	2968	22	AAI66822 Human keratinocyte
36	252.4	12.6	4699	22	AAH76213 Human keratinocyte
37	250.8	12.5	2533	21	AAH82951 Human Ser/Thr kina
38	250.8	12.5	2632	21	AAH82952 Drosophila melanog
39	249.8	12.4	614	22	ABA08924 Polynucleotide seq
40	233.4	11.6	2118	23	ABU11605 Drosophila melanog
41	233.4	11.6	2361	22	AAS06718 Polynucleotide seq
42	233.4	11.6	4118	23	ABU11604 Drosophila melanog
43	232.6	11.6	2766	23	ABU26615 Drosophila melanog
44	230.6	11.5	3234	25	ABZ77147 Human protein kina
45	229.4	11.4	2601	23	ABU13339 Drosophila melanog

ALIGNMENTS

RESULT 1
ABQ77625
ID ABQ77625 standard; cDNA; 2007 BP.
XX AC ABQ77625;
XX AC ABQ77625;
XX DT 21-OCT-2002 (first entry)
XX DE Human kinase NHP #1-encoding cDNA, SEQ ID NO:1.
XX KW Human; kinase; NHP; chromosome 11; signal transduction; cytoplasmic;
KW nuclear; brain; pituitary; hypothalamus; adipose; cerebellum;
KW adrenal gland; foetal lung; foetal brain; cancer; drug screening;
KW mental disorder; diagnostic reagent; clinical trial monitoring; cosmetic;
KW nutraceutical; mutation detection; gene expression analysis;
KW chromosome mapping; transgenic animal; cytostatic; gene therapy;
KW gene; ss.
XX OS Homo sapiens.
XX FH Key
XX CDS Location/Qualifiers
FT 1..2007
FT FT
FT /*tag= a
FT /product= "Human kinase NHP #1"
XX WO200259287-A2.
XX PD 01-AUG-2002.
XX PF 22-JAN-2002; 2002WO-US01818.
XX

23-JAN-2001; 2001US-263378P.
(LEXI-) LEXICON GENETICS INC.
Turner CA, Mathur B;
WPI; 2002-599780/64.
P-PSDB; ABB09557.
Novel polynucleotide encoding human proteins sharing sequence
similarity with animal kinases, useful for drug screening, diagnosis,
in gene therapy of disorders and diseases e.g. cancer -
Claim 1; Page 36; 40pp; English.
The invention relates to novel human kinases (ABB09557, ABB09558),
referred to as NHPs, and to nucleic acids encoding them (ABB077625,
ABB077626). The NHPs have structural similarity with animal kinases
including serine-threonine kinases, carbon catabolite repressing kinases,
calcium/calmodulin-dependent protein kinases, and cAMP-dependent protein
kinases. The NHPs do not contain consensus signal sequences, indicating
that they may be cytoplasmic or nuclear proteins, and are thought to be
involved in signal transduction. Polynucleotides encoding NHPs were
obtained using human brain, pituitary, hypothalamus, adipose, cerebellum,
adrenal gland, foetal lung, and foetal brain cDNAs and primers derived
from human genomic DNA. The gene encoding the NHPs is located on
chromosome 11. NHP nucleotides and proteins are useful for treating
mental, biological or medical disorders including cancer, and for
screening compounds useful in the treatment of such conditions. They can
also be used as diagnostic reagents, in clinical trial monitoring and in
cosmetic and nutritional applications. NHP nucleotides can additionally
be used in the detection of disease-associated mutations, in the analysis
of gene expression, for mapping chromosome 11, for the recombinant
expression of NHPs, to generate transgenic animals, in gene therapy,
and as part of ribozyme and/or triple helix sequences useful in the
modulation of NHP gene expression. The present sequence represents cDNA
encoding a 668 amino acid NHP (#1).
Sequence 2007 BP; 445 A; 626 C; 604 G; 332 T; 0 other;

Query Match 100.0%; Score 2007; DB 24; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2007; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGACATCGACGGGGAAGGACGGCGCGCAGCACGCGCAGTATGTTGGGCCCTACCGG 60
1 ATGACATCGACGGGGAAGGACGGCGCGCAGCACGCGCAGTATGTTGGGCCCTACCGG 60
61 CTGGAAGAAGCGCTGGGCAAGGGGCAGACAGGCTCTGGTGAAGCTGGGGGTTCACTGCGTC 120
61 CTGGAAGAAGCGCTGGGCAAGGGGCAGACAGGCTCTGGTGAAGCTGGGGGTTCACTGCGTC 120
121 ACCTGCCAGAGGTGGCCATCAAGATCGTCAACCGTCAGAGGCTCAGCGAGTGGTCTG 180
121 ACCTGCCAGAGGTGGCCATCAAGATCGTCAACCGTCAGAGGCTCAGCGAGTGGTCTG 180
181 ATGAAGGTGGAGCGGGAGATCGCATCTGAAGCTCATTGAGCACCCCGCAGTCTTAAAG 240
181 ATGAAGGTGGAGCGGGAGATCGCATCTGAAGCTCATTGAGCACCCCGCAGTCTTAAAG 240
241 CTGCACGACGTTTATGAACAAAAATATTTGTTACCTGGTGTAGAACACGTTGTCAGGT 300
241 CTGCACGACGTTTATGAACAAAAATATTTGTTACCTGGTGTAGAACACGTTGTCAGGT 300
301 GGTGAGCTCTTCGACTACCTGGTGAAGAGGGAGGCTGAGCGCTTAGAGGGCTCGGAAG 360
301 GGTGAGCTCTTCGACTACCTGGTGAAGAGGGAGGCTGAGCGCTTAGAGGGCTCGGAAG 360
361 TTCTTCGGCAGATCATCTCTGCGCTGAGCTTCTGCCACAGCCACTCCATATGCCACAGG 420
361 TTCTTCGGCAGATCATCTCTGCGCTGAGCTTCTGCCACAGCCACTCCATATGCCACAGG 420
421 GATCTGAAACCTGAAACCTCTCTGCTGGAAGAGAACATCCGATCGCAGACTTT 480

421 GATCTGAAACCTGAAACCTCTCTGCTGGAAGAGAACATCCGATCGCAGACTTT 480
481 GGCATGGCGTCCCTGCAGGTTGGCGACAGCCTGTTGGAGACCAGCTGGGTGCCCCAC 540
481 GGCATGGCGTCCCTGCAGGTTGGCGACAGCCTGTTGGAGACCAGCTGGGTGCCCCAC 540
541 TACGCTCTGCCCGAGGTGATCCGGGGGGAAGATATGACGGCGGAAGCGGACGCTGGG 600
541 TACGCTCTGCCCGAGGTGATCCGGGGGGAAGATATGACGGCGGAAGCGGACGCTGGG 600
601 AGCTCGGCGTCACTCTGTTGCTGTTGCTGGGGGCTCTGCTTCCATGCAATGACAAAC 660
601 AGCTCGGCGTCACTCTGTTGCTGTTGCTGGGGGCTCTGCTTCCATGCAATGACAAAC 660
661 TTGCGACAGCTCTCGAGAGGTGAAGGGGCGTGTTCACATCGCGCCTTTATCCCG 720
661 TTGCGACAGCTCTCGAGAGGTGAAGGGGCGTGTTCACATCGCGCCTTTATCCCG 720
721 CCCGACTGCGAGAGTCTGCTACGGGGCATGATCGAGGTGGACGGCGCCTCTCACG 780
721 CCCGACTGCGAGAGTCTGCTACGGGGCATGATCGAGGTGGACGGCGCCTCTCACG 780
781 CTAGAGCATTTGAGAAACACATATGTTATATAGGGGGCAAGATAGCCCCGAAACAGAG 840
781 CTAGAGCATTTGAGAAACACATATGTTATATAGGGGGCAAGATAGCCCCGAAACAGAG 840
841 CAGCCCATCTTCGCAAGGTGCAGATCGCTCGTCCCGAGCTCGAGGACATCGACCCC 900
841 CAGCCCATCTTCGCAAGGTGCAGATCGCTCGTCCCGAGCTCGAGGACATCGACCCC 900
901 GACGTGCTGGACAGCATGCACTCACTGGGCTCTTTCCGAGACCGCAACAGCTGTGCAG 960
901 GACGTGCTGGACAGCATGCACTCACTGGGCTCTTTCCGAGACCGCAACAGCTGTGCAG 960
961 GACCTGCTCTCGAGGAGAGAACACAGAGAGATGATTTACTTCTCTCTGACCGG 1020
961 GACCTGCTCTCGAGGAGAGAACACAGAGAGATGATTTACTTCTCTCTGACCGG 1020
1021 AAAGAAAGGTACCCGAGCAGGAGATGAGGACCTGCCCCCGGAAACAGATAGACCTT 1080
1021 AAAGAAAGGTACCCGAGCAGGAGATGAGGAGATGAGGACCTGCCCCCGGAAACAGATAGACCTT 1080
1081 CCCGGAAGCGTGTGACATCTCCCGATGCTGAACCGGACGCAAGCGGCGGCAAGCGC 1140
1081 CCCGGAAGCGTGTGACATCTCCCGATGCTGAACCGGACGCAAGCGGCGGCAAGCGC 1140
1141 AAATCCATGGAGGTGCTCAGCGTGAAGCGGAGCTCCCGGTGCTGCGGGCGGGCC 1200
1141 AAATCCATGGAGGTGCTCAGCGTGAAGCGGAGCTCCCGGTGCTGCGGGCGGGCC 1200
1201 ATTGAGATGGCCAGCAGCGCCAGAGGTCTCGGTCCATCAGCGGTGCTCTCTCAGGCTT 1260
1201 ATTGAGATGGCCAGCAGCGCCAGAGGTCTCGGTCCATCAGCGGTGCTCTCTCAGGCTT 1260
1261 TCCACAGCCCACTCAGCAGCCCCCGGGTGAACCCCTCACCCCTCACAAAGGGGAGTCCC 1320
1261 TCCACAGCCCACTCAGCAGCCCCCGGGTGAACCCCTCACCCCTCACAAAGGGGAGTCCC 1320
1321 CTCGCCACCCCAAGGGGACACTGTTCCACAGCGCCAAAGAGAGCCGGCTGGCAGCCC 1380
1321 CTCGCCACCCCAAGGGGACACTGTTCCACAGCGCCAAAGAGAGCCGGCTGGCAGCCC 1380
1381 AACCCCAACGCCCGCTCAGCGCCAGCTCGGAGGGGTGCTTGGAGGGCGGCTCAAC 1440
1381 AACCCCAACGCCCGCTCAGCGCCAGCTCGGAGGGGTGCTTGGAGGGCGGCTCAAC 1440
1441 TCCATCAAGAAACAGCTTTCTGGGCTCAACCCCGTTCACCGCGGAACTGCAAGTTCCG 1500
1441 TCCATCAAGAAACAGCTTTCTGGGCTCAACCCCGTTCACCGCGGAACTGCAAGTTCCG 1500
1501 ACGCCGAGGAGATGTTCCAACTGACACAGAGTCTGTTCCCGAGAGCTGGGAGAGTCC 1560

Db 1501 AGCGCGAGGAGATGCTCAACCTGACACAGAGTCTGCTCCCGAGAGCTGGCGAAGAGTCC 1560
Qy 1561 TGGTTTGGGAACCTTCATCAGCGCTGAGAGAGGAGAGAGATCTTCCTGCTCATCAAGAC 1620
Db 1561 TGGTTTGGGAACCTTCATCAGCGCTGAGAGAGGAGAGAGATCTTCCTGCTCATCAAGAC 1620
Qy 1621 AAACCTCTGAGTCTCATCAGCGCTGACATCTGTCAGCGCTTCCTGCTCATCAAGTCTC 1680
Db 1621 AAACCTCTGAGTCTCATCAGCGCTGACATCTGTCAGCGCTTCCTGCTCATCAAGTCTC 1680
Qy 1681 AGCCACAGCTCATCTCCCAACAGAGCTTCGCGGCGGAGTCAAGGCCACCGGGGGGCCA 1740
Db 1681 AGCCACAGCTCATCTCCCAACAGAGCTTCGCGGCGGAGTCAAGGCCACCGGGGGGCCA 1740
Qy 1741 GCCGTGTTCCAGAACCGGTCAAGTTCAGAGTTGATATCACCTACACGAGGGTGGGGAG 1800
Db 1741 GCCGTGTTCCAGAACCGGTCAAGTTCAGAGTTGATATCACCTACACGAGGGTGGGGAG 1800
Qy 1801 GCGCAGAGGAGAGCGGATCTACTCCGTCACCTTCACCTGCTCTAGGCCCCGAGCGGT 1860
Db 1801 GCGCAGAGGAGAGCGGATCTACTCCGTCACCTTCACCTGCTCTAGGCCCCGAGCGGT 1860
Qy 1861 CGCTTCAAGAGGGTGTGAGACCATCCAGGCCAGCTGCTGAGCACACAGCCGCT 1920
Db 1861 CGCTTCAAGAGGGTGTGAGACCATCCAGGCCAGCTGCTGAGCACACAGCCGCT 1920
Qy 1921 GCGGCCAGCAGCTTCTGACACACCACTAACTGTATGGAATGATGACGGGGCGCTTTCC 1980
Db 1921 GCGGCCAGCAGCTTCTGACACACCACTAACTGTATGGAATGATGACGGGGCGCTTTCC 1980
Qy 1981 AAATGTGAATATCCGAAAGTTAA 2007
Db 1981 AAATGTGAATATCCGAAAGTTAA 2007

RESULT 2
ABX13583
ID ABX13583 standard; cDNA; 2908 BP.
XX AC
XX ABX13583;
XX
DT 10-FEB-2003 (first entry)
XX
DE Human cDNA encoding serine protein kinase KSE336-1.
XX
KW Human; ss; gene; chromosome 11p15.5-pter; astrocytoma; meningioma;
KW pancreatic adenocarcinoma; insulin-dependent diabetes mellitus 2;
KW helicoid peripapillary chorioretinal degeneration; brain; pancreas;
KW Beckwith-Wiedemann syndrome; congenital hyperinsulinism; KSE336.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FT CDS 106..2112
FT /tag= a
FT /product= "KSE336-1"
XX
XX US6455292-B1.
XX
XX 24-SEP-2002.
XX
XX 16-AUG-2001; 2001US-0930181.
XX
XX 16-AUG-2001; 2001US-0930181.
XX
XX (ORIG-) ORIGENE TECHNOLOGIES INC.
XX
XX Shu Y, Fan W, Kovacs KF, Zidanic M, Jay G;
XX
XX WPI; 2003-066233/06.
XX
XX P-PSDB; ABG72382.
XX
XX New isolated polynucleotide coding without interruption for a human

PT KSE336 polypeptide useful for preventing or treating
PT diseases/conditions relating to brain and pancreas, e.g. meningioma,
PT insulin-dependent diabetes mellitus 2
XX Claim 3; Column 33-40; 34pp; English.
XX
CC The invention relates to an isolated polynucleotide (its complement
CC or a sequence 9% similar to it) coding without interruption for a human
CC KSE336 polypeptide, a serine protein kinase, comprising the KSE336-1 and
CC KSE336-2 splice variants appearing as ABG72382 and ABG72383. Also
CC included is a method of identifying an agent that modulates the
CC expression of KSE336 in brain, pancreas, brain progenitor or pancreas
CC progenitor cells comprising: (a) contacting a cell population comprising
CC the cells with a test agent under conditions effective for the test agent
CC to modulate the expression of KSE336; and (b) determining if the test
CC agent modulates the expression of KSE336. The polynucleotides are useful
CC as molecular targets or drug targets, and for detecting, diagnosing, or
CC staging, monitoring, prognosticating, preventing or treating diseases or
CC conditions relating to brain and pancreas, such as astrocytoma,
CC meningioma, pancreatic adenocarcinoma, insulin-dependent diabetes
CC mellitus 2, helicoid peripapillary chorioretinal degeneration, Beckwith-
CC Wiedemann syndrome or congenital hyperinsulinism. The method and
CC polynucleotides are useful in research, diagnosis, drug discovery,
CC therapy, clinical medicine, forensic science and pathology.
CC The gene for KSE336 is located on chromosome 11p15.5-pter.
CC The present sequence encodes the KSE336 variant KSE366-1.
XX
SQ Sequence 2908 BP; 603 A; 948 C; 879 G; 478 T; 0 other;
Query Match 99.9%; Score 2005.4; DB 25; Length 2908;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2006; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 ATGACATCGACGGGAGGAGCGCGCGCGCAGCAGCGCAGTATGTTGGCCCTACCGG 60
Db 106 ATGACATCGACGGGAGGAGCGCGCGCGCAGCAGCGCAGTATGTTGGCCCTACCGG 165
Qy 61 CTGGAGAAGACGCTGGGCAAGGGGCGACAGAGTCTGTTGAAGCTGGGGTTCACCTCGTC 120
Db 166 CTGGAGAAGACGCTGGGCAAGGGGCGACAGAGTCTGTTGAAGCTGGGGTTCACCTCGTC 225
Qy 121 ACCTGCCAGAGGTGGCCATCAGATCGTCAACCGTGAGAGCTCAGCGAGTCTGGTCTG 180
Db 226 ACCTGCCAGAGGTGGCCATCAGATCGTCAACCGTGAGAGCTCAGCGAGTCTGGTCTG 285
Qy 181 ATGAAGTGGAGCGGAGATCGCGATCCTGAAGCTCATTGAGACACCCCGCTCTAAAG 240
Db 286 ATGAAGTGGAGCGGAGATCGCGATCCTGAAGCTCATTGAGACACCCCGCTCTAAAG 345
Qy 241 CTGCAACGAGTTTATGAAAAACAAAAATATTTGACCTGGTGTAGAACACGTCAGGT 300
Db 346 CTGCAACGAGTTTATGAAAAACAAAAATATTTGACCTGGTGTAGAACACGTCAGGT 405
Qy 301 GGTGAGCTCTTCGACTACCTGGTGAAGAAGGGGAGCTGACCGCTAAGAGGCTCGGAAG 360
Db 406 GGTGAGCTCTTCGACTACCTGGTGAAGAAGGGGAGCTGACCGCTAAGAGGCTCGGAAG 465
Qy 361 TTCTTCCGCGAGATCATCTCTGCGCTGAGCTTCTGCGCCACAGCCACTCATATGCCACAGG 420
Db 466 TTCTTCCGCGAGATCATCTCTGCGCTGAGCTTCTGCGCCACAGCCACTCATATGCCACAGG 525
Qy 421 GATCTGAAAACTGAAAAACCTCTGCTCGAGAGAGAACCAACATCCGATCGCAGACTTT 480
Db 526 GATCTGAAAACTGAAAAACCTCTGCTCGAGAGAGAACCAACATCCGATCGCAGACTTT 585
Qy 481 GGCATGGGCTCCCTGCGAGGTGGCGACAGCTGTTGGAGCAGCTGGGTCCCCCCAC 540
Db 586 GGCATGGGCTCCCTGCGAGGTGGCGACAGCTGTTGGAGCAGCTGGGTCCCCCCAC 645
Qy 541 TACGCTGCCCGAGGTGATCCCGGGGGAGAGATGATGACCGCGGAGAGCGGAGCTGTGG 600
Db 646 TACGCTGCCCGAGGTGATCCCGGGGGAGAGATGATGACCGCGGAGAGCGGAGCTGTGG 705

601 AGCTGCGCGCTCATCTGTTGCTTGGTGGGGCTCTGCCCTTCGACGATGACAAC 660
Db AGCTGCGCGCTCATCTGTTGCTTGGTGGGGCTCTGCCCTTCGACGATGACAAC 765
661 TTGCGACAGCTGCTGGAAGGTGAAGCGGGCGTGTTCACATGCGGCACTTTATCCCG 720
Db TTGCGACAGCTGCTGGAAGGTGAAGCGGGCGTGTTCACATGCGGCACTTTATCCCG 825
721 CCGGACTGCCAGAGTCTGCTACCGGGGATCATCGAGGTGACCGCCGACCGCCCTCACG 780
Db CCGGACTGCCAGAGTCTGCTACCGGGGATCATCGAGGTGACCGCCGACCGCCCTCACG 885
781 CTAGAGCACATTGAGAAACATATGTTATATAGGGGGCAAGATGAGCCCGAACAGAG 840
Db CTAGAGCACATTGAGAAACATATGTTATATAGGGGGCAAGATGAGCCCGAACAGAG 945
841 CAGCCATTCTCGCAGGTGCGATCCGCTCCGCTCCGACCGCTGGAGGACATCGACCCC 900
Db CAGCCATTCTCGCAGGTGCGATCCGCTCCGCTCCGACCGCTGGAGGACATCGACCCC 1005
901 GAGCTGCTGGACAGCATGCACTCACTGGGCTGCTTCCGAGACCGCAACAAGCTGCTGCAG 960
Db GAGCTGCTGGACAGCATGCACTCACTGGGCTGCTTCCGAGACCGCAACAAGCTGCTGCAG 1065
961 GACTGCTGTCGAGGAGGAGAACAGAGAGATGATTTCTCTCTCTCTGAGACCGG 1020
Db GACTGCTGTCGAGGAGGAGAACAGAGAGATGATTTCTCTCTCTCTGAGACCGG 1125
1021 AAGAAAGGTACCGGACGAGGAGTGAAGCTGCGCCCGGACGAGATAGACCTT 1080
Db AAGAAAGGTACCGGACGAGGAGTGAAGCTGCGCCCGGACGAGATAGACCTT 1185
1126 AAGAAAGGTACCGGACGAGGAGTGAAGCTGCGCCCGGACGAGATAGACCTT 1140
Db AAGAAAGGTACCGGACGAGGAGTGAAGCTGCGCCCGGACGAGATAGACCTT 1245
1141 AATTCATGAGGTGCTCAGGTGACGAGCGGGTCTCCGCGTCTGCGCGCGGGCC 1200
Db AATTCATGAGGTGCTCAGGTGACGAGCGGGTCTCCGCGTCTGCGCGCGGGCC 1305
1201 ATTGAGATGGCCAGCAGCGGACAGGTCTCGGTCCATCAGCGTGTCTCTCAGGCTT 1260
Db ATTGAGATGGCCAGCAGCGGACAGGTCTCGGTCCATCAGCGTGTCTCTCAGGCTT 1365
1261 TCCACCGCCCACTCAGCAGCGCCCGGGTGAACCTTCAACCGCTTCAACGAGGGCAGTCCC 1320
Db TCCACCGCCCACTCAGCAGCGCCCGGGTGAACCTTCAACCGCTTCAACGAGGGCAGTCCC 1425
1321 CTCCCGACCCCGAGGAGACACTGTTCACACGCGCAAGGAGAGCCGCTGGACGCCC 1380
Db CTCCCGACCCCGAGGAGACACTGTTCACACGCGCAAGGAGAGCCGCTGGACGCCC 1485
1381 AACCCACCGCCCGTCCAGCGCCAGCGTCCGAGGGGTCCCTGAGGGCGCGCTCAAC 1440
Db AACCCACCGCCCGTCCAGCGCCAGCGTCCGAGGGGTCCCTGAGGGCGCGCTCAAC 1545
1441 TCCATCAAGAACAGCTTTCTGGGCTCAACCGCGCTTCCACCGCCGGAACCTCAAGTTCCG 1500
Db TCCATCAAGAACAGCTTTCTGGGCTCAACCGCGCTTCCACCGCCGGAACCTCAAGTTCCG 1605
1501 ACGCGGAGGAGATGTCACCTGACACAGAGTGTCTCCGAGAGCTGGCGAAGTCC 1560
Db ACGCGGAGGAGATGTCACCTGACACAGAGTGTCTCCGAGAGCTGGCGAAGTCC 1665
1606 ACGCGGAGGAGATGTCACCTGACACAGAGTGTCTCCGAGAGCTGGCGAAGTCC 1620
Db ACGCGGAGGAGATGTCACCTGACACAGAGTGTCTCCGAGAGCTGGCGAAGTCC 1725
1621 AAACCTCTGAGTCCATCAAGGCTGACATCGTGACGCGCTTCTGTGATTTCCAGTCTC 1680
Db AAACCTCTGAGTCCATCAAGGCTGACATCGTGACGCGCTTCTGTGATTTCCAGTCTC 1785
1681 AGCCACAGCTCATCTCCCAACAGAGCTTCCGGGCGGAGTCAAGGCCACCGGGGGGCCA 1740

1786 AGCCACAGCGTCACTCCCAACGAGCTTCCGGGCGGAGTACAGGCCACCGGGGGGCCA 1845
QY 1741 GCCGTGTTCCAAAGCCGCTCAAGTTCCAGGTTGATATCACCTACACGAGGAGTGGGGAG 1800
Db 1846 GCCGTGTTCCAAAGCCGCTCAAGTTCCAGGTTGATATCACCTACACGAGGAGTGGGGAG 1905
QY 1801 GCGCAGAGGAGAACCGCATCTACTCCGTCACTTTCACCTTCACTGCTCTCAGGCCCCAGCCCT 1860
Db 1906 GCGCAGAGGAGAACCGCATCTACTCCGTCACTTCCGTCACTTCACTGCTCTCAGGCCCCAGCCCT 1965
QY 1861 CCGTTCAAGAGGAGTGGAGACCATCCAGGCCAGCTGCTGAGCACACACACCGCCCT 1920
Db 1966 CCGTTCAAGAGGAGTGGAGACCATCCAGGCCAGCTGCTGAGCACACACACCGCCCT 2025
QY 1921 GCGGCCACGACTTGTTCAGACACCACTACTACTGTATGAAATGATGACGGGGCGGCTTTCC 1980
Db 2026 GCGGCCACGACTTGTTCAGACACCACTACTACTGTATGAAATGATGACGGGGCGGCTTTCC 2085
QY 1981 AAATGTGGAATATCCCGAAAGTTAA 2007
Db 2086 AAATGTGGAATATCCCGAAAGTTAA 2112

RESULT 3
ABX13584
ID ABX13584 standard; cDNA; 3364 BP.
XX
AC ABX13584;
XX
XX 10-FEB-2003 (first entry)
DT
DE Human cDNA encoding serine protein kinase KSE336-2.
XX
XX Human; ss; gene; chromosome 11p15.5-pter; astrocytoma; meningioma;
KW pancreatic adenocarcinoma; insulin-dependent diabetes mellitus 2;
KW helicoid peripapillary choriorretinal degeneration; brain; pancreas;
KW Beckwith-Wiedemann syndrome; congenital hyperinsulinism; KSE336-2.
XX
OS Homo sapiens.
XX
XX
XX Key Location/Qualifiers
XX CDS 482..2239
XX FT /*tag= a
XX FT /product= "KSE336-2"
XX
XX US6455292-B1.
XX
XX 24-SEP-2002.
XX
XX 16-AUG-2001; 2001US-0930181.
XX
XX 16-AUG-2001; 2001US-0930181.
XX
XX (ORIG-) ORIGENE TECHNOLOGIES INC.
XX
XX Shu Y, Fan W, Kovacs XF, Zidanic M, Jay G;
XX WPI; 2003-066233/06.
XX P-PSDB; ABG72383.
XX
XX New isolated polynucleotide coding without interruption for a human
XX KSE336 polypeptide useful for preventing or treating
XX diseases/conditions relating to brain and pancreas, e.g. meningioma,
XX insulin-dependent diabetes mellitus 2
XX
XX Claim 4; Column 43-48; 34pp; English.
XX
XX The invention relates to an isolated polynucleotide (its complement
XX or a sequence 99% similar to it) coding without interruption for a human
XX KSE336 polypeptide, a serine protein kinase, comprising the KSE336-1 and
XX KSE336-2 splice variants appearing as ABG72382 and ABG72383. Also
XX included is a method of identifying an agent that modulates the

expression of KSE336 in brain, pancreas, brain progenitor or pancreas
progenitor cells comprising: (a) contacting a cell population comprising
the cells with a test agent under conditions effective for the test agent
to modulate the expression of KSE336; and (b) determining if the test
agent modulates the expression of KSE336. The polynucleotides are useful
as molecular targets or drug targets, and for detecting, diagnosing,
staging, monitoring, prognosticating, preventing or treating diseases or
conditions relating to brain and pancreas, such as astrocytoma,
meningioma, pancreatic adenocarcinoma, insulin-dependent diabetes
mellitus 2, heliocoid petipapillary chorioretinal degeneration, Beckwith-
Wiedemann syndrome or congenital hyperinsulinism. The method and
polynucleotides are useful in research, diagnosis, pathology,
therapy, clinical medicine, forensic science and pathology.
The gene for KSE336 is located on chromosome 11p15.5-pter.
XX The present sequence encodes the KSE366 variant KSE366-2.
SQ Sequence 3364 BP; 639 A; 1078 C; 1069 G; 578 T; 0 other;

Query Match 99.3%; Score 1993; DB 25; Length 3364;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2007; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 1 ATGACATCGACGGGAAGAGCGCGCGCGAGACGCGAGCTATGTTGGGCCCTACCGG 60
DB 229 ATGACATCGACGGGAAGAGCGCGCGCGAGACGCGAGCTATGTTGGGCCCTACCGG 288

QY 61 CTGGAGAAGACGCTGGGCAAGGGGCGAGACAGCTCTGTGAAGCTGGGGGTTCACTGCGTC 120
DB 289 CTGGAGAAGACGCTGGGCAAGGGGCGAGACAGCTCTGTGAAGCTGGGGGTTCACTGCGTC 348

QY 121 ACCTGCCAGAGGTGGCCATCAAGATCGTCAACCGTGAGAGCTCAGCGAGTCGGTGTG 180
DB 349 ACCTGCCAGAGGTGGCCATCAAGATCGTCAACCGTGAGAGCTCAGCGAGTCGGTGTG 408

QY 181 ATGAAGTGGAGCGGAGATCGGATCTGAAGCTATTGAGACCCCGACCTCTTAAG 240
DB 409 ATGAAGTGGAGCGGAGATCGGATCTGAAGCTATTGAGACCCCGACCTCTTAAG 468

QY 241 CTGACGACGCTTTATGAAAACAAAATAATTT- - -GTACCTGGTGTGATGAACAGCTGC 296
DB 469 CTGACGACGCTTTATGAAAACAAAATAATTTGTAGGTACCTGTGTGATGAACAGCTGC 528

QY 297 AGTGGTGAAGCTCTTGGATACCTGGTGAAGAGGGAGGCTGAGCCCTAAGGAGGCTCG 356
DB 529 AGTGGTGAAGCTCTTGGATACCTGGTGAAGAGGGAGGCTGAGCCCTAAGGAGGCTCG 588

QY 357 GAACTTCTTCGGGAGATCATCTGCGCTGAGCTTCTGCCACAGCCACTCCATATGCCA 416
DB 589 GAACTTCTTCGGGAGATCATCTGCGCTGAGCTTCTGCCACAGCCACTCCATATGCCA 648

QY 417 CAGGATCTGAAACCTGAAAACCTCTCTGGAAGAGAAACAAACATCCGCATCGCAGA 476
DB 649 CAGGATCTGAAACCTGAAAACCTCTCTGGAAGAGAAACAAACATCCGCATCGCAGA 708

QY 477 CTTTGGCATGGGCTCCCTGAGGTGGCGACAGCCCTGTGAGACCACTGTGGTCCCC 536
DB 709 CTTTGGCATGGGCTCCCTGAGGTGGCGACAGCCCTGTGAGACCACTGTGGTCCCC 768

QY 537 CCATCTACCCCTGCCCCGAGGTGATCCGGGGGAGAGTATGACGCGCGGAAGGGGAGCT 596
DB 769 CCATCTACCCCTGCCCCGAGGTGATCCGGGGGAGAGTATGACGCGCGGAAGGGGAGCT 828

QY 597 GTGAGCTGCGCGCTCATCTGTTCCGCTTGTGTTGGGGGCTCTGCGCTTCGACGATGA 656
DB 829 GTGAGCTGCGCGCTCATCTGTTCCGCTTGTGTTGGGGGCTCTGCGCTTCGACGATGA 888

QY 657 CAATCTGCGACAGCTGCTGGAGAGGTGAAGCGGGGCTGTTCCACATGCGCGCATTTAT 716
DB 889 CAATCTGCGACAGCTGCTGGAGAGGTGAAGCGGGGCTGTTCCACATGCGCGCATTTAT 948

QY 717 CCGCGCCGACCTGCCAGAGTCTGTACGGGGCATATCGAGGTGGAGCGCGCACCGCCCT 776
DB 949 CCGCGCCGACCTGCCAGAGTCTGTACGGGGCATATCGAGGTGGAGCGCGCACCGCCCT 1008

QY 777 CACGCTAGAGCACATTTCAGAAAACACATATGTTATATAGGGGGCAAGATAGCCCGAAC 836
DB 1009 CACGCTAGAGCACATTTCAGAAAACACATATGTTATATAGGGGGCAAGATAGCCCGAAC 1068

QY 837 AGAGCAGCCCATCTCTCGCAAGGTGACATCCGCTCGCTGCCAGCTCGAGAGCATCGA 896
DB 1069 AGAGCAGCCCATCTCTCGCAAGGTGACATCCGCTCGCTGCCAGCTCGAGAGCATCGA 1128

QY 897 CCGCAGCTGCTGACAGCATGCACTCACTGGGCTGCTCCGAGACCGCAACAGCTGCT 956
DB 1129 CCGCAGCTGCTGACAGCATGCACTCACTGGGCTGCTCCGAGACCGCAACAGCTGCT 1188

QY 957 GCAGGACCTCTGCTCCGAGGAGAGAACCCAGGAGAGATGATTTACTTCTCTCTCGGA 1016
DB 1189 GCAGGACCTCTGCTCCGAGGAGAGAACCCAGGAGAGATGATTTACTTCTCTCTCGGA 1248

QY 1017 CCGGAAAGAAAGTTACCCGAGCCAGGAGATGAGGACCTGCCCGCCCGGAAACGAGATGA 1076
DB 1249 CCGGAAAGAAAGTTACCCGAGCCAGGAGATGAGGACCTGCCCGCCCGGAAACGAGATGA 1308

QY 1077 CCTTCCCGGAAGCTGTGACCTCCCGATGCTCAACCCGCAAGCGGCGGCGCAGA 1136
DB 1309 CCTTCCCGGAAGCTGTGACCTCCCGATGCTCAACCCGCAAGCGGCGGCGCAGA 1368

QY 1137 ACGCAATTCATGAGGTGCTCAGCGTGAAGCGGCGGCTCCCGGCTGCTGCGCGCG 1196
DB 1369 ACGCAATTCATGAGGTGCTCAGCGTGAAGCGGCGGCTCCCGGCTGCTGCGCGCG 1428

QY 1197 GGCATTGAGATGGCCAGCAGCGGCTGAGGTCTGGTCTCATACAGCGGTGCTCTCAGG 1256
DB 1429 GGCATTGAGATGGCCAGCAGCGGCTGAGGTCTGGTCTCATACAGCGGTGCTCTCAGG 1488

QY 1257 CTTTCCACAGCCACTCAGCAGCGCCCGGGTGAACCCCTCACCCCTCACCAAGGGGCGAG 1316
DB 1489 CTTTCCACAGCCACTCAGCAGCGCCCGGGTGAACCCCTCACCCCTCACCAAGGGGCGAG 1548

QY 1317 TCCTCTCCCAACCCCAAGGGGACACCTGTCCACACGCCCAAGAGAGCCCGGTGCGAC 1376
DB 1549 TCCTCTCCCAACCCCAAGGGGACACCTGTCCACACGCCCAAGAGAGCCCGGTGCGAC 1608

QY 1377 GCCCAACCCCAAGCGCCCGCTCAGCGCTCGAGGGGTGCTGAGAGGGCGCGGCT 1436
DB 1609 GCCCAACCCCAAGCGCCCGCTCAGCGCTCGAGGGGTGCTGAGAGGGCGCGGCT 1668

QY 1437 CAATCTCATCAAGAAAGCTTTCTGGGCTCACCCCGCTCCACCGCGCGAAACTGCAAGT 1496
DB 1669 CAATCTCATCAAGAAAGCTTTCTGGGCTCACCCCGCTCCACCGCGCGAAACTGCAAGT 1728

QY 1497 TCCGACGCGGAGAGATGTCACACCTGACACAGAGTCTGCCCGAGAGCTGGCGAAGAA 1556
DB 1729 TCCGACGCGGAGAGATGTCACACCTGACACAGAGTCTGCCCGAGAGCTGGCGAAGAA 1788

QY 1557 GTCTGTGTTGGAACTTTCATCAGCTGAGAGAGGAGGAGAGATCTTCTGTGTCATCAA 1616
DB 1789 GTCTGTGTTGGAACTTTCATCAGCTGAGAGAGGAGGAGAGATCTTCTGTGTCATCAA 1848

QY 1617 AGACAAACCTCTGAGCTTCATCAAGGCTGACATGCTGACAGCTTCTGTCGATTCCAG 1676
DB 1849 AGACAAACCTCTGAGCTTCATCAAGGCTGACATGCTGACAGCTTCTGTCGATTCCAG 1908

QY 1677 TCTCAGCACAGCGTCTATCTCCCAACAGAGCTTTCGGGGCGAGTACAAGGCGCACGGGGG 1736
DB 1909 TCTCAGCACAGCGTCTATCTCCCAACAGAGCTTTCGGGGCGAGTACAAGGCGCACGGGGG 1968

QY 1737 GCCAGCGGTGTTCCAGAGCGCGGTCAAGTTCAGAGTTGATATCACTACAGGAGGCTGG 1796
DB 1969 GCCAGCGGTGTTCCAGAGCGCGGTCAAGTTCAGAGTTGATATCACTACAGGAGGCTGG 2028

QY 1797 GGAGGGCGACAGAGAGAGCGCATCTACCTCGCTCACCTTCACCTCTGCTCAGGCCCGAG 1856
DB 2029 GGAGGGCGACAGAGAGAGCGCATCTACCTCGCTCACCTTCACCTCTGCTCAGGCCCGAG 2088

QY 1857 CCCTGCGTTCAAGAGGGTGTGGAGACCAATCCAGGCCAGCTCTGAGCAGACACAGACCC 1916
Db CCGTGGCTTCAAGAGGGTGTGGAGACCAATCCAGGCCAGCTCTGAGCAGACACAGACCC 2148
QY 1917 GCCTGGGCCAGCAGCTTGTTCAGACACCACTAATCTGTATGGAATGATGACGGGGCGGCT 1976
Db GCTGGGCCAGCAGCTTGTTCAGACACCACTAATCTGTATGGAATGATGACGGGGCGGCT 2208
QY 1977 TTCCAAATGTGGAATTATCCGAAAAGTTAA 2007
Db 2209 TTCCAAATGTGGAATTATCCGAAAAGTTAA 2239

RESULT 4
AAD34315
ID AAD34315 standard; cDNA; 2647 BP.
AC AAD34315;
XX
DT 16-JUL-2002 (first entry)
XX
DE Human PKIN-18 cDNA.
XX
KW Human; kinase; enzyme; PKIN-18 protein; immune system disorder; anaemia;
KW acquired immune deficiency syndrome; thymic hypoplasia; Crohn's disease;
KW asthma; neurological disorder; epilepsy; Charcot-Marie-Tooth disease;
KW AIDS; seizures; cell proliferative disorder; cancer; adenocarcinoma;
KW leukaemia; lymphoma; melanoma; myeloma; sarcoma; developmental disorder;
KW Down's syndrome; gene therapy; protein therapy; cytostatic; gene; ss.
XX
OS Homo sapiens.

XX
FH Key Location/Qualifiers
FT CDS 1..1995
FT FT /*tag= a
FT FT /product= "Human PKIN-18 protein"
XX
XX WO200218557-A2.
XX
XX 07-MAR-2002.
XX
XX 31-AUG-2001; 2001WO-US27219.
XX
XX 31-AUG-2000; 2000US-229873P.
PR 08-SEP-2000; 2000US-231357P.
PR 14-SEP-2000; 2000US-232654P.
PR 22-SEP-2000; 2000US-234902P.
PR 29-SEP-2000; 2000US-236499P.
PR 06-OCT-2000; 2000US-238389P.
PR 13-OCT-2000; 2000US-240542P.
XX
XX (INCY-) INCYTE GENOMICS INC.
XX
XX Bandman O, Nguyen DB, Wallia NK, Hafalia AJA, Yao MG, Gandhi AR;
PI Gururajan R, Ding L, Patterson C, Yue H, Baughn MR, Tribouley CM;
PI Thornton M, Elliott VS, Lu Y, Ison CH, Au-Young J, Tang YI;
PI Azimzai Y, Burrill JD, Marcus GA, Zingler KA, Lu DAM, Lal PG;
PI Ramkumar J, Warren BA, Kearney L, Policky JL, Thangavelu K;
PI Burford N;
XX
XX WPI; 2002-329769/36.
DR P-FSDB; AAE21723.
XX
XX New human kinases, useful for diagnosing, treating or preventing immune
PT system disorders (e.g. Crohn's disease), neurological disorders (e.g.
PT epilepsy), or cell proliferative disorders (e.g. cancers such as
PT leukemia or lymphoma) -
XX
XX Claim 97; Page 212-213; 218pp; English.
XX
XX The present invention relates to human kinases (PKIN) and polynucleotides
CC encoding such proteins. PKIN sequences of the invention are useful for
CC diagnosing, treating or preventing disorders associated with aberrant

CC expression of PKIN, particularly immune system disorders (e.g. acquired
CC immune deficiency syndrome (AIDS), thymic hypoplasia, Crohn's disease,
CC anaemia, asthma), neurological disorders (e.g. epilepsy, Charcot-Marie-
CC Tooth disease or seizures), cell proliferative disorders (e.g. cancers
CC such as adenocarcinoma, leukaemia, lymphoma, melanoma, myeloma, sarcoma),
CC and developmental disorders (e.g. Down's syndrome). They are also used
CC in gene therapy and protein therapy. The present sequence is a cDNA
CC encoding human PKIN-18 protein.
XX
QY Sequence 2647 BP; 525 A; 885 C; 789 G; 448 T; 0 other;
Query Match 98.0%; Score 1966; DB 24; Length 2647;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1966; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 42 GTATGTTGGGCCCTACCGGCTGGAGAAGACGCTGGGCAAGGGGCGAGAGTCTCTGTGAA 101
Db 30 GTATGTTGGGCCCTACCGGCTGGAGAAGACGCTGGGCAAGGGGCGAGAGTCTCTGTGAA 89
QY 102 GCTGGGGTTTCACTCGTCACTGCTGCAAGAGGTGGCCATCAAGATCGTCAACCGTGAGAA 161
Db 90 GCTGGGGTTTCACTCGTCACTGCTGCAAGAGGTGGCCATCAAGATCGTCAACCGTGAGAA 149
QY 162 GCTCAGCAGTCTGCTGCTGATGAAGGTGGGCGGAGATCGCGATCCTCAAGCTCATTGA 221
Db 150 GCTCAGCAGTCTGCTGCTGATGAAGGTGGGCGGAGATCGCGATCCTCAAGCTCATTGA 209
QY 222 GCACCCCCACGCTCTAAAGCTCAGCAGCTTTATGAAAACAAAAAATATTTGTACTCTGT 281
Db 210 GCACCCCCACGCTCTAAAGCTCAGCAGCTTTATGAAAACAAAAAATATTTGTACTCTGT 269
QY 282 GCTAGAACACGTGTCAGGTGGTGGTCTTTCAGTCTTTCAGTCTTTCAGTCTTTCAGTCT 341
Db 270 GCTAGAACACGTGTCAGGTGGTGGTCTTTCAGTCTTTCAGTCTTTCAGTCTTTCAGTCT 329
QY 342 GCTAAGGAGGCTCGAAGTCTTTCGGCAGATCATCTCGCGTGGACTCTCTGCCACAG 401
Db 330 GCTAAGGAGGCTCGAAGTCTTTCGGCAGATCATCTCGCGTGGACTCTCTGCCACAG 389
QY 402 CCACCTCATATGCCACAGGGATCTGAAACCTTGAAACCTTGAAACCTTGAAACCTTGAAAC 461
Db 390 CCACCTCATATGCCACAGGGATCTGAAACCTTGAAACCTTGAAACCTTGAAACCTTGAAAC 449
QY 462 CATCCGATCGCAGACTTTGGGATGCGCTCCCTGCGAGTGGCGACAGCTGTGGAGAC 521
Db 450 CATCCGATCGCAGACTTTGGGATGCGCTCCCTGCGAGTGGCGACAGCTGTGGAGAC 509
QY 522 CAGCTGTGGTCCCCCCTAGCCCTGCGGAGTGTATCCGGGGGAGAGTATCAGCG 581
Db 510 CAGCTGTGGTCCCCCCTAGCCCTGCGGAGTGTATCCGGGGGAGAGTATCAGCG 569
QY 582 CCGAAGGCGGAGCTGTGGAGTGGCGGCTCATCTGTTTCGCTTTCGCTTTCGCTTTCGCTTTC 641
Db 570 CCGAAGGCGGAGCTGTGGAGTGGCGGCTCATCTGTTTCGCTTTCGCTTTCGCTTTCGCTTTC 629
QY 642 GCCTTCGAGATGACAACTTGGCAGCTGCTGGAGAGGTGAAGCGGGCGGTGTCCA 701
Db 630 GCCTTCGAGATGACAACTTGGCAGCTGCTGGAGAGGTGAAGCGGGCGGTGTCCA 689
QY 702 CATGCCGCACTTTATCCCGCCGACTGCGCAGAGTCTGCTACCGGGGATGATCGAGGTGA 761
Db 690 CATGCCGCACTTTATCCCGCCGACTGCGCAGAGTCTGCTACCGGGGATGATCGAGGTGA 749
QY 762 CGCCGACCGCGCTTCACTGAGCAGATTCAGAAACATATGATGATATAGGGGGCAA 821
Db 750 CGCCGACCGCGCTTCACTGAGCAGATTCAGAAACATATGATGATATAGGGGGCAA 809
QY 822 GAATGAGCCGAAACAGAGAGCCCACTTCTCGCAGAGTGCAGATCGCTCGTGGCCAG 881
Db 810 GAATGAGCCGAAACAGAGAGCCCACTTCTCGCAGAGTGCAGATCGCTCGTGGCCAG 869
QY 882 CTTGGAGGACATGACCCGAGCTGTGGACAGCATGCACTCACTGGGTGCTTCCGAGA 941

Db 870 CTGGAGGACATCGACCCCGAGCTGCTGGACAGATGCACTCACTGGGCTGCTCCGAGA 929
QY 942 CGCAACAGCTGCTCCAGGACCTGCTGCCAGGAGAACACAGGAGAGATGATTATA 1001
Db 930 CGCAACAGCTGCTCCAGGACCTGCTGCCAGGAGAACACAGGAGAGATGATTATA 989
QY 1002 CTTCTCTCTCTGGACCGGAAGAAGATGATCCGAGCCAGGAGGATGAGGACCTGCCCCC 1061
Db 990 CTTCTCTCTCTGGACCGGAAGAAGATGATCCGAGCCAGGAGGATGAGGACCTGCCCCC 1049
QY 1062 CGGAAACAGATAGACCTCTCCCGGAAGCGTGTGACTCCCGATGCTGAACCGGACGG 1121
Db 1050 CGGAAACAGATAGACCTCTCCCGGAAGCGTGTGACTCCCGATGCTGAACCGGACGG 1109
QY 1122 CAAAGCGGGCCAGAACGCAATTCATGAGGTGCTCAGCGTGAGCGGCGGCTCCCC 1181
Db 1110 CAAAGCGGGCCAGAACGCAATTCATGAGGTGCTCAGCGTGAGCGGCGGCTCCCC 1169
QY 1182 GGTGCTGCGCGGGCCATTTGATGTCGCCAGCACGCGCAGAGGTCTCGGTCCATCAG 1241
Db 1170 GGTGCTGCGCGGGCCATTTGATGTCGCCAGCACGCGCAGAGGTCTCGGTCCATCAG 1229
QY 1242 CGGTGCTCTCTCAGGCTTTTCCACAGCCCACTCAGCAGCCCCCGGCTGACCCCTCACCC 1301
Db 1230 CGGTGCTCTCTCAGGCTTTTCCACAGCCCACTCAGCAGCCCCCGGCTGACCCCTCACCC 1289
QY 1302 CTTACCAAGGGGAGTCCCTCTCCACCCCAAGGGGACACCTGTCCACAGCCCAAGGA 1361
Db 1290 CTTACCAAGGGGAGTCCCTCTCCACCCCAAGGGGACACCTGTCCACAGCCCAAGGA 1349
QY 1362 GAGCCGGGTGCGACGCCCAACCCACCGCCCCCGTCCAGCCCCAGCGTCCGAGGGGTGCC 1421
Db 1350 GAGCCGGGTGCGACGCCCAACCCACCGCCCCCGTCCAGCCCCAGCGTCCGAGGGGTGCC 1409
QY 1422 CTGGAGGGCGGGCTCAACTCCATCAAGAAAGCTTTCTGGGCTCACCCCGTCCACCG 1481
Db 1410 CTGGAGGGCGGGCTCAACTCCATCAAGAAAGCTTTCTGGGCTCACCCCGTCCACCG 1469
QY 1482 CCGAAACTGCAAGTTCCGACCCCGAGGAGATGTCCAACTGACACAGAGTCCGTCCCC 1541
Db 1470 CCGAAACTGCAAGTTCCGACCCCGAGGAGATGTCCAACTGACACAGAGTCCGTCCCC 1529
QY 1542 AGAGTGGGAGAGTCTGTTGGAACTTATCAGCTTGGAGAGGAGGAGGAGAGAT 1601
Db 1530 AGAGTGGGAGAGTCTGTTGGAACTTATCAGCTTGGAGAGGAGGAGGAGAGAT 1589
QY 1602 CTTGCTGTGTCATCAAGACAAACCTCTGAGCTCCATCAAGGCTGACATGTCACGCTT 1661
Db 1590 CTTGCTGTGTCATCAAGACAAACCTCTGAGCTCCATCAAGGCTGACATGTCACGCTT 1649
QY 1662 CTGTGATTTCCAGTCTCAGCCACAGCGTATCTCCCAAACGAGCTTCCGGGCGGAGTA 1721
Db 1650 CTGTGATTTCCAGTCTCAGCCACAGCGTATCTCCCAAACGAGCTTCCGGGCGGAGTA 1709
QY 1722 CAAAGCCAGGGGGGCGGAGCGTGTTCAGAGCCGCTCAAGTTCAGGTTGATATAC 1781
Db 1710 CAAAGCCAGGGGGGCGGAGCGTGTTCAGAGCCGCTCAAGTTCAGGTTGATATAC 1769
QY 1782 CTACAGGAGGTGGGGGCGGAGAGGAGAGCGCATCTACTCCGTACCTTCAACCT 1841
Db 1770 CTACAGGAGGTGGGGGCGGAGAGGAGAGCGCATCTACTCCGTACCTTCAACCT 1829
QY 1842 GCTCTCAGGCCCCAGCGCTCGCTTCAAGAGGGTGGTGGAGCATCCAGGCCAGCTGCT 1901
Db 1830 GCTCTCAGGCCCCAGCGCTCGCTTCAAGAGGGTGGTGGAGCATCCAGGCCAGCTGCT 1889
QY 1902 GAGCACAGACCGGCTTGGGCGCCAGCATCTGTTCAGACACCATTAAGTATGTAAT 1961
Db 1890 GAGCACAGACCGGCTTGGGCGCCAGCATCTGTTCAGACACCATTAAGTATGTAAT 1949
QY 1962 GATGAGGGGGGCTTTCCAAATGTGAATTTATCCGAAAGCTTAA 2007
Db 1950 GATGAGGGGGGCTTTCCAAATGTGAATTTATCCGAAAGCTTAA 1995

RESULT 5
ABA02995
ID ABA02995 standard; cDNA; 2025 BP.
XX
AC ABA02995;
XX
DT 19-FEB-2002 (first entry)
XX
Human protein kinase 2246 coding sequence SEQ ID NO 3.
XX
Human; protein kinase 2246; cytostatic; immunomodulator; carcinoma;
anti-inflammatory; analgesic; cardiovascular; cancer; sarcoma;
cellular proliferation disorder; cellular differentiation disorder;
metastatic; haematopoietic disorder; leukaemia; immune disorder;
inflammatory disorder; arthritis; autoimmune disease; diabetes mellitus;
psoriasis; Crohn's disease; cardiovascular disease; virus; pain;
gene therapy; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..2025
FT /*tag= a
FT /product= "protein kinase 2246"
XX
WO200181588-A2.
XX
PD 01-NOV-2001.
XX
PF 25-APR-2001; 2001WO-US13784.
XX
PR 25-APR-2000; 2000US-19931P.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Meyers R;
XX
WPI; 2002-049281/06.
DR P-PSDB; AAM47830.
XX
New protein kinase nucleic acid and polypeptide molecules, designated
2246, useful for diagnosing, preventing or treating cancer or a
cellular proliferation/differentiation disorders, e.g. carcinoma,
sarcoma or leukaemias -
XX
Claim 1; Fig 1; 11pp; English.
XX
The invention relates to the human protein kinase 2246 gene and the
isolated encoded polypeptide with cytostatic, immunomodulator,
anti-inflammatory, analgesic and cardiovascular activity. The 2246
nucleic acid and polypeptide are useful for diagnosing, preventing or
treating a subject having cancer or a cellular proliferation and/or
differentiation disorder or at risk of developing cancer or a cellular
proliferation and/or differentiation disorder. In particular, the
disorder includes carcinoma, sarcoma, metastatic or haematopoietic
disorders (e.g. leukaemias) or cancers of the lung, breast, thyroid, head
neck, prostate or genito-urinary tract. The 2246 nucleic acid and
polypeptide are also useful for treating immune disorders, e.g.
inflammatory (e.g. respiratory inflammation or arthritis), autoimmune
disease (e.g. diabetes mellitus, psoriasis, Wegener's granulomatosis,
Crohn's disease or Grave's disease), for treating cardiovascular
diseases, endothelial cell disorder, viral diseases or pain. The nucleic
acid and polypeptide are also useful for evaluating the efficacy of a
treatment of cancer or a cellular proliferation and/or differentiation
disorder. The nucleic acid is useful for gene therapy. The present
sequence is that of the 2246 coding sequence.
XX
SQ Sequence 2025 BP; 442 A; 641 C; 616 G; 326 T; 0 other;

Query Match 96.6%; Score 1939.6; DB 24; Length 2025;
Best Local Similarity 99.8%; Pred. No. 0;

	Matches	1942;	Conservative	0;	Mismatches	4;	Indels	0;	Gaps	0;
QY	1	ATGACATCGACGGGGAAGGACGGCGCGCGCACAGCGCAGCTATGTTGGCGCCTACCGG	60							
Db	1	ATGACATCGACGGGGAAGGACGGCGCGCGCACAGCGCAGTATGTTGGGCCCTACCGG	60							
QY	61	CTGGAGAAGACGCTGGCGAAGGGCGACAGGTCCTGGTGAAGCTGGGGGTTCACTGGCTC	120							
Db	61	CTGGAGAAGACGCTGGCGAAGGGCGACAGGTCCTGGTGAAGCTGGGGGTTCACTGGCTC	120							
QY	121	ACCTGCCAGAAGGTGGCCCATCAAGATCTGTCAAACCGTGAGAAGCTCAGCGAGTCCGTGCTG	180							
Db	121	ACCTGCCAGAAGGTGGCCCATCAAGATCGTCAACCGTGAGAAGCTCAGCGAGTCCGTGCTG	180							
QY	181	ATGAAGGTGGAGCGGAGATCGCGATCCTGAAGCTCATTTGAGCACCCACACGCTCTAAAG	240							
Db	181	ATGAAGGTGGAGCGGAGATCGCGATCCTGAAGCTCATTTGAGCACCCACCGCTCTAAAG	240							
QY	241	CTGCACGACGTTTATGAAAACAAAAAATATTTCTGACTCTGGTGTCTAGAACACGCTGTGAGGT	300							
Db	241	CTGCACGACGTTTATGAAAACAAAAAATATTTGTACTCTGGTGTCTAGAACACGCTGTGAGGT	300							
QY	301	GGTGAGCTCTTGACACTACTGTGTGAAGGGGAGGCTGACGCTTAAGGAGGCTCGGAAG	360							
Db	301	GGTGAGCTCTTGACACTACTGTGTGAAGGGGAGGCTGACGCTTAAGGAGGCTCGGAAG	360							
QY	361	TTCTTCCGCGAGATCATCTGCGCTGGACTTCTGCCACAGCCACTCCATATGCCACAGG	420							
Db	361	TTCTTCCGCGAGATCATCTGCGCTGGACTTCTGCCACAGCCACTCCATATGCCACAGG	420							
QY	421	GATCTGAAACCTGAAAACCTCTGCTGGACGAGAAGAACAACTCCGCATCGCAGACTTT	480							
Db	421	GATCTGAAACCTGAAAACCTCTGCTGGACGAGAAGAACAACTCCGCATCGCAGACTTT	480							
QY	481	GGCATGGCTCCCTGCAGGTTGGCGACAGCCTGTTGGAGACACAGCTGTGGGTCCCCCACC	540							
Db	481	GGCATGGCTCCCTGCAGGTTGGCGACAGCCTGTTGGAGACACAGCTGTGGGTCCCCCACC	540							
QY	541	TACGCTTGCCCCGAGGTGATCCGGGGGGAGAGTATGACGCGCCGGAAGCGGACGCTGTGG	600							
Db	541	TACGCTTGCCCCGAGGTGATCCGGGGGGAGAGTATGACGCGCCGGAAGCGGACGCTGTGG	600							
QY	601	AGCTGGCGGTCACTCTGTTTGGCTTCTGGTGGGGCTCTGCGCTTCGACGATGACAAC	660							
Db	601	AGCTGGCGGTCACTCTGTTTGGCTTCTGGTGGGGCTCTGCGCTTCGACGATGACAAC	660							
QY	661	TTCCGACAGCTGCTGGAGAAGGTGAAGCGGGGGTGTTCACATGCCGCACTTTATCCCG	720							
Db	661	TTCCGACAGCTGCTGGAGAAGGTGAAGCGGGGGTGTTCACATGCCGCACTTTATCCCG	720							
QY	721	CCCGACTGCCAGAGTCTGCTACGGGGCATGATCGAGGTGACGCCGCAACGCCGCTCACG	780							
Db	721	CCCGACTGCCAGAGTCTGCTACGGGGCATGACGAGGTGACGCCGCAACGCCGCTCACG	780							
QY	781	CTAGACACATTCAGAAACACATATGTTATATAGGGGGCAGATGAGCCGACACAGAG	840							
Db	781	CTAGACACATTCAGAAACACATATGTTATATAGGGGGCAGATGAGCCGACACAGAG	840							
QY	841	CAGCCCATTCCTCGCAAGGTGCAGATCCGCTCGCTGCCCGAGCTGGAGGACATCGACCCC	900							
Db	841	CAGCCCATTCCTCGCAAGGTGCAGATCCGCTCGCTGCCCGAGCTGGAGGACATCGACCCC	900							
QY	901	GACGTGCTGACACGATGCACTACTGGGTGCTTCCGAGACCGGCACAAAGCTGCTCGAG	960							
Db	901	GACGTGCTGACACGATGCACTACTGGGTGCTTCCGAGACCGGCACAAAGCTGCTCGAG	960							
QY	961	GACCTGCTGTCCGAGGAGGAAACAGAGAAAGATGATTTACTTCTCTCTCTGGAACGG	1020							
Db	961	GACCTGCTGTCCGAGGAGGAAACAGAGAAAGATGATTTACTTCTCTCTCTGGAACGG	1020							
QY	1021	AAAGAAAGGTACCCGAGCAGGAGGATGAGGACTGCTCCCCCGGAAACGAGATAGACCTT	1080							
Db	1021	AAAGAAAGGTACCCGAGCAGGAGGATGAGGACTGCTCCCCCGGAAACGAGATAGACCTT	1080							

Qy	1081	CCCCGAAAGCGTGTGAATCTCCCGGATGCTGAACCGGCAAGCGGCGCGCCAGAACGC	1140
Db	1081	CCCCGAAAGCGTGTGAATCTCCCGGATGCTGAACCGGCAAGCGGCGCGCCAGAACGC	1140
Qy	1141	AAATCCATCAGAGTGCTCAGCGTGAAGCGGCGGCTCCCGGTGCTCGCGCGCGGGCC	1200
Db	1141	AAATCCATCAGAGTGCTCAGCGTGAAGCGGCGGCTCCCGGTGCTCGCGCGCGGGCC	1200
Qy	1201	ATTGAGATGGCCGACGACGGCCAGAGGTTCTGGTCCATCAGCGGTGCCCTCTCAGGCCCTT	1260
Db	1201	ATTGAGATGGCCGACGACGGCCAGAGGTTCTGGTCCATCAGCGGTGCCCTCTCAGGCCCTT	1260
Qy	1261	TCCACAGGCGCACTCAGCAGCCCCCGGGTGACCCCTCACCCCTCACCAAGGGGCACTGCC	1320
Db	1261	TCCACAGGCGCACTCAGCAGCCCCCGGGTGACCCCTCACCCCTCACCAAGGGGCACTGCC	1320
Qy	1321	CTCCCAACCCCCAAGGGGACACCTGTGCCACAGCCAAAGGAGAGCCGGCTGGCAGCCCC	1380
Db	1321	CTCCCAACCCCCAAGGGGACACCTGTGCCACAGCCAAAGGAGAGCCGGCTGGCAGCCCC	1380
Qy	1381	AACCCACAGCCCCCGTCCAGCCCCCAGCGTGGAGGGTGCCCTGGAGGGCGGGCTCAAC	1440
Db	1381	AACCCACAGCCCCCGTCCAGCCCCCAGCGTGGAGGGTGCCCTGGAGGGCGGGCTCAAC	1440
Qy	1441	TCCATCAAGAAACAGCTTTCTGGGCTCACCCCGCTTCCACCGCCGGAATCTGCAAGTTCCG	1500
Db	1441	TCCATCAAGAAACAGCTTTCTGGGCTCACCCCGCTTCCACCGCCGGAATCTGCAAGTTCCG	1500
Qy	1501	ACGCCGAGGAGATGTCACACTGACACACAGAGTGTCTCCCGAGAGCTGGCGAAGAAGTCC	1560
Db	1501	ACGCCGAGGAGATGTCACACTGACACACAGAGTGTCTCCCGAGAGCTGGCGAAGAAGTCC	1560
Qy	1561	TGGTTTTGGGAACCTTCATCAGCCTGGAGAGGAGGAGCAGACTTTCTGTGGTCATCAAGAC	1620
Db	1561	TGGTTTTGGGAACCTTCATCAGCCTGGAGAGGAGGAGCAGACTTTCTGTGTCATCAAGAC	1620
Qy	1621	AAACCTCTGAGCTCCATCAAGGCTGACATCGTGCACCGCCTCTCTGTCGATTCACAGTCTC	1680
Db	1621	AAACCTCTGAGCTCCATCAAGGCTGACATCGTGCACCGCCTCTCTGTCGATTCACAGTCTC	1680
Qy	1681	AGCCACAGCGTCATCTCCAAACGAGCTTCCGGGCGAGGTACAGGCCACCGGGGGGCCA	1740
Db	1681	AGCCACAGCGTCATCTCCAAACGAGCTTCCGGGCGAGGTACAGGCCACCGGGGGGCCA	1740
Qy	1741	GCGGTGTTCCAGAAAGCGGCTCAAGTTTCCAGTTTGATATCACTACAGGAGGTGGGGAG	1800
Db	1741	GCGGTGTTCCAGAAAGCGGCTCAAGTTTCCAGTTTGATATCACTACAGGAGGTGGGGAG	1800
Qy	1801	GCGCAGAGGAGAACGGCATCTATCTCGTCACTTCACCTTCTCAGGGCCCGAGCCGT	1860
Db	1801	GCGCAGAGGAGAACGGCATCTATCTCGTCACTTCACCTTCTCAGGGCCCGAGCCGT	1860
Qy	1861	CGCTTCAAGAGGTTGGTGAGACCATCCAGGCCCGAGCTGCTGAGCACACACGACCCGCT	1920
Db	1861	CGCTTCAAGAGGTTGGTGAGACCATCCAGGCCCGAGCTGCTGAGCACACACGACCCGCT	1920
Qy	1921	CGCGCCCGACGACTTGTTCAGACACCAAC	1946
Db	1921	CGCGCCCGACGACTTGTTCAGAACCCCC	1946

RESULT 6
APR 03 1994

ABA02994
ID ABA02994 standard: cDNA: 2217 BP.

AC ABA02994;

XX
DT 19-FEB-2002 (first entry)

XX DE Human protein kinase 2246 encoding cDNA SEQ ID NO 1.

Human; protein kinase 2246; cytostatic; immunomodulator; carcinoma; XX KW

anti-inflammatory; analgesic; cardiovascular; cancer; sarcoma;
cellular proliferation disorder; cellular differentiation disorder;
metastatic; haematopoietic disorder; leukaemia; immune disorder;
inflammatory disorder; arthritis; autoimmune disease; diabetes mellitus;
psoriasis; Crohn's disease; cardiovascular disease; virus; pain;
gene therapy; ss.

OS Homo sapiens.

	key	Location/Qualifiers
FH	CDS	51..2075
FT		/*tag= a
FT		/product= "protein

PN WO200181588-A2.

01-NOV-2001.

25-APR-2001: 2001WO-US13784.

XX
PR 25-APR-2000; 2000US-199391P.

XX PA (MILL-) MILLENNIUM PHARM INC.

XX
PI
Meyers R:

XX
DR WPI; 2002-049281/06.
DR P-PSDB; AAM47830.

PT New protein kinase nucleic acid and polypeptide molecules, designated
PT 2246, useful for diagnosing, preventing or treating cancer or a
PT cellular proliferation/differentiation disorders, e.g. carcinoma,
PT sarcoma or leukaemias.

PS Claim 1: Fig 1; 11pp: English.

The invention relates to the human protein kinase 2246 gene and the isolated encoded polypeptide with cytostatic, immunomodulator, anti-inflammatory, analgesic and cardiovascular activity. The 2246 nucleic acid and polypeptide are useful for diagnosing, preventing or treating a subject having cancer or a cellular proliferation and/or differentiation disorder or at risk of developing cancer or a cellular proliferation and/or differentiation disorder. In particular, the disorder includes carcinoma, sarcoma, metastatic or haematopoietic disorders (e.g. leukaemias) or cancers of the lung, breast, thyroid, head neck, prostate or genito-urinary tract. The 2246 nucleic acid and polypeptide are also useful for treating immune disorders, e.g. inflammatory (e.g. respiratory inflammation or arthritis), autoimmune disease (e.g. diabetes mellitus, psoriasis, Wegener's granulomatosis, Crohn's disease or Grave's disease), for treating cardiovascular diseases, endothelial cell disorder, viral diseases or pain. The nucleic acid and polypeptide are also useful for evaluating the efficacy of a treatment of cancer or a cellular proliferation and/or differentiation disorder. The nucleic acid is useful for gene therapy. The present sequence is that of the 2246 encoding cDNA.

Sequence 2217 BP; 476 A; 715 C; 682 G; 344 T; 0 other;

Query Match	96.6%	Score 1939.6;	DB 24;	Length 2217;
Best Local Similarity	99.8%	Pred. No. 0;		
Matches 1942;	Conservative	0;	Mismatches	4;
			Indels	0;
			Gaps	0;

[illegible]

Db 301 GGCAATGGCGTCCCTGACAGTTGGGACAGCCCTGTTGGAGACAGCAGTGTGGGTCCCCCAC 360
Qy 541 TACGCTCCCGGAGGTGATCCGGGGGAGAGATGACGGCCGAGAGGGCGAGTGTGG 600
Db 361 TACGCTCCCGGAGGTGATCCGGGGGAGAGATGATGACGGCCGAGAGGGCGAGTGTGG 420
Qy 601 AGCTGGGCGTATCTCTGTTCCGCTTGTGTGGGGGCTCTGCCCTTCGACGATGACAAC 660
Db 421 AGCTGGGCGTATCTCTGTTCCGCTTGTGTGGGGGCTCTGCCCTTCGACGATGACAAC 480
Qy 661 TTGGCAGAGCTGCTGGAGAGGTGAGCGGGCGTGTTCACATGCCGCACTTATCCCG 720
Db 481 TTGGCAGAGCTGCTGGAGAGGTGAGCGGGCGTGTTCACATGCCGCACTTATCCCG 540
Qy 721 CCCGACTGCCAGAGTCTCTACGGGGGATGATCAGAGTGGAGCGCGACGCGGCTCAAG 780
Db 541 CCCGACTGCCAGAGTCTCTACGGGGGATGATCAGAGTGGAGCGCGACGCGGCTCAAG 600
Qy 781 CTAGAGCAATTCAGAAACAATATGTTATATAGGGGGCAAGATGAGCCCGAACCAGAG 840
Db 601 CTAGAGCAATTCAGAAACAATATGTTATATAGGGGGCAAGATGAGCCCGAACCAGAG 660
Qy 841 CAGCCCATCTCCGACAGGTGAGATCCGCTGCTGCCAGCCTGGAGGACATGACGCC 900
Db 661 CAGCCCATCTCCGACAGGTGAGATCCGCTGCTGCCAGCCTGGAGGACATGACGCC 720
Qy 901 GACGTGCTGGACAGATGACATCTACTGGGCTGCTTCCGAGACCGCAACAGCTGCTGAG 960
Db 721 GACGTGCTGGACAGATGACATCTACTGGGCTGCTTCCGAGACCGCAACAGCTGCTGAG 780
Qy 961 GACGTGCTGCTCGAGGAGAGAACAGAGAGATGATTTACTTCTCTCTCTGAGCCGG 1020
Db 781 GACGTGCTGCTCGAGGAGAGAACAGAGAGATGATTTACTTCTCTCTCTGAGCCGG 840
Qy 1021 AAGAGAGGTATCCGAGGAGAGATGAGACCTGCCCGCCCGGAAAGAGATGACGCT 1080
Db 841 AAGAGAGGTATCCGAGGAGAGATGAGACCTGCCCGCCCGGAAAGAGATGACGCT 900
Qy 1081 CCCGAGAGCGTGTGACTTCCCGATGCTGAACCGGACCGCAAGCGCGGCCAGAACGC 1140
Db 901 CCCGAGAGCGTGTGACTTCCCGATGCTGAACCGGACCGCAAGCGCGGCCAGAACGC 960
Qy 1141 AATCATGAGAGTGTCTCAGGTGACGACGGCGGCTCCCGGTGCTTGGCGCGGCGCC 1200
Db 961 AATCATGAGAGTGTCTCAGGTGACGACGGCGGCTCCCGGTGCTTGGCGCGGCGCC 1020
Qy 1201 ATTGATGAGCGCCAGCAGCGGCGAGGTCTCGGTCCATCAGCGGTGCTCTCAGGCGTT 1260
Db 1021 ATTGATGAGCGCCAGCAGCGGCGAGGTCTCGGTCCATCAGCGGTGCTCTCAGGCGTT 1080
Qy 1261 TCCACGAGCCACTCAGCAGCGCCCGGTGACCCCTCACCCTCACCAGGGGCGAGTCCC 1320
Db 1081 TCCACGAGCCACTCAGCAGCGCCCGGTGACCCCTCACCCTCACCAGGGGCGAGTCCC 1140
Qy 1321 CTCCCCACCCCAAGGGAGACCTGTTCACAGCGCCAAAGGAGAGCCGGCTGGCACGCCC 1380
Db 1141 CTCCCCACCCCAAGGGAGACCTGTTCACAGCGCCAAAGGAGAGCCGGCTGGCACGCCC 1200
Qy 1381 AACCCGAGCCCGCTCAGCGCCAGCGTGGAGGGGTGCTGGAGGGCGCGGCTCAAC 1440
Db 1201 AACCCGAGCCCGCTCAGCGCCAGCGTGGAGGGGTGCTGGAGGGCGCGGCTCAAC 1260
Qy 1441 TCCATCAAGAACAGCTTTCTGGGCTCACCCGCTTCCACCGCCGAAACTGCAAGTTCCG 1500
Db 1261 TCCATCAAGAACAGCTTTCTGGGCTCACCCGCTTCCACCGCCGAAACTGCAAGTTCCG 1320
Qy 1501 AGCGCGGAGAGATTCACACTGACACAGAGTCTCTCCAGAGCTGGCGAAGAGTCC 1560
Db 1321 AGCGCGGAGAGATTCACACTGACACAGAGTCTCTCCAGAGCTGGCGAAGAGTCC 1380
Qy 1561 TGGTTTGGGAATTCATCAGCTGAGAGGAGGAGAGATCTTCGTGGTTCATCAAGAC 1620
Db 1381 TGGTTTGGGAATTCATCAGCTGAGAGGAGGAGGAGATCTTCGTGGTTCATCAAGAC 1440

Qy 1621 AAACCTCTGAGTCCCATCAAGGCTGACATCGTCACGCCCTTCTGTGATTTCCAGTCTC 1680
Db 1441 AAACCTCTGAGTCCCATCAAGGCTGACATCGTCACGCCCTTCTGTGATTTCCAGTCTC 1500
Qy 1681 AGCCACAGCGTCTATCTCCCAACGAGCTTCCGGGCCGAGTACAAGGCCACGCGGGGCCA 1740
Db 1501 AGCCACAGCGTCTATCTCCCAACGAGCTTCCGGGCCGAGTACAAGGCCACGCGGGGCCA 1560
Qy 1741 GCGTGTTCAGAGCGGGTCAAGTTCCAGGTTGATATCACTACAGGAGGTTGGGAG 1800
Db 1561 GCGTGTTCAGAGCGGGTCAAGTTCCAGGTTGATATCACTACAGGAGGTTGGGAG 1620
Qy 1801 GCGCAGAGAGAACGGCATCTACTCGTCACCTTCACTCCCTGCTCTCAGGCCCCAGCCGT 1860
Db 1621 GCGCAGAGAGAACGGCATCTACTCGTCACCTTCACTCCCTGCTCTCAGGCCCCAGCCGT 1680
Qy 1861 CGTTCAAGAGGTTGTGGAGACCATCCAGGCCGAGCTGCTGAGCACACAGACCCGCT 1920
Db 1681 CGTTCAAGAGGTTGTGGAGACCATCCAGGCCGAGCTGCTGAGCACACAGACCCGCT 1740
Qy 1921 GCGGCCGAGCACTTTCAGACACCACTAATCTGTAATGAAATGATGACGGGCGGCTTTC 1980
Db 1741 GCGGCCGAGCACTTTCAGACACCACTAATCTGTAATGAAATGATGACGGGCGGCTTTC 1800
Qy 1981 AAATGTGGAATTATCCCGAAAAGTTAA 2007
Db 1801 AAATGTGGAATTATCCCGAAAAGTTAA 1827

RESULT 8

AAAL51889
ID AAL51889 standard; DNA; 2799 BP.
XX
AC AAL51889;
XX
DT 08-MAY-2003 (first entry)
XX
DE Human cell cycle-regulatory factor Cdr2 coding sequence.
XX
KW Human; cell cycle-regulatory factor; Cdr2; kinase; proliferative disease;
XX anticancer agent; wound-healing drug; gene; ds.
XX OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 50..2314
FT /*tag= a
FT /product= "Human Cdr2 protein"
XX
XX W0200299110-A1.
XX
XX 12-DEC-2002.
XX
XX 03-JUN-2002; 2002WO-JP05411.
XX
XX 04-JUN-2001; 2001JP-0168792.
XX
XX (TAIH) TAIHO PHARM CO LTD.
XX (NAKA/) NAKANISHI M.
XX
XX Nakanishi M;
XX
XX WPI; 2003-156857/15.
XX P-PSDB; AAO16604.
XX
XX

Cell cycle-regulatory factor Cdr2 with kinase activity and encoded gene, applicable in diagnosis of and screening drugs for proliferative diseases e.g. anticancer agents and wound-healing drugs
Claim 2; Fig 2 A-C; 63pp; Japanese.
The invention comprises the amino acid and coding sequence of the human

Db 2103 TCCAGGCGACGCTCTGAGCACTATGACACGAGCCCTCCGTGACGGCCTTGGCAGACGAGA 2162

Qy 1946 CTAACGTG 1952

Db 2163 AGAACGG 2169

RESULT 9
ABV74557
ID ABV74557 standard; cDNA; 2337 BP.

XX: AC ABV74557;

XX: 20-JAN-2003 (first entry)

XX: Human kinase #1 coding sequence.

DE Human; kinase; chromosome 19; gene; ss.

XX: Homo sapiens.

OS Key Location/Qualifiers

XX: CDS 1..2337

FT /tag= a

FT /product= "Human kinase #1"

XX: WO200281670-A1.

XX: 17-OCT-2002.

XX: 04-APR-2002; 2002WO-US10786.

XX: 06-APR-2001; 2001US-282036P.

XX: (LEXI-) LEXICON GENETICS INC.

XX: Turner CA, Mathur B, Friddle CJ;

XX: WPI; 2003-058538/05.

XX: P-PSDB; ABB98743.

XX: New human kinase proteins useful for diagnosis, drug screening, and clinical trial monitoring, treatment of disorders and diseases, and cosmetic and nutritional applications

XX: Claim 5; Page 39; 47pp; English.

XX: The present sequence is the coding sequence for a novel human kinase. The genomic locus encoding the kinase is thought to be on human chromosome 19. The kinase and its coding sequence are useful for diagnosis, drug screening, clinical trial monitoring, treatment of disorders and diseases, and cosmetic and nutritional applications.

XX: Sequence 2337 BP; 479 A; 786 C; 586 G; 386 T; 0 other;

Query Match 48.1%; Score 965; DB 25; Length 2337;
Best Local Similarity 70.0%; Pred. No. 1.5e-199;
Matches 1484; Conservative 0; Mismatches 440; Indels 195; Gaps 6;

Qy 29 CGCAGCAGCCGACGATGTTGGGCGCTTACCGCTGGAGAACGCTGGCGGAGGCGAGA 88

Db 74 CCCAGCAGCCGCAATATGTTGGGCGCTTATCGCTGGAGAACGCTGGGCAAGGACAGA 133

Qy 89 CAGGCTCTGTTGAAGCTGGGGGTTCACTCGTCACTGCCAGAAAGTGCCCATCAAGATCG 148

Db 134 CAGGGCTGTTAACTCGGGGTTCACTGCTATCAAGGTCAGAGGTCGCCATCAAGATCG 193

Qy 149 TCAACCGTGAGAGCTCAGCAGTGGTGGTGTGATGAAGGTGGAGCGGAGATCGCGATCC 208

Db 194 TGAACCGGAGAGCTGTGCGAGTGGTGTGATGAAGGTGGAGCGGAGATCGCCATCC 253

Qy 209 TGAAGCTCATTTGAGCAGCCCACTCTTAAAGCTGCACGCTTTATGAAACAAAAAT 268

254 TGAAGCTCATCGAACCCACATGTCTCAAGCTCCACGACGTCTACGAGAACAGAAAT 313

Qy 269 ATTTGTACCTGGTGTAGAACACAGTGTGAGTGTGAGCTCTTCGACTACTGTGTGAGA 328

Db 314 ATTTGTACCTGGTGTGAGACAGCTCTCGGGGGTGTGAGCTATTGAGTACTGTGTAAGA 373

Qy 329 AGGGAGGCTGAGCCCTAAGGAGGCTCGGAAGTTCTTCCGGCAGATCATCTCTGCGCTGG 388

Db 374 AGGGAGACTGACGCCCAAGGAGGSCCCGAAAGTTCTTCCGCAGATTTGTCTGCGCTGG 433

Qy 389 ACTTCTGCGACAGCCACTCCATATGCGACAGGGATCTGAAACCTGAAACCTCTGCTGG 448

Db 434 ACTTCTGCGACAGCTACTCCATCTGCGACAGAGACCTTAAAGCCCGAGAACCTGCTTTGG 493

Qy 449 ACGAGAAAGAACACATCCGATCGCAGACTTGGCATGGGGTCCCTCAGGTTGCGGACA 508

Db 494 ATGAGAAAAAACATCCGATTTGACACTTGGCATGGGGTCCCTCAGGTTGCGGACA 553

Qy 509 GCCTGTTGGAGACGAGCTGTGGGTCCGCCCACTACGCTGCCCCAGGTGATCCGGGGG 568

Db 554 GCCTCCTGGAGACGAGCTGCGGGTCCGCCCATTTATGCGTGTCCAGAGGTGATTAAAGGGG 613

Qy 569 AGAAGTATGACGGCCGGAAGCGGACGTGTGAGCTCGGGGTCTCATCTGTTCCTGCTTCG 628

Db 614 AAAAATATGATGGCCGCGCGGCGAGACATGTGGAGCTGTGGAGTCACTCTCTCGCCCTGC 673

Qy 629 TGTGGGGGCTCTGCGCTTCGACGATGACAACTTGGCAGAGCTGCTGGAAGGTGAGC 688

Db 674 TGTGGGGGCTCTGCGCTTTGATGACGACAACTTCCGCCAGCTGCTGGAGAGGTGAAC 733

Qy 689 GGGCGGTGTTCCACATGCCGCACTTTATCCGCCGCACTGCCAGAGTCTGTACGGGGCA 748

Db 734 GGGCGGTGTTCCACATGCCGCACTTTATCCCTCCAGATTGCCAGAGCTCTCTGAGGGGA 793

Qy 749 TGATCGAGGTGAGCGCGGACGCGCTCAGCTAGAGACATTCAGAAACACATATGTT 808

Db 794 TGATCGAAGTGGAGCCCGGAAAAAGGCTCAGTCTGGAGCAAAATTCAGAAACATCTTGGT 853

Qy 809 ATATAGGGGGCAAGATGAGCCCGAACCC-----AGAGCAGCCCATCTCTCGCAAGGTGC 862

Db 854 ACCTAGCGGGGAAACAGACGACGACCCGCTGCTGGAGCCAGCCCTGGCGCGCGGGTAG 913

Qy 863 AGATCCGCTCGCTGCCAGCTCTGAGGACATCGACCCCGAGCTGTGAGCAGCATGCACT 922

Db 914 CCATGCGGAGCTGCCATCCAAACGAGAGCTGGACCCCGAGCTCTTAGAGAGCATGTCAT 973

Qy 923 CACTGGGCTCTCCGAGACCGCAACAGTGTCTGAGGACCTGTCTCTCCGAGAGAGA 982

Db 974 CACTGGGCTCTCTCAGGACCGGAGAGGCTGTCATCGCAGCTGCGCAGTGAGAGAGA 1033

Qy 983 ACCAGGAGAGATGATTACTTCTCTCTGACCGGAAAGAGTACCCGAGCCAGG 1042

Db 1034 ACCAAGAAAGATGATATATTTCTGCTTTTGGATCGAAGGAGCGGTATCCCAAGCTGTG 1093

Qy 1043 AGGATGAGGACCTGCCCGCCCGGAAACGAGATAGACCTCTCCCGGAGCGTGTGACTCCC 1102

Db 1094 AGGACGAGGACCTGCCCTCCCGGAAATGATGTTGACCCCGGAGCGTGTGATTTCTC 1153

Qy 1103 CGATGCTGAACCGGACGCGCAAGCGGCGGCGAGAAACGAAATCCATGAGAGGTCTAGCG 1162

Db 1154 CCATGCTGAGCCGTCAGGGAAGCGGACACAGAGCGGAAGTCCATGGAAGTCTCTGAGCA 1213

Qy 1163 TGAC-----GGAGCGGGCTCCCGGTGCTGCGCGCGGGCCATTGAGATGSCCC 1213

Db 1214 TCACCGATGCGGGGGTGTGGTCCCTGTATCCACCCGACGGGCTTGGAGATGSCCC 1273

Qy 1214 AGCAGCGCAGAGGTCTCGGTCCATCAGCGGTGCTCTCTCAGGCTTTTCCACGAGCCAC 1273

Db 1274 AGCAGCGCAGAGATCCGCTAGGTGAGTGGAGGCTCCACGGGTCTCTCTCCAGCCCTC 1333

Qy 1274 TCAGCAGCCCCCGGT----- 1289

Db 1334 TAAGCAGCCCCAAGGAGTCCGGTCTTTTCTTTTTCACCGGAGCGGGGCTGGAGATGAGG 1393

QY 1290 ----- 1289
 Db 1394 CTGAGGCGGGGCTCCCGACTTCCAAACGACAGCGTGCCTTCTCGGGGCCCCAGGG 1453
 QY 1290 -----GACCCCTCACCCCTTCAACGAGGCGAGTCCCTCCCC----- 1326
 Db 1454 GTGGGGCGCGGGAGCAGCCCGCGCCCGAGTGCCTCCACACCCCTCCCGGCG 1513
 QY 1327 -----ACCCCAAGGGGACACCTGTCCACACGCCAA 1357
 Db 1514 CCCCAGGCTCCCGCGCTCTCTGCGGGAGCCCTTGCACCTGCCTGTCAACGCCCC 1573
 QY 1358 AGGAGAGCCCGGCTGGCAGCCGCAACCCACGCGCCCGCTCCAGCCCC-----AGGCTCG 1411
 Db 1574 GGCCAGTCCACCGGACCCCGGGGACACACACCCCGCGCGGTGGCGTCG 1633
 QY 1412 GAGGGTGCCTGAGGCGCGGCTCAACTCCATCAAGAAACAGTTCCTGGGCTCACCC 1471
 Db 1634 GGGAGCGGCTGGAGAGTCTCTCACTTCCATCCGCAACAGTTCCTGGGCTCCCTC 1693
 QY 1472 GCTTCCACCGCGGAACTGCAAGTTCGAGCGCGGAGGAGATGTCCAACTGACACCCAG 1531
 Db 1694 GCTTTCACCGCGCAAGATGAGTCTCCCTACCGCTGAGGAGATGTCCAGCTTGACGCCAG 1753
 QY 1532 AGTCGTCCTCCAGAGCTGGCGAAGAGTCTCTGGTTTGGAACTTTCATCAGCTCGAGAAGG 1591
 Db 1754 AGTCCTCCCGGAGCTGGCAAAACGCTCTCTGGTTTCGGGAATTCATCTCTTGACAAAG 1813
 QY 1592 AGGAGAGATCTTCGTGGTGTCAAGAACAACTCTGAGTCTCATCAAGCGGTCAATCG 1651
 Db 1814 AAGAACAAATATCTCTGTGTAAAGGACAAACCTCTCAGCAGCATCAAAAGCAGACATCG 1873
 QY 1652 TGCAAGCTTCTCTCGATTCCTAGTCTCAGCCACAGCGTATCTCCCAACGAGCTTCC 1711
 Db 1874 TCCATGCTTCTCTCGATTCCTAGTCTCAGCGTGTGTCAGTGTCTGTCACACACGCTTCA 1933
 QY 1712 GGGCGGAGTCAAGGCCACCGGGGGGCGAGCGGTGTTCAGAAACCGGTCAAGTTCAGG 1771
 Db 1934 GGGCGGAGTCAAGGCCACCGGTGGGGGCGCTCTCGTTCCTCAAAAGCCGCTCCAGG 1993
 QY 1772 TTGATATCACTACACGAGGCT-----GGGAGCGCGAGAGAGA 1813
 Db 1994 TGGACATCAGCTCTCTGAGGCTCAGAGCCCTCCCGCGACGCGGACGCGAGGAGTG 2053
 QY 1814 ACAGCATCTACTCGTCACTTCACTTCACTCTCAGCGCCCGAGCGTCTCAAGAGGG 1873
 Db 2054 GTGGATCTACTCTGCTACCTTCACTCTCTCGGTCCAGCGCTCGGTTCAGCGAG 2113
 QY 1874 TGGTGGAGACCATCCAGGCCAGCTCTGAGCAGACACGACCCCGCTGCGGCCAGCACT 1933
 Db 2114 TGGTGGAGACCATCCAGGCCAGCTCTGAGCAGACACGACCCCGCTGCGGCCAGCACT 1933
 QY 1934 TGTACAGACCACTAACTG 1952
 Db 2174 TGGCAGACGAGAAGACGG 2192

RESULT 10

AA06717
 ID AA06717 standard; cDNA; 2385 BP.
 XX AC AA06717;
 XX DT 12-SEP-2001 (first entry)
 XX DE Polynucleotide sequence encoding human protein kinase #17.
 XX KW Human; protein kinase; PTK; STK; cancer; cardiovascular disease;
 XX KW metabolic disorder; immune related disease; neurological disorder;
 XX KW neurodegenerative disorder; inflammatory disorder; infectious disease;
 XX KW reproductive disorder; gene therapy; ss.

OS Homo sapiens.
 XX WO200138503-A2.
 PN 31-MAY-2001.
 XX 22-NOV-2000; 2000WO-US32085.
 PF 24-NOV-1999; 99US-0167482.
 XX (SUGEN-) SUGEN INC.
 PA Plowman GD, Whyte D, Manning G, Sudarsanam S, Martinez R;
 PI Flanagan P, Clary D;
 XX WPI: 2001-343950/36.
 DR P-PSDB; AAU03517.
 XX Nucleic acids encoding human kinase polypeptides, useful for preventing
 PT diagnosing and/or treating e.g. cancer, immune, cardiovascular and
 PT neuronal-associated diseases, and microbial infections -
 PS Example 1; Figure 1; 433pp; English.
 XX AA06701-AA06757 encode for novel human protein kinases #1-57. The
 CC novel protein kinases have been identified as members of the tyrosine
 CC or serine/threonine kinase (PTK and STK) families. The polynucleotides
 CC encoding protein kinases and the polypeptides may be used in the
 CC prevention, diagnosis and treatment of diseases associated with
 CC inappropriate kinase expression. For example, they may be used to treat
 CC cancers (especially cancers of haematopoietic origin), cardiovascular
 CC disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes),
 CC immune related diseases (e.g. rheumatoid arthritis), neurological
 CC disorders (e.g. schizophrenia), neurodegenerative disorders (e.g.
 CC Parkinson's disease), inflammatory disorders (e.g. asthma), infectious
 CC disease (e.g. HIV) and reproductive disorders (e.g. infertility).
 CC Additionally, polynucleotides encoding protein kinases may be
 CC used for gene therapy and as DNA probes in diagnostic assays.
 CC The protein kinase polypeptides may be used as antigens in the production
 CC of antibodies against the protein kinases and in assays to identify
 CC modulators of protein kinase expression and activity.
 XX SQ Sequence 2385 BP; 494 A; 768 C; 731 G; 392 T; 0 other;

Query Match 48.1%; Score 964.4; DB 22; Length 2385;
 Best Local Similarity 69.8%; Pred. No. 2e-199;
 Matches 1490; Conservative 0; Mismatches 451; Indels 195; Gaps 6;
 QY 12 GGGGAAGGACGGCGCGCGCAGCAGCGCGAGTATGTTGGGCCCTACCGCTGGAGAAGAC 71
 Db 105 GGAGGCCGAAGAGAGAGAGAGGGCGCCACGCCCAATATGTGGGCCCTATCGGCTGGAGAAGAC 164
 QY 72 GCTGGGCAAGGGGACACAGGCTGTGTTGAAGCTGGGGGTTCACTGCTCACCTGCCAGAA 131
 Db 165 GCTGGGCAAGGGGACACAGGCTGTGTTGAAGCTGGGGGTTCACTGCTCACCGGTGAGAA 224
 QY 132 GGTGGCCATCAGATCGTCAACCGTGGAGAAGCTCAGCGAGTGGTGTCTGATGAAGTGA 191
 Db 225 GGTGCCCATCAGATCGTGAACCGGAGAGAGCTGTCCGAGTGGTGTCTGATGAAGTGA 284
 QY 192 GCGGAGATCGCGATCTCCTGAGCTATTGAGACACCCCGCTCTTAAGCTGACACGCT 251
 Db 285 GCGGAGATCGCGATCTCCTGAGCTATTGAGACACCCCGCTCTTAAGCTGACACGCT 344
 QY 252 TTATGAACCAAAAAATATTTGTACCTGGTGTGCTAGAACAGCTGCTAGGTGGTGTCTT 311
 Db 345 CTACGAGAACAGAAATATTTGTACCTGGTGTGCTAGAACAGCTGCTAGGTGGTGTCTT 404
 QY 312 CGACTACCTGGTGAAGAGGGGAGGCTGAGCCCTTAAGAGGCTCGGAAGTTCTTCCGGCA 371
 Db 405 CGACTACCTGGTGAAGAGGGGAGCTGAGCCCGCAAGAGGCGCCGAAAGTTCTTCCGCCA 464
 QY 372 GATCATCTCTGCGCTGAGCTTTCTGCGACAGCCACTCATATATGCCACAGGGATCTGAAC 431

1305	Db	GGCCTTGGAGATGGCCAGACACACCGCAGAGATCCGTAGCTAGTGGAGCCTCCACGGG	1364
1357	Qy	CTTTTCCACAGCCCACTCAGCAGCCCCCGGGT-----	1289
1365	Db	TCCTCTCCAGCCCTCTAAGCAGCCCAAGSAGTCCGGTCTTTTCTTTTCAACGGAGCC	1424
1390	Qy	-----	1289
1425	Db	GGGGCTGGAGATAGGCTCGAGCGGGGCTCCCGACTTCCAAAACGAGAGCGTGC	1484
1490	Qy	-----GACCCTTCACCCCTCACCAGGGG	1313
1485	Db	TTCTCGGGGCCCAAGGGTGGGGCGCGGGAGCAGCCCGCCCCCAGTGC	1544
1514	Qy	CAGTCCCTCCCTC-----ACCCCAAGGGGAC	1340
1545	Db	CACACCTTGCCCGGCCCCAGGCTCCCGCGCTCTCTGGGGGACCCCTTGCACTC	1604
1541	Qy	ACCTGTCCACAGCCAAAGGAGAGCCCGGTGGCAGCCCAACCCCAAGCCCGCGTCCAG	1400
1605	Db	GCCTCTGCACAGCCCGCGGCAGTCCCAACCGGACCCCGGGACAAACACACCCCCAG	1664
1401	Qy	CCCC-----AGCGTCGAGGGGTCCCTCGAGGGCGGGCTCAACTCCATCAAGACAG	1454
1665	Db	CCCCGGCGGTGGCTCGGGGGAGCCGCTGGAGAGTCTCAACTCCATTCGCAACAG	1724
1455	Qy	CTTTCTGGGCTCACCCGCTTCCACCGCCGAAACTGCAAGTTCAGAGCCGCGGAGAGAT	1514
1725	Db	CTTCTGGGCTCCCTCGCTTTACCCGGCGCAGATGCAGGTCCCTACCGCTGAGGAGAT	1784
1515	Qy	GTCCAACTTGACAACAGAGTCGTCCCAGAGCTGGCGAAGTCTCTGGTTTGGGAACCT	1574
1785	Db	GTCAGAGTTGACGCGCAGAGTCTCTCCCGGAGCTGGCAAAACGCTCTCTGGTTTGGGAACCT	1844
1575	Qy	CATCAGCTTGAGAGGAGGAGCAGATCTTCGTGGTTCATCAAGACAAACCTCTGAGCTC	1634
1845	Db	CATCTCTTGGACAAAGAAACAAATATTCCTCTGCTCTAAGAGACAAACCTCTCAGCAG	1904
1635	Qy	CATCAAGCTGACATCTGTGACGCTTCTCTGCTCATCCAGTCTCAGGCACACAGCGTCAT	1694
1905	Db	CATCAAGCAGACATCTTCATGCTTCTGTCTCATCCCAAGCTTGATCAGTGTGCT	1964
1695	Qy	CTCCAAACGAGCTTCGGGCGGAGTACAAGGCCACGGGGGGGCGAGCCGTGTTCAGAA	1754
1965	Db	GTCACAGCAGCTTCAGGGCCGAGTACAAGGCCAGTGGCGGCCCTCTTCCTTCCAAA	2024
1755	Qy	GCCGCTCAGTTTCCAGTTTGATATCACTTCAACGAGGGT-----GG	1796
2025	Db	GCCCGTCCGCTTCCAGSTGGACATCAGCTCTCTTGAGGGTCCAGAGCCCTCCCGCGACG	2084
1797	Qy	GGAGCGCAGAAGAGAGAACGCACTACTCCGTCACTTCACTCCCTGTCTCAGGCCCCAG	1856
2085	Db	GGACGGCAGCGGAGGTGGTGCACTACTCCGTCACTTCACTCTCATCTCGGGTCCAG	2144
1857	Qy	CCGTCTGCTTCAAGAGGTTGGTGGAGACCATCCAGGCCAGCTGTGAGCACACACGCC	1916
2145	Db	CCGTCTGTTCAAGCGAGTGGTGGAGACCATCCAGGCACAGCTCTTGAGCACTCATGACCA	2204
1917	Qy	GCCTGGGCCCGCAGCACTTGTTCAGACACCACTAACTG	1952
2205	Db	GCCCTCCGTGAGGCCCTGGCAGACGAGAGAACGG	2240

RESULT 12

ABV74559

ID ABV74559 standard; cDNA; 2112 BP.

AC ABV74559;

XX

DT 20-JAN-2003 (first entry)

[illegible]

DE Human kinase #3 coding sequence.

XX

KW	Human; kinase; chromosome 19; gene; ss.
XX	Homo sapiens.
FX	Key Location/Qualifiers
FH	CDS 1..2112
FT	/*tag= a
FT	/product= "Human kinase #3"
XX	
XX	WO200281670-A1.
FN	
XX	
XX	17-OCT-2002.
PD	
XX	
XX	04-APR-2002; 2002WO-US10786.
PP	
XX	
XX	06-APR-2001; 2001US-282036P.
PR	
XX	(LEXI-) LEXICON GENETICS INC.
PA	
XX	
PI	Turner CA, Mathur B, Friddle CJ;
XX	
XX	WPI: 2003-058538/05.
DR	P-PSDB; ABB98745.
DR	
XX	New human kinase proteins useful for diagnostic clinical trial monitoring, treatment of diseases and nutritional applications -
PT	
PT	cosmetic and nutritional applications -
XX	
XX	Claim 5; Page 44; 47pp; English.
PS	
XX	The present sequence is the coding sequence
CC	genomic locus encoding the kinase is thought
CC	19. The kinase and its coding sequence are
CC	screening, clinical trial monitoring, treat
CC	diseases, and cosmetic and nutritional appl
CC	
XX	
SQ	Sequence 2112 BP; 432 A; 711 C; 615 G; 354
 Query Match 42.4%; Score 851.4; Best Local Similarity 68.9%; Pred. No. 6.2e Matches 1356; Conservative 0; Mismatches	
QY	181 ATGAAGTGTGAGCGGGAGATCGCGATCCTGAAAC
Db	1 ATGAAGTGTGAGCGGGAGATCGCATCCTGAAAC
QY	241 CTGCACGACGTTATTGAAAACAATAAATATTTGT
Db	61 CTCACGACGCTACGAGAACAAGAAATATTTGT
QY	301 GGTCAGCTCTTCGACTACCTGTGTGAAGAGGGA
Db	121 GGTCAGCTATTCGACTACCTGTGTGAAGAGGGA
QY	361 TTCTTCGGCAGATCATCTCTGCGCTGGACTTCT
Db	181 TTCTTCGGCAGATGTGCTGCGCTGGACTTCT
QY	421 GATCTGAAACCTGAAACCTCTCTGCTGGACGAGA
Db	241 GACCTAAGCCCGAGAACCTGCTTTTGATGAGA
QY	481 GGCAATGGCGTCCCTGCAGGTTGGCGCACGCCCTGT
Db	301 GGCAATGGCGTCCCTGCAGGTTGGCGCACGCCCTGT
QY	541 TAGCGCTGCCCCGAGGTGATCCGGGGGGGAGAGCT
Db	361 TATGCGTGTCCAGGTGATTAAGGGGGGAAAAAT
QY	601 AGCTGGCGGCTCATCTCTGTTTCGCTTCTGCTGGTGG
Db	421 AGCTGTGAGTCAATCTCTCTGCGCTGCTGCTGGTGG

QY 661 TTGGCAGAGCTGTGGAGAGGTGAAGCGGGCGTGTTCACATGCGCACTTTATCCCG 720
 Db |||||
 QY 481 CTCCGCCAGCTGTGGAGAGGTGAAGCGGGCGTGTTCACATGCCCACTTCATTCCT 540
 Db |||||
 QY 721 CCCAGCTGCCAGAGCTGTGTACGGGGCATGATCAGAGTGGACCGCGCCGCTCAGC 780
 Db |||||
 QY 541 CCAGATTGCCAGAGCTCTCTGAGGGGAATGATCAAGTGGAGCCCGAAAAAGGCTCAGT 600
 Db |||||
 QY 781 CTAGAGCACATTCAAGAACACATATGTATATAGGGGGCAAGATAGCCCGAACCC--- 836
 Db |||||
 QY 601 CTGAGGCAAAATTCAGAAACATCTCTTGTGTACCTAGCGGGGAAACAGAGCCAGACCCGTGC 660
 Db |||||
 QY 837 --AGAGCAGCCCATTCCTCGAAGGTGCAGATCCGCTCGCTGCCAGCCTGGAGGACATC 894
 Db |||||
 QY 661 CTGAGCAGCCCTCTGGCGCGCGGTAGCATCGGAGCCTGCCATCAACGGAGAGCTG 720
 Db |||||
 QY 895 GACCCGAGCTGTGGACAGATGATCACTAGTGGCTGTTCGAGACCGCAACAGCTG 954
 Db |||||
 QY 721 GACCCGAGCTGTAGAGAGCATGGCATCACTGGGCTGTTCAGGGACCGCGAGAGCTG 780
 Db |||||
 QY 955 CTGAGGACCTGTGTCCGAGGAGGAGAACAGAGAGATGATTACTTCTCTCTCTG 1014
 Db |||||
 QY 781 CATCGGAGCTGCGAGTGGAGGAGAACCAAGAAAGATATATATCTCTCTTTG 840
 Db |||||
 QY 1015 GACCGGAAGAAAGTATCCGAGCGCAGAGGATGAGGACCTGCCCGCCCGGAAACGAGATA 1074
 Db |||||
 QY 841 GATCGGAGGAGCGGTATCCAGCTGTGAGGACAGGACCTGCCCTCCCGGAATGATGT 900
 Db |||||
 QY 1075 GACCTCTCCCGAAGCTGTGGATCTCCCGATGTGAACCGGACGGCAAGCGCGGCCA 1134
 Db |||||
 QY 901 GACCCCGCCGGAAGCTGTGGATTCTCCATGCTGAGCCGTCAAGGAAAGCGCGACCA 960
 Db |||||
 QY 1135 GAACGCAATCCATGAGGTGCTAGCGTGACGA-----CGGCGGCTCCCGGTG 1185
 Db |||||
 QY 961 GAGCGGAAGTCAATGGAAGTCTGAGCATCACGATGCCGGGGTGTGGCTCCCTGTGTA 1020
 Db |||||
 QY 1186 CTTGCGCGCGGGCCATTTAGATGCGCCAGACCGCCAGAGGTCTCGGTCCATCAGCGGT 1245
 Db |||||
 QY 1021 CCCACCCGACGGCTTGGAGATGGCCCGACAGCAGCAGATCCCGTAGGCTCAGTGA 1080
 Db |||||
 QY 1246 GCCTCTCAGGCTTTCACACAGCCACTCAGAGCCCCCGG----- 1288
 Db |||||
 QY 1081 GCCTCCAGGGTCTGTCTCCAGCCCTTAAGCAGCCCAAGGAGTCCGGTCTTTTCTCTTT 1140
 Db |||||
 QY 1289 ----- 1288
 Db |||||
 QY 1141 TCACCGAGCCGGGGCTGGAGATGAGGCTCGAGGCGGGGGCTCCCGACTTCCAAAACG 1200
 Db |||||
 QY 1289 -----TGACCCCTCAGCCC 1302
 Db |||||
 QY 1201 CAGACGCTGCTTCTCGGGGCCCCAGGGGTGGGGCGCGCGGAGCAGCCCCCGCCCC 1260
 Db |||||
 QY 1303 TCACCAAGGGGAGTCCCTCTCCG-----ACC 1329
 Db |||||
 QY 1261 AGTCCCGCTCCACACCCCTGCCCCCGCCCCCAGGCTCTCTCTGCGGGGACC 1320
 Db |||||
 QY 1330 CCCAAGGGGACACCTGTCCACACGCCAAAGGAGAGCCCGGTGGCACGCCCAACCCACAG 1389
 Db |||||
 QY 1321 CCTTTGCACTCGCTCTGACACGCCCCCGGGCCAGTCCCAACGGGACCCCGGGGACACA 1380
 Db |||||
 QY 1390 CCCCCGTCCAGCCCC-----AGCTGGAGGGGTGCTCTGAGGGCGCGGTCAACTCC 1443
 Db |||||
 QY 1381 CCACCCCGCAGCCCGGGGTGGCGTCCGGGGAGCGCGCTGAGGAGTCTCTCAACTCC 1440
 Db |||||
 QY 1444 ATCAGAGACGCTTCTGGGCTCACCCGCTTCCACCGCGGAACTCAAGTTCGAGC 1503
 Db |||||
 QY 1441 ATCCGCAACAGCTTCTGGGCTTCTCTCTTTCACCGGCGCAAGATGAGGTCTCTTACC 1500
 Db |||||
 QY 1504 CCGGAGGAGATCTCAACCTGACACAGAGTCTCTCCAGAGCTGGCGAAGAGTCTCTGG 1563
 Db |||||
 QY 1501 GCTGAGGAGATCTCAGCTTGGAGCGCAGAGTCTCTCCCGAGCTGGCAAAACGCTCTCTGG 1560
 Db |||||

RESULT 13

ABV74558
 ID ABEV74558 standard; cDNA; 2289 BP.
 XX AC ABV74558;
 XX AC
 XX DT 20-JAN-2003 (first entry)
 XX DE Human kinase #2 coding sequence.
 XX KW Human; kinase; chromosome 19; gene; ss.
 XX OS Homo sapiens.
 XX PH Key Location/Qualifiers
 XX CDS 1..2289
 XX FT /*tag= a
 XX FT /product= "Human kinase #2".
 XX PN W0200281670-A1.
 XX PD 17-OCT-2002.
 XX PF 04-APR-2002; 2002MO-US10786.
 XX PR 06-APR-2001; 2001US-282036P.
 XX PA (LEXI-) LEXICON GENETICS INC.
 XX PI Turner CA, Mathur B, Friddle CJ;
 XX WPI; 2003-058538/05.
 XX DR P-PSDB; ABB98744.
 XX PT New human kinase proteins useful for diagnosis, drug screening, and
 XX PT clinical trial monitoring, treatment of disorders and diseases, and
 XX PT cosmetic and nutritional applications
 XX PS Claim 5; Page 41-42; 47pp; English.
 XX CC The present sequence is the coding sequence for a novel human kinase. The
 XX CC genomic locus encoding the kinase is thought to be on human chromosome
 XX CC 19. The kinase and its coding sequence are useful for diagnosis, drug
 XX CC screening, clinical trial monitoring, treatment of disorders and

QY 1564 TTGGGAATCTCATCAGCCTGGAGAGGAGGAGAGATCTTCGTGGTCAATAAGACAAA 1623
 Db |||||
 QY 1561 TTCCGGAACTTCATCTCTTGGCAAAAGAGAAACAAATATTCTCTGTGCTAAAGACAAA 1620
 Db |||||
 QY 1624 CTTCTGAGCTCCATCAAGGCTGACATCGTGGACGCTTCCTGTCGATTCCTCCAGTCTCAGC 1683
 Db |||||
 QY 1621 CTTCTCAGCAGCATCAAAAGCAGACATCGTCCATGCTTCTGTGATCCCCAGCTGAGT 1680
 Db |||||
 QY 1684 CACAGCGTCATCTCCCAACAGAGCTTCCGGGCGGAGTACAAGGCCACCGGGGGGCCAGCC 1743
 Db |||||
 QY 1681 CACAGTGTCTGTACAGACACAGCTTCAGGGCCGAGTACAAGGCCAGTGGCGGCCCTCC 1740
 Db |||||
 QY 1744 GTGTTCCAGAACCGCGTCAAGTTCAGGTTGATATCACTACACGAGAGGT----- 1794
 Db |||||
 QY 1741 GTCTTCAAAAGCCCGTCCGCTTCCAGGTGGACATCAGCTCTCTGAGGTCCAGAGCCC 1800
 Db |||||
 QY 1795 -----GGGGAGCGCAGAAAGGAGAACGGCATCTACTCCGTCACTTCACTTCACTCTCTC 1845
 Db |||||
 QY 1801 TCCCCCGCAGCGGACCGCAGCGGAGGTGGTGGATCTACTCCGTCACTTCACTTCACTCTCATC 1860
 Db |||||
 QY 1846 TCAGGCCCCCAGCGCTCGCTTCAAGAGGGTGGTGGAGACCATCCAGGCCCAGCTGTGAGC 1905
 Db |||||
 QY 1861 TCGGGTCCAGCGCTCGGTTCAAGCGAGTGGTGGAGACCATCCAGGCACAGCTCTCTGAGC 1920
 Db |||||
 QY 1906 ACACAGACCCCGCTCCGCGCCAGCAGCACTTGTTCAGACACCACTAACTG 1952
 Db |||||
 QY 1921 ACTCATGACGAGCCCTCCGTGCGAGGCCCTGGCAGACGAGAAGACGG 1967
 Db |||||

XX	Human; gene; ss; nervous system disorder; peripheral neuropathy;
KW	Huntington's disease; amyotrophic lateral sclerosis; haemophilia;
KW	neurodegenerative disease; Parkinson's disease; Alzheimer's disease;
KW	autoimmune disease; systemic lupus erythematosus; rheumatoid arthritis;
KW	insulin-dependent diabetes mellitus; anaemia; thrombocytopaenia; wound;
KW	ulcer; burn; bone disorder; osteoporosis; osteoarthritis; stroke;
KW	fibrosis; reperfusion injury; infection; allergic rhinitis; asthma;
KW	coagulation disorder; cancer; tumour; inflammatory disease;
KW	septic shock; Crohn's disease; anaphylaxis; proliferation; chemotactic;
KW	differentiation; stem cell growth factor; haematopoiesis; chemokinetic;
KW	haemostatic; antiinflammatory; expressed sequence tag; EST.
XX	
OS	Homo sapiens.
XX	
PN	WO200281731-A2.
FN	
PD	17-OCT-2002.
PD	
PF	29-JAN-2002; 2002WO-US01222.
PF	
PF	30-JAN-2001; 2001US-0774528.
FR	(HYSE-) HYSEQ INC.
XX	(GOOD/) GOODRICH R. W.
PA	
PA	
PI	Tang TY, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;
PI	Xue AJ, Yang Y, Wehrman T, Wang J, Wang D, Drmanac RT;
XX	
DR	WPI; 2003-058563/05.
XX	
PT	Novel polypeptide useful for treating neurodegenerative diseases,
PT	myeloid or lymphoid cell disorders, bone disorders, mechanical and
PT	traumatic disorders, coagulation disorders, and inflammatory diseases
PT	-
XX	
XX	Claim 1; Page -; 612pp; English.
XX	
PS	This invention relates to the cDNA sequences encoding an isolated
CC	novel human polypeptide. The protein encoded by the nucleic acid of
CC	the invention is useful for treating central and peripheral nervous
CC	system diseases (e.g. peripheral neuropathy, Huntington's disease,
CC	amyotrophic lateral sclerosis); neurodegenerative diseases (e.g.
CC	Parkinson's disease, Alzheimer's disease); autoimmune disease (e.g.
CC	systemic lupus erythematosus, rheumatoid arthritis, insulin-dependent
CC	diabetes mellitus); myeloid or lymphoid cell disorders (e.g. anaemia
CC	and thrombocytopaenia); wounds, ulcers, burns; bone disorders (e.g.
CC	osteoporosis, osteoarthritis); mechanical and traumatic disorders (e.g.
CC	stroke, head trauma); lung or liver fibrosis; reperfusion injury in
CC	various tissues; bacterial, viral or fungal infections; allergic
CC	conditions such as allergic rhinitis, asthma; coagulation disorders
CC	(e.g. haemophilia); cancer and tumours; and inflammatory diseases (e.g.
CC	septic shock, Crohn's disease, anaphylaxis). The protein may be used to
CC	inhibit the growth, infection or function of infectious agents such as
CC	bacteria, fungi, viruses, or to effect bodily characteristics,
CC	biohythms or circadian cycles of rhythms. The protein may also
CC	have proliferation/differentiation, stem cell growth factor,
CC	haematopoiesis regulation, immune stimulating or suppressing,
CC	chemotactic/chemokinetic, haemostatic and thrombolytic, receptor/ligand
CC	and antiinflammatory activities. The cDNA sequences of the invention are
CC	useful for expressing recombinant protein for analysis. The present
CC	sequence represents a novel human cDNA sequence of the invention,
CC	this sequence is an expressed sequence tag (EST) and was identified
CC	using subtractive hybridisation.
CC	

Query Match 29.3%; Score 588.8; DB 25; Length 1797;
Best Local Similarity 77.1%; Pred. No. 5.2e-118;
Matches 748; Conservative 0; Mismatches 207; Indels 15; Gaps 2;
Qy 273 GTACCTGGTGCTAGAACCGTGTCAGGTGGTGACCTCTTCGACTACCTGGTGGAAGAGG 332

Db	89	GTACCTGGTTCTTGGAGCACGCTCTCGGGGGGTGAGCTATTTCGACTACCTGCTGTTAAAGAGGG	148
Qy	333	GAGGCTGACGCCCTTAAGAGAGGCTCGGAAGTTCTTCCGGCAGATCATCTCTGCGCTGGACTT	392
Db	149	GAGACTGACGCCCAAGAGAGGCCGGAAGTTCTTCCGCCAGATTGTGTCTGCGCTGGACTT	208
Qy	393	CTGCGCACAGCACTCCATATGCGACAGGATCTGAAACCTGAAACCTCTCTCTGGACGA	452
Db	209	CTGCCACAGCTACTCCATCTGCCACAGACCTTAAAGCCCGAGAACCCTGCTTTTGATGA	268
Qy	453	GAGAAACAACATCCGCATCGCAGACTTTTGGCATGGCGTCCCTGCGAGTTTGGGACAGCCT	512
Db	269	GAAAAACAACATCCGCATTTGCAGACTTTCGSCATGGCTCCCTGCGAGTGGGGGACAGCCT	328
Qy	513	GTTTGGAGCAGCTGTGGTCCCCCACTACGCTGCCCGGAGGTGATCCGGGGGAGAA	572
Db	329	CCTGGAGACAGCTGGGGTCCCCCATTTATGCGTGTCCAGAGGTGATTAAGGGGGAAAA	388
Qy	573	GTATGACGGCCGGAAGCGGACGTGTGGAGCTCGGCGCTCATCTGTTCGCCCTTGTCTGGT	632
Db	389	ATATGATGGCCGCGGCGAGACATGTGGAGCTGTGGAGTCATCTCTTGCCTCTGCTCGT	448
Qy	633	GGGGGCTCTGCCCTTCGACGATGACAACTTGGCAGCTGCTGGAGAAAGGTGAAGCGGG	692
Db	449	GGGGGCTCTGCCCTTTGATGACGACAACTCCGCCAGCTGCTGGAGAGGTGAAACGGGG	508
Qy	693	CGTGTTCACATGCCGCACTTTATCCGGCCGACTGCCAGAGCTGCTACGCGGGCATGAT	752
Db	509	CGTCTTCCATGCCCCCACTTATCTCTCCAGATTGCCAGAGCTCTCGAGGGGAATGAT	568
Qy	753	CGAGGTGGACGCCGCGACGCGCTCTACGCTAGAGCACATTCAGAAACATATGGTATAT	812
Db	569	CGAAGTGGAGCCCGAAAAAGGCTCAGTCTGGAGCAAATTCAGAAACATCTTGGTACCT	628
Qy	813	AGGGGCGAAGATGAGCCCGAACA-----GAGCAGCCCATCTCTCGCAAGGTGCAGAT	866
Db	629	AGCGGGGAACACGAGCCACAGACCCGTGCTGGAGCCAGCCCTTGGCCCGCGGTAGCCAT	688
Qy	867	CCGCTCGCTGCCCAGCGCTGGAGGACATCGAACCCGACGTGCTGGACAGCATGCACTCACT	926
Db	689	CGCGAGCCTGCCATCAAACGAGAGCTGGACCCCGACGTCTTAGAGCATGSCATCACT	748
Qy	927	GGGCTGTTCCGAGACCGGCAACAGCTGCTGACGACCTGCTGCTCCGAGGAGAGAACCA	986
Db	749	GGGCTGTTCCAGGGACCGGAGAGGCTGCATCGCAGCTGCGCAGTGGAGGAGAGAACCA	808
Qy	987	GGAGAGATGATTTACTTCTCTCTCTGACCGGAAGAAAGTACCCGAGCCAGAGGA	1046
Db	809	AGAAAGATGATATATATCTGCTTTTGATCGGAAGAGCGGTATCCACGCTGTGAGGA	868
Qy	1047	TGAGGACCTGCCCCCCCGGAACAGATAGACCTCTCCCGGAAGCGTGTGGACTCCCGCAT	1106
Db	869	CCAGGACCTGCTCTCCCGGAATGATGTGACCCCGCCCGGAGCGTGTGGATTTCTCCCAT	928
Qy	1107	GCTGMAACCGCACGGCAAGCGGGCCAGAACCAATCCATGGAGGTGCTCAGCGTGAC	1166
Db	929	GCTGAGCCGTGACGGGAAGCGGCGACAGAGCGGAAGTCCATGGAAGTCTCTGAGCATCAC	988
Qy	1167	-----GGACGGGGGCTTCCCCGGTGGCTGCGCGCGCGGCCCATTTGAGATGCCCGACGA	1217
Db	989	CGATGCCGGGGTGGTGGCTCCCCCTGTACCACCCGACGGGCTTGGAGATGCCCAGCA	1048
Qy	1218	CGGCCAGAG	1227
Db	1049	CAGCCAGAG	1058

RESULT 15

ABL10489

ID ABL10489 standard; cDNA; 2720 BP.

XX ABL10489;

XX

DT 26-MAR-2002 (first entry)
XX Drosophila melanogaster expressed polynucleotide SEQ ID NO 25949.
DE XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ss.
XX Drosophila melanogaster.
OS
XX WO200171042-A2.
XX 27-SEP-2001.
XX 23-MAR-2001; 2001WO-US09231.
PF 23-MAR-2000; 2000US-191637P.
XX 11-JUL-2000; 2000US-0614150.
PR
XX (PEKE) PE CORP NY.
XX Venter JC, Adams M, Li PWD, Myers EW;
PI WPI; 2001-656960/75.
XX P-PSDB; AB566386.
DR
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX Claim 1; SEQ ID NO 25949; 21pp + Sequence Listing; English.
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
CC sequences (AB101840-AB116175) and the encoded proteins
CC (AB57737-AB572072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 2720 BP; 661 A; 715 C; 759 G; 585 T; 0 other;

Query Match 26.9%; Score 539.8; DB 23; Length 2720;
Best Local Similarity 70.4%; Pred. No. 2.4e-107;
Matches 737; Conservative 0; Mismatches 307; Indels 3; Gaps 1;

QY 9 GACGGGGAAGGACGGCGGCGGAGCAGCGGAGTATGTTGGGCGCTACCGCTGGAGAA 68
DB 6 GAAGGAGAAACAATGTACCGCGGAGAAATGCCAATTTGTGGGCGCTATCGCTGGAGAA 65

QY 69 GACGCTGGGCAAGGGGACACAGGCTCTGTGAAGCTTGGGGGTTCACTGGCTCACCTGCCA 128
DB 66 AACCTTGGCAAGGGTCAACAGGGTCTCTCAAGTTGGCGGTCATGTGTGATTTGGCAA 125

QY 129 GAAGGTGGCCATCAAGATCGTCAACCGTGAGAGCTCAGCGAGTCGGTCTGATGAAGT 188
DB 126 GAAGGTGGGATTAATAATCAATCGCGAGAACTCAGCGAATCGGTCTAATGAAGT 185

QY 189 GGAGCGGGAGATCGGATCCTGAAGCTCATTTGAGCACCCCGCTCTTAAGCTGACGA 248
DB 186 TGAACGTGAATCGCCATAATGAACATAATCGATCATCCACACGCTCTTGGGCTGAGCGA 245

QY 249 CGTTTATGAAACAAATAATTTGTACCTGGTGTGTAGAACACGCTGTCAAGTGGTGAGCT 308
DB 246 TGTGTACGAGAACAGAACTATTTGTTATTTGATTTGAGCATGATCCGCGGAGAGCT 305

QY 309 CTTCCGACTACCTGGTGAAGAGGGAGGCTGACGCTCAAGAGGCTCGGAAGTCTTCCG 368
DB 306 CTTCCGATTACCTGGTGAAGAGGGTGTGATTGACCGCGAAGGAGGCGCGCAAGTCTTCCAG 365

QY 369 GCAGATCATCTCTGGCGTGGACTTCTGCCACAGCCACTCCATATGCCACAGGATCTGAA 428
DB 366 GCRAATCATCTCCGCCCTGGATTTCTGCCATTCGATTCGATTTGCCATCGCGACTTGA 425

QY 429 ACCTGAAAACTCTCTGTGACAGAGAGAAACAACATCCGATCCGACATTTGGCATGGC 488
DB 426 GCCGAGANTCTGTCTGGACGAGAGAAATACATTAAGATAGCGACTTTGGATGGC 485

QY 489 GTCCCTCAGGTTGGCGACAGCCTGTTGGAGACAGCTGTGGGTCCCCCACTAGCGCTG 548
DB 486 TTCCCTGCAGCCAGCTGGCAGCATGTTGGAGACCTCTCTGGCGAGCCACACTACCGGTG 545

QY 549 CCCGAGGTGATCCGGGGGAGAGTATGACGGCGGAGAGCGGACGCTGTGGAGCTGGC 608
DB 546 TCCAGAGGTATACCGGGGCGAGAGTACGATGGCGCGAAGCGGATGCTCTGGTCTCTGG 605

QY 609 CGTCATCTGTTTCGCTTGTGTGGGGGCTCTGCCCTTCGACGATGACAACTTTGCCACA 668
DB 606 GGTCTATCTCTATGCCCTCTCTGGTGGGTGCGTTCGCTTCGACGACGACAACTTTGGCCA 665

QY 669 GCTCTGAGAGAGGTGAAGCGGGCGTGTTCACATGCCGCACTTTATCCCGCCGACTG 728
DB 666 GCTCTGAGAGAGGTCAAGCGGGCGTCTTTTACATACCGCACTTTGTGCGCGGACTG 725

QY 729 CCAGAGTCTGTCAGGGGCGATGTCGAGGTGGACCGCGCAGCGCCCTCAGCTAGAGCA 788
DB 726 CCAGAGTCTGTCGCGGCGCATGATTGAGGTCAATCCCGACCGCGGCTCAGCTGGCTGA 785

QY 789 CATTTCAGAAACACATATGGTATATA---GGGGGCAAGAAATGAGCCCGAACCCAGAGCAGCC 845
DB 786 AATCAACCGGATCCGTGGGTCAAGCTGGCGGCAAGGGGAGCTGGAGCTGGAGCTGCC 845

QY 846 CATTCTCGCAAGGTGAGATCCGCTCGTCCGAGCTGGAGGACATCGACCCGCGAGT 905
DB 846 AATGATGGAGGTGTGCAGACACACGTTATTCACACAGCCACCGCGGTGGATCCGGATGT 905

QY 906 GCTGGACAGCATGCACTCAGTGGGCTGTTCCGAGACCGCAACAGCTGCTGCGAGGACT 965
DB 906 GTTGAACGCGATTTGCTGCTGGGCTGTTTCAAGGAGAGGAGAACTCATCCAGGAACT 965

QY 966 GCTGTCGAGGAGAGAACACAGGAGAGATGATTTACTTCTCTCTGAGACCGGAAAGA 1025
DB 966 GCTCAGTTCAAGTCACATACGAGAGAGGTATATATTTCTCTGTTGCTCGAGCGCAACG 1025

QY 1026 AAGGTACCCGAGCCAGGAGGATGAGGA 1052
DB 1026 AAGACGACCTCGCTGGAGGATGATGA 1052

Search completed: November 27, 2003, 05:14:47
Job time : 524.488 secs

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OM nucleic - nucleic search, using sw model

Run on: November 27, 2003, 02:00:45 ; Search time 7183.11 Seconds
(without alignments)
11430.368 Million cell updates/sec

Title: US-10-054-579-1
Perfect score: 2007
Sequence: 1 atgacatcgacggggaagga.....gaattatccgaaagttaa 2007

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: gb_ba.*
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10: gb_ro.*
11: gb_ats.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*
15: em_ba.*
16: em_fun.*
17: em_hum.*
18: em_in.*
19: em_mu.*
20: em_om.*
21: em_or.*
22: em_ov.*
23: em_pat.*
24: em_ph.*
25: em_pl.*
26: em_ro.*
27: em_sts.*
28: em_un.*
29: em_vi.*
30: em_htg_hum.*
31: em_htg_inv.*
32: em_htg_other.*
33: em_htg_mus.*
34: em_htg_pln.*
35: em_htg_rtd.*
36: em_htg_mam.*
37: em_htg_vrt.*
38: em_sy.*
39: em_htgo_hum.*
40: em_htgo_mus.*
41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2007	100.0	2007	6	AX661191	AX661191 Sequence
2	2005.4	99.9	3516	6	AR232170	AR232170 Sequence
3	2005.4	99.9	3516	9	AY168857	AY168857 Homo sapi
4	1993	99.3	3364	6	AR232171	AR232171 Sequence
5	1939.6	96.6	2025	6	AX327995	AX327995 Sequence
6	1939.6	96.6	2219	6	AX327993	AX327993 Sequence
7	1827	91.0	1827	6	AX661193	AX661193 Sequence
8	1727	86.0	1956	9	HSAG701	AJ006701 Homo sapi
9	1330.4	66.3	3156	9	AK074411	AK074411 Homo sapi
10	965	48.1	3109	9	AF479827	AF479827 Homo sapi
11	964.4	48.1	2385	6	AX166526	AX166526 Sequence
12	964.4	48.1	2897	6	AX642966	AX642966 Sequence
13	964.4	48.1	3007	9	AF479826	AF479826 Homo sapi
14	946	47.1	2720	9	HSAG05307	AL834275 Homo sapi
15	878.8	43.8	2576	9	AB058714	AB058714 Homo sapi
16	594	29.6	2333	9	AF020089	BC024091 Homo sapi
17	583.2	29.1	1873	9	BC024291	BC024291 Homo sapi
18	432.2	21.5	3933	3	AB014885	AB014885 Halocynthia
19	426.6	21.3	3059	3	AF316542	AF316542 Caenorhab
20	426	21.2	5609	3	AY060288	AY060288 Drosophila
21	410.2	20.4	2123	3	AK116009	AK116009 Ciona int
22	391	19.5	2128	9	BC016681	BC016681 Homo sapi
23	265.8	13.2	3529	9	AB088047	AB088047 Homo sapi
24	265.8	13.2	3609	9	AB049127	AB049127 Homo sapi
25	265.6	13.2	2259	10	AY151083	AY151083 Mus muscu
26	265	13.2	1594	6	AX056390	AX056390 Sequence
27	264.2	13.2	1549	6	AX685979	AX685979 Sequence
28	264.2	13.2	2462	6	AX399987	AX399987 Sequence
29	264.2	13.2	2650	9	AY120867	AY120867 Homo sapi
30	264.2	13.2	2954	6	BD127952	BD127952 Primer fo
31	264.2	13.2	2954	9	AK075272	AK075272 Homo sapi
32	264.2	13.2	3226	9	AY057448	AY057448 Homo sapi
33	264.2	13.2	3269	6	AX680149	AX680149 Sequence
34	264.2	13.2	3312	6	AX305105	AX305105 Sequence
35	264.2	13.2	3392	6	AX305106	AX305106 Sequence
36	264.2	13.2	4917	9	AB058763	AB058763 Homo sapi
37	262.4	13.1	3170	6	AX305103	AX305103 Sequence
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ALIGNMENTS

RESULT 1
AX661191
LOCUS AX661191 2007 bp DNA linear PAT 22-MAR-2003
DEFINITION Sequence 1 from Patent WO02059287.
ACCESSION AX661191
VERSION AX661191.1 GI:29162844
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Turner, C.A. and Mathur, B.
TITLE Novel human kinases and polynucleotides encoding the same
JOURNAL Patent: WO 02059287-A 1 01-AUG-2002;

Db 1981 AATGTGGAATTATCCGAAAGTTAA 2007
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RESULT 2
AR232170 2908 bp DNA linear PAT 20-DEC-2002
LOCUS
DEFINITION
Sequence 1 from patent US 6455292.
ACCESSION
AR232170
VERSION
AR232170.1 GI:27274061
KEYWORDS
Unknown.
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 2908)
AUTHORS
Shu, Y., Fan, W., Kovacs, K.F., Zidanic, M. and Jay, G.
TITLE
Full-length serine protein kinase in brain and pancreas
JOURNAL
Patent: US 6455292-A 1 24-SEP-2002;
FEATURES
Location/Qualifiers
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/organism="unknown"
BASE COUNT 603 a 948 c 879 g 478 t
ORIGIN
Query Match 99.9%; Score 2005.4; DB 6; Length 2908;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2006; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 106 ATGACATCAGCGGGAAGACGCGCGCGCAGCAGCGCCAGTATGTTGGGCGCTACCGG 165
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RESULT 4
AR232171
LOCUS AR232171 3364 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 3 from patent US 6455292.
ACCESSION AR232171
VERSION AR232171.1 GI:27274062
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 3364)
AUTHORS Shu,Y., Fan,W., Kovacs,K.F., Zidanic,M. and Jay,G.
TITLE Full-length serine protein kinase in brain and pancreas

JOURNAL Patent: US 6455292-A 3 24-SEP-2002;
FEATURES Location/Qualifiers
source 1. 3364
BASE COUNT 639 a 1078 c 1069 g 578 t
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Query Match 99.3%; Score 1993; DB 6; Length 3364;
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AX327995
LOCUS AX327995 2025 bp DNA linear PAT 07-JAN-2002
DEFINITION Sequence 3 from Patent WO0181588.
ACCESSION AX327995
VERSION AX327995.1 GI:18098148
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 Meyers, R.
2246, protein kinase molecules and uses therefor
Patent: WO 0181588-A 3 01-NOV-2001;
Millennium Pharmaceuticals, Inc. (US)

FEATURES

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/organism="Homo sapiens"
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BASE COUNT 442 a 641 c 616 g 326 t
ORIGIN

Query Match 96.6%; Score 1939.6; DB 6; Length 2025;
Best Local Similarity 99.8%; Pred. No. 0;
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DEFINITION Sequence 1 from Patent WO0181588.
ACCESSION AX327993
VERSION AX327993.1 GI:18098146
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Meyers,R.
TITLES 2246, protein kinase molecules and uses therefor
JOURNAL Patent: WO 0181588-A 1 01-NOV-2001;
Millennium Pharmaceuticals, Inc. (US)
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ORIGIN
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RESULT 7

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AX661193
LOCUS 1827 bp DNA linear PAT 22-MAR-2003
DEFINITION Sequence 3 from Patent WO02059287.
ACCESSION AX661193
VERSION AX661193.1 GI:29162845
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Turner, C.A. and Mathur, B.
TITLE Novel human kinases and polynucleotides encoding the same
JOURNAL Patent: WO 02059287-A 3 01-AUG-2002;
Lexicon Genetics Incorporated (US)
FEATURES
source 1. 1827
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 406 a 581 c 535 g 305 t
ORIGIN
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Query Match 91.0%; Score 1827; DB 6; Length 1827;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1827; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	181	ATGAAGTGGAGCGGAGATCCGATCTGTAAGCTCATTGAGACCCGCCAGTCTTAAG	240
DB	1	ATGAAGTGGAGCGGAGATCCGATCTGTAAGCTCATTGAGACCCGCCAGTCTTAAG	60
QY	241	CTGACGACGCTTTATGAACAAAAATATTTGTAACCTGTGTAGAACACGCTGCAGGT	300
DB	61	CTGACGACGCTTTATGAACAAAAATATTTGTAACCTGTGTAGAACACGCTGCAGGT	120
QY	301	GGTGAAGTCTTCGACTACCTGGTGAAGAGGGAGGCTGACGCCCTAAGAGAGCTCGAAG	360
DB	121	GGTGAAGTCTTCGACTACCTGGTGAAGAGGGAGGCTGACGCCCTAAGAGAGCTCGAAG	180
QY	361	TTCTTTCCGGCAGATCATCTCTGCGCTGACCTTCTGCCACAGCCATCCATATGCCACAGG	420
DB	181	TTCTTTCCGGCAGATCATCTCTGCGCTGACCTTCTGCCACAGCCATCCATATGCCACAGG	240
QY	421	GATCTGAACCTGAAACCTCTCTGCTGGACGAGAGAAACAACATCCGATCGCAGACTTT	480
DB	241	GATCTGAACCTGAAACCTCTCTGCTGGACGAGAGAAACAACATCCGATCGCAGACTTT	300
QY	481	GGCATGGCGTCCCTGACAGGTTGGCGACAGCCTGTTGGAGACAGCTGTGGTCCGCCAC	540
DB	301	GGCATGGCGTCCCTGACAGGTTGGCGACAGCCTGTTGGAGACAGCTGTGGTCCGCCAC	360
QY	541	TACGCTCCGCCGAGTGCATCCGGGGGAGAGATGACGGCCGAGAGCGGAGCTGTGG	600
DB	361	TACGCTCCGCCGAGTGCATCCGGGGGAGAGATGACGGCCGAGAGCGGAGCTGTGG	420
QY	601	AGCTGCGCGCTCATCTCTGCTGCTTGTGTGGGGGCTCTGCCCTTCGACGATGACAAC	660
DB	421	AGCTGCGCGCTCATCTCTGCTGCTTGTGTGGGGGCTCTGCCCTTCGACGATGACAAC	480
QY	661	TTGGACAGCTGCTGGAGAGGTGAAGCGGGCGTGTTCACATGCGCCACTTTATCCCG	720
DB	481	TTGGACAGCTGCTGGAGAGGTGAAGCGGGCGTGTTCACATGCGCCACTTTATCCCG	540
QY	721	CCCGACTCCAGAGTCTGCTACGGGGCATGATCGAGGTGAGCGCGCGCTCAGC	780
DB	541	CCCGACTCCAGAGTCTGCTACGGGGCATGATCGAGGTGAGCGCGCGCTCAGC	600
QY	781	CTAGAGCATTTCAGAAACACATATGTTATAGGGGGCAAGATGAGCCCGAACCCAGAG	840
DB	601	CTAGAGCATTTCAGAAACACATATGTTATAGGGGGCAAGATGAGCCCGAACCCAGAG	660
QY	841	CAGCCCATTCCTCGCAAGGTGAGATCCGCTGCTGCGCCAGCTGGAGGACATCGACCCC	900
DB	661	CAGCCCATTCCTCGCAAGGTGAGATCCGCTGCTGCGCCAGCTGGAGGACATCGACCCC	720
QY	901	GACGTGCTGGACAGCATGCACTCACTGGGCTGCTTCGAGACCGCAACAAGCTGTGCG	960
DB	721	GACGTGCTGGACAGCATGCACTCACTGGGCTGCTTCGAGACCGCAACAAGCTGTGCG	780
QY	961	GACCTGCTGCTCCGAGGAGAACACAGAGAGATGATTTACTTCTCTCTCTGACCGG	1020
DB	781	GACCTGCTGCTCCGAGGAGAACACAGAGAGATGATTTACTTCTCTCTCTGACCGG	840
QY	1021	AAAGAAAGGTATCCGAGCAGAGAGATGAGACCTGCGCCCGGAAACGAGATAGACCT	1080
DB	841	AAAGAAAGGTATCCGAGCAGAGAGATGAGACCTGCGCCCGGAAACGAGATAGACCT	900
QY	1081	CCCCGGAAGCTGTGACTTCCCGGATGCTGAACCGGACGCGCAAGCGGCGCAGAACGC	1140
DB	901	CCCCGGAAGCTGTGACTTCCCGGATGCTGAACCGGACGCGCAAGCGGCGCAGAACGC	960
QY	1141	AAATCCATGAGGTGCTCAGCGTGAAGCGCGGCTCCCGGTGCTTCCGCGGGCGG	1200
DB	961	AAATCCATGAGGTGCTCAGCGTGAAGCGCGGCTCCCGGTGCTTCCGCGGGCGG	1020
QY	1201	ATTGAGTGGCCAGACAGGCGGAGAGGTCTCGGTTCATCAGCGGTGCTCTCAGGCGCTT	1260

DB	1021	ATTGAGTGGCCAGACGCGCCAGAGGTCTCGGTCCATCAGCGGTGCTCTCAGGCGCTT	1080
QY	1261	TCCACAGAGCCCTCAGCAGAGCCCGGGTGACCCCTCACCCTCACCAGGGGAGTCCC	1320
DB	1081	TCCACAGAGCCCTCAGCAGAGCCCGGGTGACCCCTCACCCTCACCAGGGGAGTCCC	1140
QY	1321	CTCCCAAGAGGAGACACCTGTCCACAGCCAAAGAGAGAGCCGGTGGCAGCGCC	1380
DB	1141	CTCCCAAGAGGAGACACCTGTCCACAGCCAAAGAGAGAGCCGGTGGCAGCGCC	1200
QY	1381	AACCCACAGCCCGCTCCAGCCCGAGGGTGGCCCTGGAGGGCGCGGCTCAAC	1440
DB	1201	AACCCACAGCCCGCTCCAGCCCGAGGGTGGCCCTGGAGGGCGCGGCTCAAC	1260
QY	1441	TCCATCAAGAAACAGCTTCTGCGCTCACCCTGCTCCACCGCGGAAACTGCAAGTTCCG	1500
DB	1261	TCCATCAAGAAACAGCTTCTGCGCTCACCCTGCTCCACCGCGGAAACTGCAAGTTCCG	1320
QY	1501	ACGCCGAGAGATGTCCAACTGACACACAGAGTCTGCTCCAGAGCTGGGAGAAAGTCC	1560
DB	1321	ACGCCGAGAGATGTCCAACTGACACACAGAGTCTGCTCCAGAGCTGGGAGAAAGTCC	1380
QY	1561	TGGTTGGGAACTTCATCAGCCTGGAGAGGAGAGAGATCTTCTGTTGTCATCAAGAC	1620
DB	1381	TGGTTGGGAACTTCATCAGCCTGGAGAGGAGAGAGATCTTCTGTTGTCATCAAGAC	1440
QY	1621	AAACCTCTGAGCTCCATCAAGGCTGACATCGTGCAGCCCTCTGTCGATTCGAGTCTC	1680
DB	1441	AAACCTCTGAGCTCCATCAAGGCTGACATCGTGCAGCCCTCTGTCGATTCGAGTCTC	1500
QY	1681	AGCCACAGCTCTATCTCCAAACGAGCTTCCGGGCGCGAGTACAAGGCCACGGGGGGCCA	1740
DB	1501	AGCCACAGCTCTATCTCCAAACGAGCTTCCGGGCGCGAGTACAAGGCCACGGGGGGCCA	1560
QY	1741	GCGTGTTCAGAAAGCGGTCAAGTTCCAGGTTGATATCACTTACAGGAGGTGGGGAG	1800
DB	1561	GCGTGTTCAGAAAGCGGTCAAGTTCCAGGTTGATATCACTTACAGGAGGTGGGGAG	1620
QY	1801	GCGCAGAGGAGAAAGGCTACTCTCGTCACTTCACTTCACTTCACTTCACTTCACTTCA	1860
DB	1621	GCGCAGAGGAGAAAGGCTACTCTCGTCACTTCACTTCACTTCACTTCACTTCACTTCA	1680
QY	1861	CGTTTCAAGAGGTGGTGGAGACCATCCAGCCAGCTGTGAGACACACAGCCCGCT	1920
DB	1681	CGTTTCAAGAGGTGGTGGAGACCATCCAGCCAGCTGTGAGACACACAGCCCGCT	1740
QY	1921	GCGGCCAGCACTTGTGAGACACCACTAATGTAATGTAATGTAATGTAATGTAATGTAAT	1980
DB	1741	GCGGCCAGCACTTGTGAGACACCACTAATGTAATGTAATGTAATGTAATGTAATGTAAT	1800
QY	1981	AAATGTGAATTTATCCCGAAAGTTAA	2007
DB	1801	AAATGTGAATTTATCCCGAAAGTTAA	1827

RESULT 8

LOCUS	HSA6701
DEFINITION	Homo sapiens mRNA for putative serine/threonine protein kinase, partial.
ACCESSION	AJ006701
VERSION	AJ006701.1
KEYWORDS	putative; serine/threonine protein kinase.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	1 Stanchi, F., Bertocco, E., Toppo, S., Dioguardi, R., Simonati, B., Cannata, N., Zimbellio, R., Lanfranchi, G. and Valle, G. Characterization of 16 novel human genes showing high similarity to yeast sequences
AUTHORS	
TITLE	

JOURNAL	Yeast 18 (1), 69-80 (2001)	QY	692	GGGTGTTCCACATGCGCACATTATCCCGCCGACTCTCCAGAGTCTGTCACGGGCAATGA	751
MEDLINE	21064499	Db	481	GGGTGTTCCACATGCGCACATTATCCCGCCGACTCTCCAGAGTCTGTCACGGGCAATGA	540
PUBMED	11124703				
REFERENCE	2 (bases 1 to 1956)	QY	752	TCAGAGTGGACCCCGCAGCCGCTTACGCTAGAGCAATTCAGAAACATATGTATATA	811
AUTHORS	Stanchi, F.	Db	541	GGAGGTGGACCCCGCAGCCGCTTACGCTAGAGCAATTCAGAAACATATGTATATA	600
TITLE	Submitted (02-JUN-1998) Stanchi F., CRIBI Biotechnology Centre,	QY	812	TAGGGGGGAGAGTGGAGGACATCGACCCCGAAGCAAGCAAGCCATTCCTCGAAGGTGAGATCCGCT	871
JOURNAL	Universita' di Padova, Via G. Colombo 3, 35121 Padova, 35121, ITALY	Db	601	TAGGGGGGAGAGTGGAGGACATCGACCCCGAAGCAAGCAAGCCATTCCTCGAAGGTGAGATCCGCT	660
FEATURES	Location/Qualifiers	QY	872	CGCTGCCAGAGCTGGAGGACATCGACCCCGAAGCAAGCAAGCCATTCCTCGAAGGTGAGATCCGCT	931
source	1. 1956	Db	661	CGCTGCCAGAGCTGGAGGACATCGACCCCGAAGCAAGCAAGCCATTCCTCGAAGGTGAGATCCGCT	720
	/organism="Homo sapiens"	QY	932	GTTTCGAGACCGCAACAAAGCTGCTGCGAGGACCTGCTGTCGAGGAGGAGAACCCAGGAGA	991
	/mol_type="mRNA"	Db	721	GCTTCGAGACCGCAACAAAGCTGCTGCGAGGACCTGCTGTCGAGGAGGAGAACCCAGGAGA	780
	/db_xref="taxon:9606"	QY	992	AGATGATTTTACTTCTCTCTCTGACCCGGAAGAAAGTACCCGAGCCAGGAGGATGAGG	1051
	/sex="female"	Db	781	AGATGATTTTACTTCTCTCTCTGACCCGGAAGAAAGTACCCGAGCCAGGAGGATGAGG	840
	/tissue_type="whole brain"	QY	1052	ACCTGCCCGCCCGGAAACGAGATAGACCCCTCCCGGAAAGCTGTGGAATCCCGATGCTGA	1111
	/clone_lib="Soares infant brain INIB"	Db	841	ACCTGCCCGCCCGGAAACGAGATAGACCCCTCCCGGAAAGCTGTGGAATCCCGATGCTGA	900
	/dev_stage="73 days post natal"	QY	1112	ACCGGACCGGCAAGCGGCGGCGAGAAACGCAAAATTCATGAGAGTGTCTGAGGTGACGGAGC	1171
	<1. 1814	Db	901	ACCGGACCGGCAAGCGGCGGCGAGAAACGCAAAATTCATGAGAGTGTCTGAGGTGACGGAGC	960
CDS	/codon_start=3	QY	1172	GGGGTCCCGCGGTGCTGCGCGCGGCGGCAATTCAGATGAGTGGCCGAGGAGGATGCTC	1231
	/product="putative serine/threonine protein kinase"	Db	961	GGGGTCCCGCGGTGCTGCGCGCGGCGGCAATTCAGATGAGTGGCCGAGGAGGATGCTC	1020
	/protein_id="CAA07196.1"	QY	1232	GGTCCATCAGCGGTGCTCTCTCAGGCGCTTTCACACAGCCCACTCAGACGCCCCCGGGTGA	1291
	/db_xref="SPIRIT:060843"	Db	1021	GGTCCATCAGCGGTGCTCTCTCAGGCGCTTTCACACAGCCCACTCAGACGCCCCCGGGTGA	1080
	/translation="LIEHPHVLKLDVYENKLYLVLHVSGGELFDYLVKKGRITP	QY	1292	CGCTCAGCCCTCACAAGGGGAGTCCCTCTCCACACCCGCGGAGGAGACCTGTGTCACA	1351
	KEARFQRIISALDFEHSIICHRDLKPNELLDKNNIRIADFGWASLDGDSLLLE	Db	1081	CGCTCAGCCCTCACAAGGGGAGTCCCTCTCCACACCCGCGGAGGAGACCTGTGTCACA	1140
	TSCGSPHVAPEVIRGKDYGRKADVMSGVILFALLVAGLPFDNDNLRLLLEKVRG	QY	1352	CGCCAAAGGAGAGCCGCGTGGCAGCCCAACCCAGCCGCGGCTCCAGCCGCGGAGTGG	1411
	VFMHPHPIPDQCSSLGMSVDAAERLTLEHIOKHLYWYIGKNEPEPQPIPRKQI	Db	1141	CGCCAAAGGAGAGCCGCGTGGCAGCCCAACCCAGCCGCGGCTCCAGCCGCGGAGTGG	1200
	RSPLSDIDPDLVDLSWHSIGCFDRNKLQDLLEENQRMYYFILLDRKIEFSQ	QY	1412	GAGGGTGGCTTGGAGGGCGCGGCTCAACTCCATCAAGAAACAGCTTCTTGGGCTCACCCC	1471
	EDEDLPNRNIDPPKRVDFMLNRHGRKRPERSMEVLSVTDGGSPVPARRAIEWAQ	Db	1201	GAGGGTGGCTTGGAGGGCGCGGCTCAACTCCATCAAGAAACAGCTTCTTGGGCTCACCCC	1260
	HGQRSISIGASGLSTSPSSPRVTPHSPRGSPLTPKGTPTVHTPKESPAGTNPPT	QY	1472	GCTTCCACCGCGGAAACTGCAAGTTCGACCGCGGAGAGATGTCCAACTTGCACACAG	1531
	PPSPSGVGVPMRRLNLSIKNSFLGSPRHRKLOVTPREMSNLTPESPPELAKXSW	Db	1261	GCTTCCACCGCGGAAACTGCAAGTTCGACCGCGGAGAGATGTCCAACTTGCACACAG	1320
	FGNFIKKEEQIPVTKDPLKSLIKADIVHFLSIPLSHVSISOTSPRAEYKATGG	QY	1532	AGTCTGCTCCCGAGAGTGGCGAAGAGTCTGCTTGGGAACTTTCATCAGCTGGGAGAGG	1591
	PAVQKPVKQVDITTEGEAKENGKGIYVETLLSGPSRRPKRVVETIQAOQLSTH	Db	1321	AGTCTGCTCCCGAGAGTGGCGAAGAGTCTGCTTGGGAACTTTCATCAGCTGGGAGAGG	1380
	DPFAQLSEFPFPPAPGLSWGGLGKVAISTESSL"	QY	1592	AGGAGCAGATCTTCTGTTGTTTCATCAAGAAACAACTCTTGAGCTCCCATCAAGGCTGACATCG	1651
BASE COUNT	427 a 640 c 579 g 310 t	Db	1381	AGGAGCAGATCTTCTGTTGTTTCATCAAGAAACAACTCTTGAGCTCCCATCAAGGCTGACATCG	1440
ORIGIN		QY	1652	TGCAAGCTTCTGTTGTTTCATCAAGAAACAACTCTTGAGCTCCCATCAAGGCTGACATCG	1711
Query Match	86.0%; Score 1727; DB 9; Length 1956;	Db	1441	TGCAAGCTTCTGTTGTTTCATCAAGAAACAACTCTTGAGCTCCCATCAAGGCTGACATCG	1500
Best Local Similarity	99.7%; Pred. No. 2e-298;	QY	1712	GGSCCGAGTACAAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	1771
Matches 1730; Conservative	0; Mismatches 5; Indels 0; Gaps 0;	Db	1501	GGSCCGAGTACAAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	1560
212	AGCTCATGTAGACACCCCAAGCTCTTAAAGCTGTCAGACGCTTTATGAAAAACAAATATT	QY	1772	TTGATATACCTACACGAGGGGTGGGGAGGCGGAGAGGAGAACCGGCATCTTACTCCGTCAC	1831
Db	1 AGCTCATGTAGACACCCCAAGCTCTTAAAGCTGTCAGACGCTTTATGAAAAACAAATATT				
60	60				
272	TGTACCTGGTGTAGACACGCTGTGAGTGTGAGCTTTCGACTACCTGCTGAGAGAGG	QY			
Db	61 TGTACCTGGTGTAGACACGCTGTGAGTGTGAGCTTTCGACTACCTGCTGAGAGAGG	Db			
120	120				
332	GGAGGCTGACGCTTAAAGGAGGCTCGAAGTTCCTCCGCGCAGATCATCTCTGCGCTGAGCT	QY			
Db	121 GGAGGCTGACGCTTAAAGGAGGCTCGAAGTTCCTCCGCGCAGATCATCTCTGCGCTGAGCT	Db			
391	391				
392	TCTGCCACAGCACTCCATATGCCACAGGATGTGAAACCTGAAAAACCTCTGCTGAGC	QY			
Db	181 TCTGCCACAGCACTCCATATGCCACAGGATGTGAAACCTGAAAAACCTCTGCTGAGC	Db			
240	240				
452	AGAGAACACATCCGATCCGACACTTGGCATGGGCTCCCTGACGTTGGCGACAGCC	QY			
Db	241 AGAGAACACATCCGATCCGACACTTGGCATGGGCTCCCTGACGTTGGCGACAGCC	Db			
511	511				
512	TGTTGGAGACAGCTGTGGGTCCCGCCACTACGCTGCGCGGAGTGCATCCGGGGGAGG	QY			
Db	301 TGTTGGAGACAGCTGTGGGTCCCGCCACTACGCTGCGCGGAGTGCATCCGGGGGAGG	Db			
360	360				
572	AGTATGACGCGCGGAGCGGACGTGTGAGAGTCCGCGCTCATCTGTCCTGCTGCTGG	QY			
Db	361 AGTATGACGCGCGGAGCGGACGTGTGAGAGTCCGCGCTCATCTGTCCTGCTGCTGG	Db			
631	631				
632	TGGGGGCTCTGCCCTTCGACCATGACAACTTGGCAGACGCTGCTGAGAGAGTGAAGCGG	QY			
Db	421 TGGGGGCTCTGCCCTTCGACCATGACAACTTGGCAGACGCTGCTGAGAGAGTGAAGCGG	Db			
480	480				


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QY 1659 CTTCTCTGATCCAGTCTCAGCCACAGCGTCATCTCCCAACAGAGCTTCCGGCCGA 1718
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Db 1228 GTACAGGCCACCGGGGGCCAGCCGCTGTTCCAGAAAGCCGCTCAAGTTCCAGTTGATAT 1287
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Db 1288 CACTACAGGAGGTGGGAGGGCGAGAGGAGAGCGGCATCTACTCCGTCACTTCC 1347
QY 1839 CTTGCTCTCAGGCCACAGCCGCTGCTTCAAGAGGGTGGTGGAGACCATCCAGGCCAGCT 1898
Db 1348 CTTGCTCTCAGGCCACAGCCGCTGCTTCAAGAGGGTGGTGGAGACCATCCAGGCCAGCT 1407
QY 1899 GCTGAGCACACAGCCGCTGCGGCCCGCCAGCACTTGTTCAGACACAC 1946
Db 1408 GCTGAGCACACAGCCGCTGCGGCCCGCCAGCACTTGTTCAGACACCC 1455

RESULT 10
AF479827 AF479827 3109 bp mRNA linear PRI 12-MAR-2002
LOCUS Homo sapiens protein kinase-like protein mRNA, complete cds.
DEFINITION
ACCESSION AF479827
VERSION AF479827.1 GI:19401873
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 3109)
AUTHORS She,X.Y., Yu,L. and Guo,J.H.
TITLE Direct Submission
JOURNAL Submitted (02-FEB-2002) School of Life Sciences, Laboratory of
Human Genes Research, Institute of Genetics, Fudan University, 220
Handan Road, Shanghai 200433, P. R. China
FEATURES
Location/Qualifiers
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BASE COUNT 611 a 1033 c 957 g 508 t
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QY 29 CGCAGCAGCGGAGTATGTTGGGCCCTTACCGCTCGAGAACACGCTGGGCAAGGGGCGAGA 88
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QY 1163 TGAC-----GGACGGCGGCTCCCGGTGCTTCCCGCGGGGCCATTGAGATGGCCC 1213
Db 1491 TCACCGATGCCGGGGTGGTGGCTCCCTGTACCCACCCCGAGCGGCTTGAGATGGCCC 1550
QY 1214 AGCAGCGGACAGGTCTCGGTCCATCAGCGGTGCTTCTCAGGGCTTTTCACACAGCCAC 1273
Db 1551 AGCAGCGGACAGATCCCGGTAGCGTCACTGAGCGCTCCACGGGTCTGTCTCCAGCCCTC 1610
QY 1274 TCAGCAGCCCGCGGT----- 1289
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QY 1290 ----- 1289
Db 1671 CTCGAGCGGGGCTCCCGACTTCCAAACGACAGCGCTGCTTCTCGGGGCCCCAGGG 1730
QY 1290 -----GACCCCTACCCCTCACCAAGGGGAGTCCCTCCCTCC----- 1326
Db 1731 GTGGGGCGCGGGAGCAGCCCCCGCCCGCCAGTGCCTCCACACCCCTGCCCCGCGCC 1790
QY 1327 -----ACCCCAAGGGGACACCTGTCCACAGCCAA 1357
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QY 1358 AGGAGAGCCCGGCTGGCACGCGCCAAACCCAGCCCGCCCTCCAGCCCC-----AGCGTGG 1411
Db 1851 GGGCCAGTCCACCGGGACCCCGGGGCAACACACACCCCGCCCGGGGCTGGGTGCTG 1910
QY 1412 GAGGGTCCCTGGAGGGCGGCTCACTCCATCAGAACAGCTTTCTGGGCTACCCC 1471
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QY 1472 GCTTCCACCGCGGAACTGCAAGTTCCGACGCGCGAGGAGATGCCAACTGACACAG 1531
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QY 1532 AGTCGTCCCGAGAGTGGCGAAGAGTCTCGTTGGGAACTTCATCAGCGCTGGAGAAGG 1591
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QY 1592 AGGAGCAGATCTTCTGTGTCTAAGAGAAACCTCTGAGCTCCATCAGCTGACATCG 1651
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Db 2271 TGGACATCAGTCTCTGAGGCTCAGAGCGCTCCCGCGACGGGACGGCAGCGAGGTG 2330
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Db 2331 GTGGCATCTACTCCGTACCTTCACTCTGCTGAGGCTCCAGCGCTGCTTCAAGCGAG 2390
QY 1874 TGGTGGAGACCATCAGGCCAGTGTGTGAGCACACAGCCCGCTGCGGCCAGCACT 1933
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QY 1934 TGTACAGACACTTAATG 1952
Db 2451 TGGCAGACGAGAAGAACGG 2469
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RESULT 11
AX166526
LOCUS

2395 bp DNA linear PAT 22-JUN-2001

DEFINITION Sequence 17 from Patent WO0138503.
ACCESSION AX166526
VERSION AX166526.1 GI:14546871
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Florman,G.D., Whyte,D., Manning,G.S., Sudarsanam,S.S., Martinez,R.,
Flanagan,P. and Clardy,D.S.
TITLE Novel human protein kinases and protein kinase-like enzymes
JOURNAL Patent: WO 0138503-A 17 31-MAY-2001;
Sugen, Inc. (US)
FEATURES Location/Qualifiers
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/organism="Homo sapiens"
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BASE COUNT 494 a 768 c 731 g 392 t
ORIGIN

Query Match 48.1%; Score 964.4; DB 6; Length 2385;
Best Local Similarity 69.8%; Pred. No. 2.9e-162;
Matches 1490; Conservative 0; Mismatches 451; Indels 195; Gaps 6;
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LOCUS
DEFINITION Sequence 43 from Patent WO01096547.
ACCESSION AX642966
VERSION AX642966.1 GI:29550113
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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1 Yue,H., Lal,P., Bandman,O., Borowsky,M., Au-Young,J., Lu,Y.,
Gandhi,A.R., Tribouley,C.M., Walla,N., Yao,M.G., Lu,D.A.,
Greenwald,S.B., Ramkumar,J., Griffin,J.A., Kearney,L., Burford,N.,
Nguyen,D.B., Tang,Y.T., Baughn,M.R., He,A., Thornton,M.,
Hafalia,A., Patterson,C., Gururajan,R., Lo,T.P., Khan,F.,
Recipon,S.A., Azimzal,Y., Pollock,J.L., Ding,L., Grether,M.,
Elliot,V.S., Thangavelu,K., Batra,S. and Ison,C.H.
Humain kinases
TITLE Patent: WO 01096547-A 43 20-DEC-2001;
Incyte Genomics, Inc. (US)
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ORIGIN
Query Match 48.1%; Score 964.4; DB 6; Length 2897;
Best Local Similarity 69.8%; Pred. No. 2.8e-162;
Matches 1490; Conservative 0; Mismatches 451; Indels 195; Gaps 6;
QY 12 GGGGAGGAGCGGGCGCGCAGCAGCGCGCTATGTTGGGCCCTACCGCTGGAGAGAC 71
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DEFINITION	Homo sapiens putative serine/threonine protein kinase mRNA,		
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ACCESSION	AF479826		
VERSION	AF479826.1	GI:19401870	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
	She,X.Y., Guo,J.H. and Yu,L		
	1 (bases 1 to 3007)		

TITLE Direct Submission
Submitted (02-FEB-2002) School of Life Sciences, Laboratory of
Human Genes Research, Institute of Genetics, Fudan University, 220
Handan Road, Shanghai 200433, P. R. China

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VERSION AL834275.1 GI:21739846
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 2720)
AUTHORS Koshner, K., Beyer, A., Mewes, H.W., Weil, B. and Wiemann, S.
JOURNAL Direct Submission
COMMENT Submitted (09-JUL-2002) 1, D-85764 Neuherberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by BMFZ (Biomedical Research Center at the Charite,
Berlin/Germany) within the cDNA sequencing consortium of the German
Genome Project.
This clone (DKFZp547E1613) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
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2041 TGAGCATCATGACGAGCCCTCGTCCAGGCGCTGCGACAGCGAAGAACGG 2092

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LOCUS Homo sapiens mRNA for KIAA1811 protein, partial cds.
DEFINITION AB058714
ACCESSION AB058714.1 GI:14017838
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2576)
AUTHORS Nagase, T., Nakajima, M., Nakajima, D., Kikuno, R. and Ohara, O.
TITLE Prediction of the coding sequences of unidentified human genes. XX.
The complete sequences of 100 new cDNA clones from brain which code
for large proteins in vitro
JOURNAL DNA Res. 8 (2), 85-95 (2001).
MEDLINE 21245130
PUBMED 11347906
REFERENCE 2 (bases 1 to 2576)
AUTHORS Ohara, O., Nagase, T. and Kikuno, R.
TITLE Direct Submission
JOURNAL Submitted (27-MAR-2001) Osamu Ohara, Kazusa DNA Research Institute,
Department of Human Gene Research, 1532-3, Yana, Kisarazu, Chiba
292-0812, Japan (E-mail:cdnaifc@kazusa.or.jp,
URL: <http://www.kazusa.or.jp/huge>, Tel:81-438-52-3913,
Fax:81-438-52-3914)

FEATURES
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Qy	1929	GCACTTGTCTAGACACCACTTACTG	1952
Db	1981	GGCCCTGGCAGACGAGAAGACGG	2004

Search completed: November 27, 2003, 09:03:57
Job time : 7207.61 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 27, 2003, 09:04:30 ; Search time 1165.25 Seconds
(without alignments)
5674.682 Million cell updates/sec

Title: US-10-054-579-1

Perfect score: 2007

Sequence: 1 atgacatcgacgggaagga.....gaattatccgaaagtaa 2007

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2190069 seqs, 1647345023 residues

Total number of hits satisfying chosen parameters: 4380138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1993	99.3	3364	14	US-10-195-072-3
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6	1966	98.0	2647	12	US-10-288-798-42
7	1941.2	96.7	2025	14	US-10-283-247-1
8	1939.6	96.6	2025	10	US-09-842-582-3
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10	1827	91.0	1827	13	US-10-054-579-3
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18	291.6	14.5	512	10	US-09-960-253-87	Sequence 87, Appl
19	265.8	13.2	3609	12	US-10-161-565-19	Sequence 19, Appl
20	265	13.2	1594	14	US-10-284-060-1	Sequence 1, Appli
21	265	13.2	1594	14	US-10-284-060-3	Sequence 3, Appli
22	264.2	13.2	2085	12	US-10-161-565-20	Sequence 20, Appl
23	264.2	13.2	2278	12	US-10-161-565-21	Sequence 21, Appl
24	264.2	13.2	3226	12	US-10-161-565-23	Sequence 23, Appl
25	264.2	13.2	4917	12	US-10-161-565-22	Sequence 22, Appl
26	262.6	13.1	3270	10	US-09-835-081-1	Sequence 1, Appli
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28	252.4	12.6	2352	12	US-10-393-316-3	Sequence 3, Appli
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31	229.4	11.4	3154	10	US-09-919-585-19	Sequence 19, Appl
32	223.4	11.1	2349	11	US-09-823-187-25	Sequence 25, Appl
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36	214.6	10.7	5983	9	US-09-799-875-4	Sequence 4, Appli
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38	214.2	10.7	2112	10	US-09-919-585-4	Sequence 4, Appli
39	214.2	10.7	2112	12	US-10-161-565-7	Sequence 7, Appli
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41	214.2	10.7	2248	12	US-10-161-565-5	Sequence 5, Appli
42	214.2	10.7	2701	12	US-10-161-565-6	Sequence 6, Appli
43	214.2	10.7	2784	12	US-10-161-565-2	Sequence 2, Appli
44	214.2	10.7	2946	12	US-10-161-565-1	Sequence 1, Appli
45	214.2	10.7	3103	12	US-10-161-565-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1

US-10-054-579-1

; Sequence 1, Application US/10054579

; Publication No. US20020137913A1

; GENERAL INFORMATION:

; APPLICANT: Turner, C. Alexander Jr.

; APPLICANT: Mathur, Brian

; TITLE OF INVENTION: No. US20020137913A1 Human Kinases and Polynucleotides Encoding t

; FILE REFERENCE: LEX-0300-USA

; CURRENT APPLICATION NUMBER: US/10/054,579

; CURRENT FILING DATE: 2002-01-22

; PRIOR APPLICATION NUMBER: US 60/263,378

; PRIOR FILING DATE: 2001-01-23

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 2007

; TYPE: DNA

; ORGANISM: homo sapiens

; US-10-054-579-1

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Best Local Similarity 100.0%; Pred. No. 0;

Matches 2007; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ATGACATCGACGGGAAGGACGCGCGCGAGCAGCCGCGAGTATGTTGGCCCTACCGG 60

QY 61 CTGGAGAAGCGTGGCGAAGGGGAGAGCAGCGTCTGTTAGCTGGGGTTCATCGGTC 120

Db 61 CTGGAGAAGCGTGGCGAAGGGGAGAGCAGCGTCTGTTAGCTGGGGTTCATCGGTC 120

QY 121 ACCTGCCAGAGTGGCCATCAAGATCGTCAACCGTGAAGCTCAGCGAGTCGGTCTG 180

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QY 181 ATGAAGTGGAGCGGGAGATCGCGATCTCTGAAGCTCATTGAGCACCCCAAGCTCTTAAAG 240

Db 181 ATGAAGTGGAGCGGGAGATCGCGATCTCTGAAGCTCATTGAGCACCCCAAGCTCTTAAAG 240

Query Match 99.9%; Score 2005.4; DB 14; Length 2908;			
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US-10-195-071-1
; Sequence 1, Application US/10195071
; Publication No. US20030096271A1

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GENERAL INFORMATION:

APPLICANT: Origene Technologies
TITLE OF INVENTION: Full-Length Serine Protein Kinase in Brain and Pancreas
FILE REFERENCE: 16U 101 C1
CURRENT APPLICATION NUMBER: US/10/195,071
CURRENT FILING DATE: 2002-07-15
PRIOR APPLICATION NUMBER: US 09/930,181
PRIOR FILING DATE: 2001-08-16
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 2908
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (106)..(2112)
OTHER INFORMATION:
US-10-195-071-1

Query Match		99.9%	Score 2005.4;	DB 14;	Length 2908;
Best Local Similarity		100.0%	Pred. No. 0;		
Matches 2006;		Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
Qy	1	ATGACATCGACGGGGAAGGACGCGCGCGCAGACGCGCAGTATGTTGGGCCCTACCGG	60		
Db	106	ATGACATCGACGGGGAAGGACGCGCGCGCAGCAGCAGCGCAGTATGTTGGGCCCTACCGG	165		
Qy	61	CTGGAGAAGACGCTGGGCAAGGGGACACAGCTCTGCTGAAGCTGGGGGTTCACTCGTC	120		
Db	166	CTGGAGAAGACGCTGGGCAAGGGGACACAGCTCTGCTGAAGCTGGGGGTTCACTCGTC	225		
Qy	121	ACCTGCCAGAGGTGGCCATCAAGATCGTCAACCGTGAGAAGCTCAGCGAGTGGTGCTG	180		
Db	226	ACCTGCCAGAGGTGGCCATCAAGATCGTCAACCGTGAGAAGCTCAGCGAGTGGTGCTG	285		
Qy	181	ATGAAGTGGAGCGGGAGATCGCATCTGAGCTCATTTAGAGCAACCCCAAGCTCTTAAG	240		
Db	286	ATGAAGTGGAGCGGGAGATCGCATCTGAGCTCATTTAGAGCAACCCCAAGCTCTTAAG	345		
Qy	241	CTGCACGACGTTTATGAACAACAAAAATATTTGCTGCTGAGAACACGTTGTCAGGT	300		
Db	346	CTGCACGACGTTTATGAACAACAAAAATATTTGCTGCTGAGAACACGTTGTCAGGT	405		
Qy	301	GGTGAGCTCTTCGACTACCTGGTGAAGAAGGGAGGCTGACCGCTAAGAGGCTCGGAAG	360		
Db	406	GGTGAGCTCTTCGACTACCTGGTGAAGAAGGGAGGCTGACCGCTAAGAGGCTCGGAAG	465		
Qy	361	TTCTTCCGGGAGATCATCTCGCGTGGACTTCTGCCACAGCCACTCCATATGCCAAG	420		
Db	466	TTCTTCCGGGAGATCATCTCGCGTGGACTTCTGCCACAGCCACTCCATATGCCAAG	525		
Qy	421	GATCTGAACCTGAAACCTCTGCTGGACAGAGAACAACATCCGCTATCGCAGACTTT	480		
Db	526	GATCTGAACCTGAAACCTCTGCTGGACAGAGAACAACATCCGCTATCGCAGACTTT	585		
Qy	481	GGCATAGCGCTCCCTGCAAGTTGGCGACAGCTGTGAGAGCACAGCTGTTGGTCCCCCAC	540		
Db	586	GGCATAGCGCTCCCTGCAAGTTGGCGACAGCTGTGAGAGCACAGCTGTTGGTCCCCCAC	645		
Qy	541	TACGCTGCCCGGAGGTGATCCGGGGGAGAGTATGACGGCGGAGGCGGAGCTGTGG	600		
Db	646	TACGCTGCCCGGAGGTGATCCGGGGGAGAGTATGACGGCGGAGGCGGAGCTGTGG	705		
Qy	601	AGCTGCGCGCTCATCTCTGCTGCTGCTGGGGGCTCTGCGCTTCGACGATGACAAC	660		
Db	706	AGCTGCGCGCTCATCTCTGCTGCTGCTGGGGGCTCTGCGCTTCGACGATGACAAC	765		
Qy	661	TTGGGACAGCTGCTGGAGAAAGTGAAGCGGGCGGTGTTCCACATGCCCACTTTATCCCG	720		
Db	766	TTGGGACAGCTGCTGGAGAAAGTGAAGCGGGCGGTGTTCCACATGCCCACTTTATCCCG	825		
Qy	721	CCCGACTGCCAGAGTCTCTACGGGGCATGATCGAGGTGGACGGCGGACCGGCTCACG	780		

Db	826	CCCGACTGCCAGAGTCTCTACGGGGCATGATCGAGGTGGACGGCGGCTCTACG	885		
Qy	781	CTAGAGCATTTCAGAAACACATATGTTATAGGGGCAAGAAATGAGCCGAAACAGAG	840		
Db	886	CTAGAGCATTTCAGAAACACATATGTTATAGGGGCAAGAAATGAGCCGAAACAGAG	945		
Qy	841	CAGCCCATCTTCGCAAGGTGAGATCCGCTCGCTGCGCAGCTGGAGACATGACACCC	900		
Db	946	CAGCCCATCTTCGCAAGGTGAGATCCGCTCGCTGCGCAGCTGGAGACATGACACCC	1005		
Qy	901	GACGTGCTGGACAGCATGCACTCACTGGGCTGCTTCCGAGACCGCAACAGCTGCTGAG	960		
Db	1006	GACGTGCTGGACAGCATGCACTCACTGGGCTGCTTCCGAGACCGCAACAGCTGCTGAG	1065		
Qy	961	GACCTGCTGCTCCGAGGAGGAGAACAGGAGAGATGATTTACTTCTCTCTGAGACCG	1020		
Db	1066	GACCTGCTGCTCCGAGGAGGAGAACAGGAGAGATGATTTACTTCTCTCTGAGACCG	1125		
Qy	1021	AAAGAAAGTACCCGAGCGCAGAGATGAGGACCTGCCCCCCCCCGGAACAGATAGACCT	1080		
Db	1126	AAAGAAAGTACCCGAGCGCAGGAGATGAGGACCTGCCCCCCCCCGGAACAGATAGACCT	1185		
Qy	1081	CCCGGAGACGCTGTGACTCCCGGATGCTGAACCGGACGCAAGCGCGGCGCAAGACG	1140		
Db	1186	CCCGGAGACGCTGTGACTCCCGGATGCTGAACCGGACGCAAGCGCGGCGCAAGACG	1245		
Qy	1141	AAATCCATCGAGGTGCTCAGCGTGACGACGGCGGCTCCCGGCTGCTCGCGGCGGCG	1200		
Db	1246	AAATCCATCGAGGTGCTCAGCGTGACGACGGCGGCTCCCGGCTGCTCGCGGCGGCG	1305		
Qy	1201	ATTGAGATGGCCAGCAGCGCCAGAGGTCTCGGTCCATCAGCGGTGCTCTCAGGCTTT	1260		
Db	1306	ATTGAGATGGCCAGCAGCGCCAGAGGTCTCGGTCCATCAGCGGTGCTCTCAGGCTTT	1365		
Qy	1261	TCCACAGACCCACTCAGCAGACCCCGGGTGACCCCTCACCTCACAAAGGGGAGTCCC	1320		
Db	1366	TCCACAGACCCACTCAGCAGACCCCGGGTGACCCCTCACCTCACAAAGGGGAGTCCC	1425		
Qy	1321	CTCCCCACCCCAAGGGGACACCTGTCCACACGCGCAAGAGGAGCGGCTGSCAGCCCC	1380		
Db	1426	CTCCCCACCCCAAGGGGACACCTGTCCACACGCGCAAGAGGAGCGGCTGSCAGCCCC	1485		
Qy	1381	AACCCACAGCCCGCTGACAGCCGCTGAGGGGTCCTTGGAGGGGCGGCTCAAC	1440		
Db	1486	AACCCACAGCCCGCTGACAGCCGCTGAGGGGTCCTTGGAGGGGCGGCTCAAC	1545		
Qy	1441	TCCATCAAGAAACAGCTTTCTGGGCTCACCCCGCTTCCACCGCGGAAACTGCAAGTTCCG	1500		
Db	1546	TCCATCAAGAAACAGCTTTCTGGGCTCACCCCGCTTCCACCGCGGAAACTGCAAGTTCCG	1605		
Qy	1501	ACGCCGAGGAGATGTCCAACCTGACACACAGAGTCTGTCCTCCAGAGCTGGCGAAGATCC	1560		
Db	1606	ACGCCGAGGAGATGTCCAACCTGACACACAGAGTCTGTCCTCCAGAGCTGGCGAAGATCC	1665		
Qy	1561	TGTTTGGGAACTTCTATCAGCTGGAGAGGAGGAGAGATCTTCTGCTGTCATCAAGAC	1620		
Db	1666	TGTTTGGGAACTTCTATCAGCTGGAGAGGAGGAGAGATCTTCTGCTGTCATCAAGAC	1725		
Qy	1621	AAACCTCTGAGCTCCATCAAGGCTGACATGCTGACGCGCTTCTGCTGATTTCCAGTCTC	1680		
Db	1726	AAACCTCTGAGCTCCATCAAGGCTGACATGCTGACGCGCTTCTGCTGATTTCCAGTCTC	1785		
Qy	1681	AGCCACAGCGTCTATCTCCAAACAGAGCTTCCGGGCGGAGTACAAAGGCCACGGGGGGCCA	1740		
Db	1786	AGCCACAGCGTCTATCTCCAAACAGAGCTTCCGGGCGGAGTACAAAGGCCACGGGGGGCCA	1845		
Qy	1741	GCGTGTTCAGAGACCGGTCAGTTCCAGTTGATATCACCTACACGGAGGGTGGGGAG	1800		
Db	1846	GCGTGTTCAGAGACCGGTCAGTTCCAGTTGATATCACCTACACGGAGGGTGGGGAG	1905		
Qy	1801	GCGCAGAGGAGAACGCGACTACTCTCCTCACCTTCACTCTCAGGCGGCGGCTCACG	1860		

Db	1906	CGCAGAAAGGAGAACGGCATCTACTCCGTACCTTCACTCCCTGTCTCAGGCCCAAGCCGT	1961
Qy	1861	CGCTTCAAGAGGGTGGTGAGAGACCATCCAGGCCCGAGCTGTGAGCACAACAGACCCGCGCT	1920
Db	1966	CGCTTCAAGAGGGTGGTGAGAGACCATCCAGGCCCGAGCTGTGAGCACAACAGACCCGCGCT	2025
Qy	1921	CGCGCCCGAGCACTTGTTCAGACACCACTTAATCTGTATGGAATATGATGAGCGGGCGGCTTTCC	1980
Db	2026	CGCGCCCGAGCACTTGTTCAGACACCACTTAATCTGTATGGAATATGATGAGCGGGCGGCTTTCC	2085
Qy	1981	AAATGTGGAATTATCCCGAAAGTTAA	2007
Db	2086	AAATGTGGAATTATCCCGAAAGTTAA	2112

RESULT 4

US-10-195-072-3

; Sequence 3, Application US/10195072

; Publication NO. US20030092036A1

; GENERAL INFORMATION:

; APPLICANT: Origene Technologies

; TITLE OF INVENTION: Full-Length Serine Protein Kinase in Brain and Pancreas

; FILE REFERENCE: 16U 101 C2

; CURRENT APPLICATION NUMBER: US/10/195,072

; CURRENT FILING DATE: 2002-07-15

; PRIOR APPLICATION NUMBER: US 09/930,181

; PRIOR FILING DATE: 2001-08-16

; NUMBER OF SEQ ID NOS: 18

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 3

; LENGTH: 3364

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (482)..(2239)

; OTHER INFORMATION:

US-10-195-072-3

Qy	1	ATGACATCGACGGGGAAGGACGGCGCGCAGCAGCGCAGTATGTTGGGCCCTACCCGG	60
Db	229	ATGACATCGACGGGGAAGGACGGCGCGCAGCAGCGCAGTATGTTGGGCCCTACCCGG	288
Qy	61	CTGGAGAGAGCGTGGCCAAAGGGGACAGACAGGTCTGTGAAGCTGGGGGTTCACTGGCTC	120
Db	289	CTGGAGAGAGCGTGGCCAAAGGGGACAGACAGGTCTGTGAAGCTGGGGGTTCACTGGCTC	348
Qy	121	ACCTGCCAGAAAGTGGCCATCAAGATCGTCAACCGTGAGAAGCTCAGCAGAGTCGGTGCTG	180
Db	349	ACTTGCCAGAAAGTGGCCATCAAGATCGTCAACCGTGAGAAGCTCAGCAGAGTCGGTGCTG	408
Qy	181	ATGAAGGTGGAGCGGGAGATCGCGATCCTTGAAGCTCAATTGAGCACCCCGCAGCTCTAAAG	240
Db	409	ATGAAGGTGGAGCGGGAGATCGCGATCCTTGAAGCTCAATTGAGCACCCCGCAGCTCTAAAG	468
Qy	241	CTGCACGACGTTTATGAAAAACAAAAATATTTTGTAGGTACCTGGTCTAGAACACAGTGC	296
Db	469	CTGCACGACGTTTATGAAAAACAAAAATATTTTGTAGGTACCTGGTCTAGAACACAGTGC	528
Qy	297	AGGTGGTGACCTCTTCGACTACCTGGTGAGAGGGGAGGCTGACGCGCTAAGGAGGCTCG	356
Db	529	AGGTGGTGACCTCTTCGACTACCTGGTGAGAGGGGAGGCTGACGCGCTAAGGAGGCTCG	588
Qy	357	GAAGTCTTCCGGCAGATCATCTCTGGCTGGACTCTCTGCGCAGAGCCATCCCATATGCCA	416
Db	589	GAAGTCTTCCGGCAGATCATCTCTGGCTGGACTCTCTGCGCAGAGCCATCCCATATGCCA	648
Qy	417	CAGGGATCTGAAACCTTGAAAACTCTCTGTGGACGAGAGAAACAACATCCGCATCCGAGA	476

Query Match 99.3%; Score 1993; DB 14; Length 3364;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 2007; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

Db	649	CAGGGATCTGAAACCTGAAACCTCTCTGTGGACGAGAAAGAAACAAACATCCGATCGCAGAG	708
Qy	477	CTTTTGGCATGGCGCTCCCTCTGCAGGTTCGGACACACCTGTTTGGAGACACAGCTGTGGGTCCCCC	536
Db	709	CTTTTGGCATGGCGCTCCCTCTGCAGGTTCGGACACACCTGTTTGGAGACACAGCTGTGGGTCCCCC	768
Qy	537	CCACTAGCGCTGCCCGAGAGGTGATCCGGGGGGAGAAAGTATGACGGCCGGGAAGCGCGACGT	596
Db	769	CCACTAGCGCTGCCCGAGAGGTGATCCGGGGGGAGAAAGTATGACGGCCGGGAAGCGCGACGT	828
Qy	597	GTGAGACTGGCGGCTCATCTCTGTTCCGCTTGTCTGTGGGGGCTCTGCCCTTCACAGCATGA	656
Db	829	GTGAGACTGGCGGCTCATCTCTGTTCCGCTTGTCTGTGGGGGCTCTGCCCTTCACAGCATGA	888
Qy	657	CAACTTTCGACACAGCTGTGTGAGAAAGTGAAGCGGGCGTGTTCACATGATCCGCGACATTTAT	716
Db	889	CAACTTTCGACACAGCTGTGTGAGAAAGTGAAGCGGGCGTGTTCACATGATCCGCGACATTTAT	948
Qy	717	CCGCGCCGACTGCCAGATCTGCTTACGGGGCATGATCGAGGTGGAGCGCCGCAACGCCGCCT	776
Db	949	CCGCGCCGACTGCCAGATCTGCTTACGGGGCATGATCGAGGTGGAGCGCCGCAACGCCGCCT	1008
Qy	777	CAGCTTAGAGCAATTCAGNAACACATATGTTATATAGGGGGCAAGATGAGCCCGAACCC	836
Db	1009	CAGCTTAGAGCAATTCAGNAACACATATGTTATATAGGGGGCAAGATGAGCCCGAACCC	1068
Qy	837	AGAGCAGCCCATTCCTCGCAAGGTGCAGATCCGCTCGCTGCCCCAGCGCTGGAGGACATCGA	896
Db	1069	AGAGCAGCCCATTCCTCGCAAGGTGCAGATCCGCTCGCTGCCCCAGCGCTGGAGGACATCGA	1128
Qy	897	CCCGCAGCTGCTGGACAGCATGCACTCACTTGGGCTGCTTCGAGACCGCAACAAAGCTGCT	956
Db	1129	CCCGCAGCTGCTGGACAGCATGCACTCACTTGGGCTGCTTCGAGACCGCAACAAAGCTGCT	1188
Qy	957	GCAGGACCTGCTGTCGAGGAGAGAGAACCAAGAGAGATGATTTACTTCTCTCTCTGGA	1016
Db	1189	GCAGGACCTGCTGTCGAGGAGAGAGAACCAAGAGAGATGATTTACTTCTCTCTCTGGA	1248
Qy	1017	CCGGAAGAAAGGTACCCGAGCCAGAGGATGAGGACTGCCCCCCCCGGAACAGAGATAGA	1076
Db	1249	CCGGAAGAAAGGTACCCGAGCCAGAGGATGAGGACTGCCCCCCCCGGAACAGAGATAGA	1308
Qy	1077	CCCTCCCGGAAGCGTGTGGACTCCCCCGATGTGAAACCGGACAGGAAGCGGGCCAGA	1136
Db	1309	CCCTCCCGGAAGCGTGTGGACTCCCCCGATGTGAAACCGGACAGGAAGCGGGCCAGA	1368
Qy	1137	ACGCAATCCATGGAGGTGCTCAGCTGTACGGACGGGCGGCTCCCCGGTGCTTCGCGGGC	1196
Db	1369	ACGCAATCCATGGAGGTGCTCAGCTGTACGGACGGGCGGCTCCCCGGTGCTTCGCGGGC	1428
Qy	1197	GGCCATTGATGGCCCGACAGCGGCCAGAGGTCTCGGTTCATCAGCGGTGCTTCCTCAGG	1256
Db	1429	GGCCATTGATGGCCCGACAGCGGCCAGAGGTCTCGGTTCATCAGCGGTGCTTCCTCAGG	1488
Qy	1257	CCTTTCCACAGCCCACTCAGCAGCCCCCGGGGTGACCCCTCACCCCTCACAAAGGGCAG	1316
Db	1489	CCTTTCCACAGCCCACTCAGCAGCCCCCGGGGTGACCCCTCACCCCTCACAAAGGGCAG	1548
Qy	1317	TCCCTTCCCAACCCCAAGGGGACACTGTGTCAACAGCCAAAGAGAGAGCCCGCTGGCAC	1376
Db	1549	TCCCTTCCCAACCCCAAGGGGACACTGTGTCAACAGCCAAAGAGAGAGCCCGCTGGCAC	1608
Qy	1377	GCCCAACCCCAACCCCGTTCAGCGCCCAAGCGTTCGAGGGGTGCTTCCTGGAGGGCGGGCT	1436
Db	1609	GCCCAACCCCAACCCCGTTCAGCGCCCAAGCGTTCGAGGGGTGCTTCCTGGAGGGCGGGCT	1668
Qy	1437	CAACTCCATCAAGAACAGCTTTCTGGGGCTCACCCCGCTTCCACCGCGGAAAACTGCAAGT	1496
Db	1669	CAACTCCATCAAGAACAGCTTTCTGGGGCTCACCCCGCTTCCACCGCGGAAAACTGCAAGT	1728
Qy	1497	TCCGACCGCGGAGGAGATGTCCAACTGTACACAGAGTGTGTCCCAAGAGCTGCGCAAGAA	1556
Db	1729	TCCGACCGCGGAGGAGATGTCCAACTGTACACAGAGTGTGTCCCAAGAGCTGCGCAAGAA	1788

1257	Qy	CTTTTCACAGCCCACTCAGACGCCACCCCGGGTGAACCCCTCACCCCTCACCAAGGGCAG	1311
1489	Db	CTTTTCACAGCCCACTCAGACGCCACCCCGGGTGAACCCCTCACCCCTCACCAAGGGCAG	1548
1317	Qy	TCCCTCCCAACCCCAAGGGGACCTGTTCACAGCCCAAGGAGAGCCCGCTGGCAC	1376
1549	Db	TCCCTCCCAACCCCAAGGGGACCTGTTCACAGCCCAAGGAGAGCCCGCTGGCAC	1608
1377	Qy	GCCCAACCCCAACCCCGCTCAGAGCCCAAGCTCGAGGGGTGCCCTGGAGGGCGCGGT	1436
1609	Db	GCCCAACCCCAACCCCGCTCAGAGCCCAAGCTCGAGGGGTGCCCTGGAGGGCGCGGT	1668
1437	Qy	CAACTCATCAAGAACAGCTTTCTGGCTCACCCCGCTTCCACCGCGGAAACTGCAAGT	1496
1669	Db	CAACTCATCAAGAACAGCTTTCTGGCTCACCCCGCTTCCACCGCGGAAACTGCAAGT	1728
1497	Qy	TCCGACGCGGAGGAGATGTCCAACTGACACAGAGTCTGCCAGAGCTGGCGAGAA	1556
1729	Db	TCCGACGCGGAGGAGATGTCCAACTGACACAGAGTCTGCCAGAGCTGGCGAGAA	1788
1557	Qy	GTCTCTGTTTGGGAACCTTCATCAGCCTGGAGAGGAGGACAGATCTTCGTGGTCAATCA	1616
1789	Db	GTCTCTGTTTGGGAACCTTCATCAGCCTGGAGAGGAGGACAGATCTTCGTGGTCAATCA	1848
1617	Qy	AGACAAACCTCTGAGCTCCATCAAGGCTGACATCGTGACCGCTTCGTGCAATCCCCAG	1676
1849	Db	AGACAAACCTCTGAGCTCCATCAAGGCTGACATCGTGACCGCTTCGTGCAATCCCCAG	1908
1677	Qy	TCTCAGCCACAGCGTCATCTCCCAACGAGCTTCCGGGCGGAGTACAGGCCACGGGGGG	1736
1909	Db	TCTCAGCCACAGCGTCATCTCCCAACGAGCTTCCGGGCGGAGTACAGGCCACGGGGGG	1968
1737	Qy	GCCAGCCGTGTTCCAGAGCCGCTCAAGTTCACAGTGTGATATCACTTACACGAGAGGTGG	1796
1969	Db	GCCAGCCGTGTTCCAGAGCCGCTCAAGTTCACAGTGTGATATCACTTACACGAGAGGTGG	2028
1797	Qy	GGAGGCGCAGAGAGAACGGCATCTACTCCGTCACTTCACCCCTGCTCTCAGGCCCCCAG	1856
2029	Db	GGAGGCGCAGAGAGAACGGCATCTACTCCGTCACTTCACCCCTGCTCTCAGGCCCCCAG	2088
1857	Qy	CCGTCCGCTTCAAGGGTGTGGAGACCATCCAGGCCACGCTGCTGAGCACACACACCC	1916
2089	Db	CCGTCCGCTTCAAGGGTGTGGAGACCATCCAGGCCACGCTGCTGAGCACACACACCC	2148
1917	Qy	GCCTGGGGCCAGCACTTGTTCAGACACCACTAACTGTATGAAATGATACGGGGCGGT	1976
2149	Db	GCCTGGGGCCAGCACTTGTTCAGACACCACTAACTGTATGAAATGATACGGGGCGGT	2208
1977	Qy	TTCCAAATGTGGAATTATCCGAAAAGTTAA	2007
2209	Db	TTCCAAATGTGGAATTATCCGAAAAGTTAA	2239

RESULT 6

US-10-288-798-42

; Sequence 42, Application US/10288798

Publication No. US20030207299A1

GENERAL INFORMATION:

; APPLICANT: BANDMAN, Olga NGUYEN, Damiel B ;
 ; APPLICANT: WALIA, Narinder K.; HAFALIA, April J.A.;
 ; APPLICANT: YAO, Monique G.; GANDHI, Ameena R.;
 ; APPLICANT: GURURAJAN, Rajagopal.; DING, Li;
 ; APPLICANT: PATTERSON, Chandra; YUE, Henry;
 ; APPLICANT: BAUGHN, Mariah R.; TRIBOULEY, Catherine M.;
 ; APPLICANT: THORNTON, Michael; ELLIOTT, Vicki S.;
 ; APPLICANT: LU, Yan; ISON, Craig H.;
 ; APPLICANT: AU-YOUNG, Janice; TANG, Y. Tom;
 ; APPLICANT: AZIMZAI, Yalda; BURRILL, John D.;
 ; APPLICANT: MARCUS, Gregory A.; ZINGLER, Kurt A.;
 ; APPLICANT: LU, Dying Aina M.; IAL, Preeti G.;
 ; APPLICANT: RAMKUMAR, Jayalaxmi; WARRIN, Bridget A.;
 ; APPLICANT: KEARNEY, Liam; POLICKY, Jennifer L.;
 ; APPLICANT: THANGAVELU, Kavitha; BURFORD, Neil

Db 570 CCGAAGCGGACGTGTGGAGCTGCGGCGTATCTCTGTTCGCTTGTGTGTGGGGCTCT 629
Qy 642 GCCCTTCGACGATGACAACTTTCGACAGCTGCTGGAGAAAGGTGAGCGGGGCGCTGTCCA 701
Db 630 GCCCTTCGACGATGACAACTTTCGACAGCTGCTGGAGAAAGGTGAGCGGGGCGCTGTCCA 699
Qy 702 CATGCCGACATTTATCCGCGCGGACTGCCAGAGTCTCTACGGGGCATGATCGAGGTGGA 761
Db 690 CATGCCGACATTTATCCGCGCGGACTGCCAGAGTCTCTACGGGGCATGATCGAGGTGGA 749
Qy 762 CGCGCAACGCGGCTCAGCTAGAGCAATTCAGAAACAATATGGTATATAGGGGCAA 821
Db 750 CGCGCAACGCGGCTCAGCTAGAGCAATTCAGAAACAATATGGTATATAGGGGCAA 809
Qy 822 GAATGAGCCGGAACGAGAGAGCCATTCCTCGCAAGGTGCAGATCCGCTCGTCCGAG 881
Db 810 GAATGAGCCGGAACGAGAGAGCCATTCCTCGCAAGGTGCAGATCCGCTCGTCCGAG 869
Qy 882 CTTGGAGGACATCGAACCCGAGCTGTGGAGCATGCACTCACTGGGCTGTTCGAG 941
Db 870 CTTGGAGGACATCGAACCCGAGCTGTGGAGCATGCACTCACTGGGCTGTTCGAG 929
Qy 942 CCGCAACAGCTGTGAGAGACTGTCTGTGAGGAGGAGAACGAGAGAGATGATTTA 1001
Db 930 CCGCAACAGCTGTGAGAGACTGTCTGTGAGGAGGAGAACGAGAGAGATGATTTA 989
Qy 1002 CTTCTCTCTCTGACCGGAAAGAGTACCCGAGCCAGAGGATGAGGACCTGCCCCC 1061
Db 990 CTTCTCTCTCTGACCGGAAAGAGTACCCGAGCCAGAGGATGAGGACCTGCCCCC 1049
Qy 1062 CCGAAGCAGATAGACCTCTCCCGAAGCGTGTGGACTCCCCGATGCTGAACCGGCACGG 1121
Db 1050 CCGAAGCAGATAGACCTCTCCCGAAGCGTGTGGACTCCCCGATGCTGAACCGGCACGG 1109
Qy 1122 CAAGCGGGCCAGAACGCAATTCATGGAGGTCTCAGCGTACGACCGCGCTCCCC 1181
Db 1110 CAAGCGGGCCAGAACGCAATTCATGGAGGTCTCAGCGTACGACCGCGCTCCCC 1169
Qy 1182 GGTGCTCTCGCGGGCGCATTTAGATGGCCAGCAGCGGCGAGAGTCTCGGTCCATCAG 1241
Db 1170 GGTGCTCTCGCGGGCGCATTTAGATGGCCAGCAGCGGCGAGAGTCTCGGTCCATCAG 1229
Qy 1242 CGGTGCTCTCTCAGGCTTTTCCACAGCCACTCAGCAGGCCCCGGGTGACCCCTCACCC 1301
Db 1230 CGGTGCTCTCTCAGGCTTTTCCACAGCCACTCAGCAGGCCCCGGGTGACCCCTCACCC 1289
Qy 1302 CTCACCAAGGGGAGTCCCTTCCCAACCCCAAGGGGACACTGTTCACACGCGCAAGGA 1361
Db 1290 CTCACCAAGGGGAGTCCCTTCCCAACCCCAAGGGGACACTGTTCACACGCGCAAGGA 1349
Qy 1362 GAGCCCGGCTGGCAGCGCCCAACCCCGCCGCTCCAGCCCGGAGGGGTGCC 1421
Db 1350 GAGCCCGGCTGGCAGCGCCCAACCCCGCCGCTCCAGCCCGGAGGGGTGCC 1409
Qy 1422 CTGAGGGGCGGCTCAACTCATCAAGAACAGCTTTCTGGGCTCACCCGCTTCCACCG 1481
Db 1410 CTGAGGGGCGGCTCAACTCATCAAGAACAGCTTTCTGGGCTCACCCGCTTCCACCG 1469
Qy 1482 CCGGAAACTGCAAGTTCCGACGCGGAGGAGATGTCCAACTGACACACAGAGTCTGCC 1541
Db 1470 CCGGAAACTGCAAGTTCCGACGCGGAGGAGATGTCCAACTGACACACAGAGTCTGCC 1529
Qy 1542 AGAGCTGGCAGAGTCTCTGTTTGGAACTTTCATCAGCTGGAGAGGAGGAGAGAT 1601
Db 1530 AGAGCTGGCAGAGTCTCTGTTTGGAACTTTCATCAGCTGGAGAGGAGGAGAGAT 1589
Qy 1602 CTTGTGTGTCATCAAGAACAACTCTGAGCTTCATCAAGGCTGACATCGTGCAGCCTT 1661
Db 1590 CTTGTGTGTCATCAAGAACAACTCTGAGTCTCATCAAGGCTGACATCGTGCAGCCTT 1649
Qy 1662 CTTGTGATTCCTCAGCTCAGCCAGCGTCTATCTCCCAAGAGCTTCCGGGCGGAGTA 1721
Db 1650 CTTGTGATTCCTCAGCTCAGCCAGCGTCTATCTCCCAAGAGCTTCCGGGCGGAGTA 1709

Qy 1722 CAAGCCACGGGGGCGCAGCGCTGTTCAGAACCGGTCAAGTTCCAGTTGATATCAC 1781
Db 1710 CAAGCCACGGGGGCGCAGCGCTGTTCAGAACCGGTCAAGTTCCAGTTGATATCAC 1769
Qy 1782 CTACACGGAGGTGGGGAGCGCAGAGGAGAACCGCATCTACTCCGTCACTTCAACCT 1841
Db 1770 CTACACGGAGGTGGGGAGCGCAGAGGAGAACCGCATCTACTCCGTCACTTCAACCT 1829
Qy 1842 GCTCTCAGGCCCCAGCGCTCGCTTCAAGAGGTGGTGGAGACATCCAGGCCAGCTGCT 1901
Db 1830 GCTCTCAGGCCCCAGCGCTCGCTTCAAGAGGTGGTGGAGACATCCAGGCCAGCTGCT 1889
Qy 1902 GAGCACACAGCACCGCCCTCGCGCCCGACACTTGTTCAGACACCACTAACTGTATGAAAT 1961
Db 1890 GAGCACACAGCACCGCCCTCGCGCCCGACACTTGTTCAGACACCACTAACTGTATGAAAT 1949
Qy 1962 GATGACGGGGCGCTTTCAAATGTGGAATATTCGGAAGTTAA 2007
Db 1950 GATGACGGGGCGCTTTCAAATGTGGAATATTCGGAAGTTAA 1995

RESULT 7

US-10-283-247-1

; Sequence 1, Application US/10283247

; Publication No. US20030119037A1

; GENERAL INFORMATION:

; APPLICANT: NEELAM, Beena et al.

; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

; FILE REFERENCE: CL001304

; CURRENT APPLICATION NUMBER: US/10/283,247

; CURRENT FILING DATE: 2002-10-30

; NUMBER OF SEQ ID NOS: 10

; SOFTWARE: fastseq for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 2025

; TYPE: DNA

; ORGANISM: Homo sapiens

; US-10-283-247-1

Query Match 96.7%; Score 1941.2; DB 14; Length 2025;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 1943; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ATGACATCGACGGGAGGACGGCGCGCAGCAGCGCGCAGTATGTTGGGCCCTACCGG 60
Db 1 ATGACATCGACGGGAGGAGGACGGCGCGCAGCAGCGCGCAGTATGTTGGGCCCTACCGG 60
Qy 61 CTGGAGAGACGCTGGGCAAGGGGCGCAGACAGGCTCTGGTGAAGCTGGGGGTTCACTGCGTC 120
Db 61 CTGGAGAGACGCTGGGCAAGGGGCGCAGACAGGCTCTGGTGAAGCTGGGGGTTCACTGCGTC 120
Qy 121 ACCTGCCAGAGTGGGCATCAAGATCGTCAACCGTGAAGCTCAGCGAGTGGTGGCTG 180
Db 121 ACCTGCCAGAGTGGGCATCAAGATCGTCAACCGTGAAGCTCAGCGAGTGGTGGCTG 180
Qy 181 ATGAAGTGGAGCGGAGATCGCGATCCTGAAGCTCATTGAGCACCCCGCAGCTCTAAAG 240
Db 181 ATGAAGTGGAGCGGAGATCGCGATCCTGAAGCTCATTGAGCACCCCGCAGCTCTAAAG 240
Qy 241 CTGCACGACCTTTATGAAAACAAAAATATTTGTACCTGGTGTAGAACACGTGTCAAGT 300
Db 241 CTGCACGACCTTTATGAAAACAAAAATATTTGTACCTGGTGTAGAACACGTGTCAAGT 300
Qy 301 GGTGAGCTCTTCAGTACCTGGTGAAGAGGAGGCTGACCGCTAAGAGGCTCGGAAG 360
Db 301 GGTGAGCTCTTCAGTACCTGGTGAAGAGGAGGCTGACCGCTAAGAGGCTCGGAAG 360
Qy 361 TTCTTCGGGAGATCATCTCTGGCTGGACTTCTGCCACAGCCACTTCATATGCCACAGG 420
Db 361 TTCTTCGGGAGATCATCTCTGGCTGGACTTCTGCCACAGCCACTTCATATGCCACAGG 420

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QY 421 GATCTGAAACCTGAAACCTCTCTCTGGAAGAGAAACAAATCCGCATCGCAGACTTT 480
Db 421 GATCTGAAACCTGAAACCTCTCTCTGGAAGAGAAACAAATCCGCATCGCAGACTTT 480
QY 481 GGCATGCGCTCCCTGCGAGCTTGGGACAGCTGTGAGACCAAGCTGTGGGTCCCCCAC 540
Db 481 GGCATGCGCTCCCTGCGAGCTTGGGACAGCTGTGAGACCAAGCTGTGGGTCCCCCAC 540
QY 541 TAGCCCTGCCCGAGGTGATCCCGGGGGAGAGATGACCGCGGAAAGCGGAGCTGTGG 600
Db 541 TAGCCCTGCCCGAGGTGATCCCGGGGGAGAGATGACCGCGGAAAGCGGAGCTGTGG 600
QY 601 AGCTGCGGCGTCATCTCTGTTCCGCTTCTGCTGGTGGGGCTCTGCCCTTCGACGATGACAAC 660
Db 601 AGCTGCGGCGTCATCTCTGTTCCGCTTCTGCTGGTGGGGCTCTGCCCTTCGACGATGACAAC 660
QY 661 TTGGCAGACGTCTGCGAGAGAGTGAAGCGGGGCTGTTCCACATGCGCGCACTTTATCCCG 720
Db 661 TTGGCAGACGTCTGCGAGAGAGTGAAGCGGGGCTGTTCCACATGCGCGCACTTTATCCCG 720
QY 721 CCCGACTGCCAGAGTCTGCTACCGGGGATGATCGAGGTGGAACGCGCAGCGCCTCACG 780
Db 721 CCCGACTGCCAGAGTCTGCTACCGGGGATGATCGAGGTGGAACGCGCAGCGCCTCACG 780
QY 781 CTAGAGCACATTGAGAAACACATATGTTATATAGGGGGGCAAGATGAGCCGCAACAGAG 840
Db 781 CTAGAGCACATTGAGAAACACATATGTTATATAGGGGGGCAAGATGAGCCGCAACAGAG 840
QY 841 CAGCCCATCTCTCGAAGGTGCAGATCGCTCGCTGCCAGCTTGGAGGACATCGACCCC 900
Db 841 CAGCCCATCTCTCGAAGGTGCAGATCGCTCGCTGCCAGCTTGGAGGACATCGACCCC 900
QY 901 GACGTGTGGACACGATGCACTCACTGGGTGCTTCCGAGACCGCAACAGCTGCTGAG 960
Db 901 GACGTGTGGACACGATGCACTCACTGGGTGCTTCCGAGACCGCAACAGCTGCTGAG 960
QY 961 GACCTGTGTCGAGGAGGAGAAACAGAGAGATGATTTACTTCCTCTCTCTGGACCGG 1020
Db 961 GACCTGTGTCGAGGAGGAGAAACAGAGAGATGATTTACTTCCTCTCTCTGGACCGG 1020
QY 1021 AAAGAAAGGTACCCGAGCAGAGGATGAGACCTGCCCCCGGAAACGAGATAGACCTT 1080
Db 1021 AAAGAAAGGTACCCGAGCAGAGGATGAGACCTGCCCCCGGAAACGAGATAGACCTT 1080
QY 1081 CCCCGAAGCGTGTGGAATCTCCCGATGCTGAACCGGCAACGCGCGGCGCCAGAACGC 1140
Db 1081 CCCCGAAGCGTGTGGAATCTCCCGATGCTGAACCGGCAACGCGCGGCGCCAGAACGC 1140
QY 1141 AAATCCATGGAGGTGCTCAGCGTGACGAGCGGCGGCTCCCCGGTGCCTGCGCGCGGGCC 1200
Db 1141 AAATCCATGGAGGTGCTCAGCGTGACGAGCGGCGGCTCCCCGGTGCCTGCGCGCGGGCC 1200
QY 1201 ATTGAGATGGCCAGCAGCGGAGAGGTCTCGGTCCATCAGCGGTGCTCTCTCAGGCTT 1260
Db 1201 ATTGAGATGGCCAGCAGCGGAGAGGTCTCGGTCCATCAGCGGTGCTCTCTCAGGCTT 1260
QY 1261 TCCACCGACCCACTCAGCAGCCCCCGGTGACCCCTCAGCCCTCAACAAAGGGGAGTCCC 1320
Db 1261 TCCACCGACCCACTCAGCAGCCCCCGGTGACCCCTCAGCCCTCAACAAAGGGGAGTCCC 1320
QY 1321 CTCCCGACCCCGAGGGACACCTGTCCACAGCGCAAGAGAGCCCGGTGGACGCGCC 1380
Db 1321 CTCCCGACCCCGAGGGACACCTGTCCACAGCGCAAGAGAGCCCGGTGGACGCGCC 1380
QY 1381 AACCCCAACGCCCCGTCCAGCGCCAGCGTGGAGGGGTGCCCTGAGGGCGCGCTCAAC 1440
Db 1381 AACCCCAACGCCCCGTCCAGCGCCAGCGTGGAGGGGTGCCCTGAGGGCGCGCTCAAC 1440
QY 1441 TCCATCAAGAACAGCTTTCTGGGCTCAACCGGCTTCCACCGCGGAAACTGCAAGTTCCG 1500
Db 1441 TCCATCAAGAACAGCTTTCTGGGCTCAACCGGCTTCCACCGCGGAAACTGCAAGTTCCG 1500
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QY 1501 AGCCCGGAGAGATGTCCAACTGACACACAGAGTCTCTCCCGAGAGCTGGGAAAGATGCC 1560
Db 1501 AGCCCGGAGAGATGTCCAACTGACACACAGAGTCTCTCCCGAGAGCTGGGAAAGATGCC 1560
QY 1561 TGGTTTGGGAACCTTCATCAGCCTTGGAGAGGAGGACAGATCTTCTGTGTCATCAAGAC 1620
Db 1561 TGGTTTGGGAACCTTCATCAGCCTTGGAGAGGAGGAGCAGATCTTCTGTGTCATCAAGAC 1620
QY 1621 AAACCTCTCAGCTCCATCAAGGCTGACATCGTGACCGCTTCTCTCGATTTCCAGTCTC 1680
Db 1621 AAACCTCTCAGCTCCATCAAGGCTGACATCGTGACCGCTTCTCTCGATTTCCAGTCTC 1680
QY 1681 AGCCACAGCTCATCTCCCAAACGAGCTTCCGGGCGGAGTACAGGCCACGGGGGGCCCA 1740
Db 1681 AGCCACAGCTCATCTCCCAAACGAGCTTCCGGGCGGAGTACAGGCCACGGGGGGCCCA 1740
QY 1741 GCGGTGTTCCAGAGCGCGTCAAGTTCAGAGTTGATATCACTTACACCTTCTCAGGCCCGT 1800
Db 1741 GCGGTGTTCCAGAGCGCGTCAAGTTCAGAGTTGATATCACTTACACCTTCTCAGGCCCGT 1800
QY 1801 GCGCAGAGGAGAACCGCATCTACTCCGTCACTTCCAGCTTCTCAGGCCCGGAGCGT 1860
Db 1801 GCGCAGAGGAGAACCGCATCTACTCCGTCACTTCCAGCTTCTCAGGCCCGGAGCGT 1860
QY 1861 CGCTTCAAGAGGGTGTGGAGACCATCCAGGCCAGCTGCTGAGGACACACAGCCGCT 1920
Db 1861 CGCTTCAAGAGGGTGTGGAGACCATCCAGGCCAGCTGCTGAGGACACACAGCCGCT 1920
QY 1921 GCGGCCCGAGCACTTGTGAGACACAC 1946
Db 1921 GCGGCCCGAGCACTTGTGAGACACAC 1946
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RESULT 8

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US-09-842-582-3
; Sequence 3, Application US/09842582
; Patent No. US20020155570A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Meyers, Rachel
; TITLE OF INVENTION: 2246, NOVEL PROTEIN KINASE MOLECULES AND
; FILE OF INVENTION: USES THEREFOR
; FILE REFERENCE: 38155-20054.00
; CURRENT APPLICATION NUMBER: US/09/842,582
; CURRENT FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 60/199,391
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2025
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-842-582-3
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Query Match 96.8%; Score 1939.6; DB 10; Length 2025;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1942; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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QY 1 ATGACATCGACGGGGAAGGACGCGCGGCGGAGACAGAGTCTGTTGAAGCTGGGGGTTCATCTCGTC 60
Db 1 ATGACATCGACGGGGAAGGACGCGCGGCGGAGACAGAGTCTGTTGAAGCTGGGGGTTCATCTCGTC 60
QY 61 CTGGAGAAGACGCTGGGGCAAGGGGCGAGACAGAGTCTGTTGAAGCTGGGGGTTCATCTCGTC 120
Db 61 CTGGAGAAGACGCTGGGGCAAGGGGCGAGACAGAGTCTGTTGAAGCTGGGGGTTCATCTCGTC 120
QY 121 ACCTGCGAGAGGTGGCCATCAAGATCGTCAACCGTGAGAGCTCAGCGAGTGGTCTG 180
Db 121 ACCTGCGAGAGGTGGCCATCAAGATCGTCAACCGTGAGAGCTCAGCGAGTGGTCTG 180
QY 181 ATGAAGTGGAGCGGAGAGATCGGATCCCTGAAGCTCATTTGAGCACCCCGCTCTAAAG 240
Db 181 ATGAAGTGGAGCGGAGAGATCGGATCCCTGAAGCTCATTTGAGCACCCCGCTCTAAAG 240
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	Matches	1942;	Conservative	0;	Mismatches	4;	Indels	0;	Gaps	0;
QY	1	ATGACATCGACGGGGAAGGACGGCGCGCAGCACGCGCAGTATGTTGGGCCCTACCGG	60							
Db	53	ATGACATCGACGGGGAAGGACGGCGCGCAGTATGTTGGGCCCTACCGG	112							
QY	61	CTGGAGAACGCTGGGCAAGGGGCAGACAGGTCTGGTGAAGCTGGGGTTCACTCGCTC	120							
Db	113	CTGGAGAACGCTGGGCAAGGGGCAGACAGGTCTGGTGAAGCTGGGGTTCACTCGCTC	172							
QY	121	ACCTGCCAGAAAGTGGCCATCAAGATCGTCAAACCGTGAGAAAGCTCAGCAGAGTCGGTGCTG	180							
Db	173	ACCTGCCAGAAAGTGGCCATCAAGATCGTCAAACCGTGAGAAAGCTCAGCAGAGTCGGTGCTG	232							
QY	181	ATGAAGGTGAGCGGGAGATCGCGATCTCTGAAGCTCAATTGAGCACCCCAACGCTCTAAAG	240							
Db	233	ATGAAGGTGAGCGGGAGATCGCGATCTCTGAAGCTCAATTGAGCACCCCAACGCTCTAAAG	292							
QY	241	CTGCACGAGTTTATGAAAAAATAATTTTGTACTGTGTGTAGNACAGGTGTCAAGT	300							
Db	293	CTGCACGAGTTTATGAAAAAATAATTTTGTACTGTGTGTAGNACAGGTGTCAAGT	352							
QY	301	GGTGAGCTCTTGACATACCTTGTTGAAGAGGGAGGCTGACGCTTAAGGAGGCTCGGAAG	360							
Db	353	GGTGAGCTCTTGACATACCTTGTTGAAGAGGGAGGCTGACGCTTAAGGAGGCTCGGAAG	412							
QY	361	TTCTTCCGGCAGATCATCTCTGGCGTGGACTTTCTGCCACAGCCACTCCATATGCCACAGG	420							
Db	413	TTCTTCCGGCAGATCATCTCTGGCGTGGACTTTCTGCCACAGCCACTCCATATGCCACAGG	472							
QY	421	GATCTGAAACCTGAAACCTCTCTGTGTGGACGAGAGAAACAATCCGCATCGCAGACTTT	480							
Db	473	GATCTGAAACCTGAAACCTCTCTGTGTGGACGAGAGAAACAATCCGCATCGCAGACTTT	532							
QY	481	GGCATGCGCTCCCTGCAAGTTGGCGACAGCCTGTTGGAGACCAAGCTGTGGTCCCCCCAC	540							
Db	533	GGCATGCGCTCCCTGCAAGTTGGCGACAGCCTGTTGGAGACCAAGCTGTGGTCCCCCCAC	592							
QY	541	TACGCCTGCCCCGAGGTGATCCGGGGGGAGAAAGTATGACGGCCGGAGGCGGACGTGTGG	600							
Db	593	TACGCCTGCCCCGAGGTGATCCGGGGGGAGAAAGTATGACGGCCGGAGGCGGACGTGTGG	652							
QY	601	AGCTGCGGCGTATCTGTTGCGCTTCTGGTGGGGGCTCTGCCCTTCGACGATGACAAC	660							
Db	653	AGCTGCGGCGTATCTGTTGCGCTTCTGGTGGGGGCTCTGCCCTTCGACGATGACAAC	712							
QY	661	TTGCGACAGCTGCTGGAGAAAGGTGAAGCGGGGCGTGTCCACATGCCGCACTTTATCCCG	720							
Db	713	TTGCGACAGCTGCTGGAGAAAGGTGAAGCGGGGCGTGTTCACATGCCGCACTTTATCCCG	772							
QY	721	CCGACCTGCCAGAGTCTGCTACGGGGGATGATCGAGGTGACGCCGCGACGCGCTCACG	780							
Db	773	CCGACCTGCCAGAGTCTGCTACGGGGGATGATCGAGGTGACGCCGCGACGCGCTCACG	832							
QY	781	CTAGACACATTCAGAAACAATATGTTATATAGGGGGCAAGAAATAGGCCGCAACACAGAG	840							
Db	833	CTAGACACATTCAGAAACAATATGTTATATAGGGGGCAAGAAATAGGCCGCAACACAGAG	892							
QY	841	CAGCCCATCTCTGCAAGGTGCAGATCGCTGCTGCCAGCTTCGAGGACATCGACCCC	900							
Db	893	CAGCCCATCTCTGCAAGGTGCAGATCGCTGCTGCCAGCTTCGAGGACATCGACCCC	952							
QY	901	GACGTGCTGACACATGCACTCACTGGGCTGCTTCGAGACCCCAACAGTCTCTCGAG	960							
Db	953	GACGTGCTGACACATGCACTCACTGGGCTGCTTCGAGACCCCAACAGTCTCTCGAG	1012							
QY	961	GACCTGCTGTCGAGGAGGAAACGAGGAAAGATGATTTACTTCTCTCTCTGACCGG	1020							
Db	1013	GACCTGCTGTCGAGGAGGAAACGAGGAAAGATGATTTACTTCTCTCTCTGACCGG	1072							
QY	1021	AAAGAAAGGTATCCGACGACGAGGAGATGAGACCTGCCCCCCCCCGAACGAGATAGACCT	1080							
Db	1073	AAAGAAAGGTATCCGACGACGAGGAGATGAGACCTGCCCCCCCCCGAACGAGATAGACCT	1132							

;; PRIOR APPLICATION NUMBER: US 60/263,378
;; PRIOR FILING DATE: 2001-01-23
;; NUMBER OF SEQ ID NOS: 4
;; SOFTWARE: fastseq for Windows Version 4.0
;; SEQ ID NO 3
;; LENGTH: 1827
;; TYPE: DNA
;; ORGANISM: homo sapiens
US-10-054-579-3

Query Match 91.0%; Score 1827; DB 13; Length 1827;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1827; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 181 ATGAAGTGGAGCGGGAGATCGCATCTCTGAAGCTCATTTAGAGACCCCGCTCTAAAG 240
Db 1 ATGAAGTGGAGCGGGAGATCGCATCTCTGAAGCTCATTTAGAGACCCCGCTCTAAAG 60

Qy 241 CTGACGACGTTTATGAAACAAAAATATTTGTACCTGTGTAGAACACGTTGTCAGGT 300
Db 61 CTGACGACGTTTATGAAACAAAAATATTTGTACCTGTGTAGAACACGTTGTCAGGT 120

Qy 301 GGTGAGCTCTTCGACTACCTGCTGAAGAAGGGAGGCTGACGCTTAAGGAGGCTCGGAAG 360
Db 121 GGTGAGCTCTTCGACTACCTGCTGAAGAAGGGAGGCTGACGCTTAAGGAGGCTCGGAAG 180

Qy 361 TTCTTCGGCGAGATCATCTCTGCGCTGGACTTCTGCCACAGCCACTCCATATGCCACAGG 420
Db 181 TTCTTCGGCGAGATCATCTCTGCGCTGGACTTCTGCCACAGCCACTCCATATGCCACAGG 240

Qy 421 GATCTGAACCTGAAACCTCTCTGTCGACGAGAACAAACATCCGCATCGCAGACTTT 480
Db 241 GATCTGAACCTGAAACCTCTCTGTCGACGAGAACAAACATCCGCATCGCAGACTTT 300

Qy 481 GGCATGGCTCCCTGCAAGTTGGCGACAGCTGTTGAGACACAGCTGTGGTCCCCCAG 540
Db 301 GGCATGGCTCCCTGCAAGTTGGCGACAGCTGTTGAGACACAGCTGTGGTCCCCCAG 360

Qy 541 TACGCTGCCCGGAGGTGATCGGGGGGAGAGATGATGACGCGCGGAGGCGGAGTGG 600
Db 361 TACGCTGCCCGGAGGTGATCGGGGGGAGAGATGATGACGCGCGGAGGCGGAGTGG 420

Qy 601 AGCTGGCGGCTCATCTGTTGCTGCTGCTGGTGGGGCTCTGCCCTTCGACGATGACAC 660
Db 421 AGCTGGCGGCTCATCTGTTGCTGCTGCTGGTGGGGCTCTGCCCTTCGACGATGACAC 480

Qy 661 TTGCGACAGCTGCTGGAGAGGTGAGCGGGCGTGTTCACATGCCGCACTTTATCCCG 720
Db 481 TTGCGACAGCTGCTGGAGAGGTGAGCGGGCGTGTTCACATGCCGCACTTTATCCCG 540

Qy 721 CCCGACTGCCAGAGTCTGCTACGGGGCATGATCGAGGTGGACGCGCAGCGCGCTCACG 780
Db 541 CCCGACTGCCAGAGTCTGCTACGGGGCATGATCGAGGTGGACGCGCAGCGCGCTCACG 600

Qy 781 CTAGAGCACATTCAGAACACATATGTTATATAGGGGCGAGATGAGCCGACACGAG 840
Db 601 CTAGAGCACATTCAGAACACATATGTTATATAGGGGCGAGATGAGCCGACACGAG 660

Qy 841 CAGCCCATTCCTCGCAAGGTGAGATCGCTCGCTGCGCCAGCCTGGAGGACATCGACCCC 900
Db 661 CAGCCCATTCCTCGCAAGGTGAGATCGCTCGCTGCGCCAGCCTGGAGGACATCGACCCC 720

Qy 901 GAGTGTGGACAGCATGCACTCATGCGGCTGCTTCGAGACCGGACCAAGCTGCTGAG 960
Db 721 GAGTGTGGACAGCATGCACTCATGCGGCTGCTTCGAGACCGGACCAAGCTGCTGAG 780

Qy 961 GACCTGCTCGGAGGAGAACACGAGAGATGATTTACTTCTCTCTCGACCGG 1020
Db 781 GACCTGCTCGGAGGAGAACACGAGAGATGATTTACTTCTCTCTCTCGACCGG 840

Qy 1021 AAAGAAAGGTACCCGAGCAGGAGATGAGGACCTGCGCCCCCGGACGAGATAGACCT 1080
Db 841 AAAGAAAGGTACCCGAGCAGGAGATGAGGACCTGCGCCCCCGGACGAGATAGACCT 900

RESULT 11
US-10-283-247-4
; Sequence 4, Application US/10283247
; Publication No. US20030119037A1
; GENERAL INFORMATION:
; APPLICANT: NEELAM, Beena et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

Qy 1081 CCCGGAAGCGTGTGGACTCTCCCGATGCTGAAACCGGACGCGGCGCGGCGGCGG 1140
Db 901 CCCGGAAGCGTGTGGACTCTCCCGATGCTGAAACCGGACGCGGCGCGGCGGCGGCGG 960

Qy 1141 AAATCATGGAGTGTCTAGCGTGAAGACGCGGCGGCTCCCGGCTGCTGCGGCGGCGG 1200
Db 961 AAATCATGGAGTGTCTAGCGTGAAGACGCGGCGGCTCCCGGCTGCTGCGGCGGCGGCGG 1020

Qy 1201 ATTGAGATGGCCAGCAGCGGCGGAGGCTCTCGGTCCATCAGCGGCTGCTCTCAGGCTTT 1260
Db 1021 ATTGAGATGGCCAGCAGCGGCGGAGGCTCTCGGTCCATCAGCGGCTGCTCTCAGGCTTT 1080

Qy 1261 TCCACAGCCCACTCAGCAGACCCCGGCTGACCCCTCACCCCTCACAAAGGCGAGTCCC 1320
Db 1081 TCCACAGCCCACTCAGCAGACCCCGGCTGACCCCTCACCCCTCACAAAGGCGAGTCCC 1140

Qy 1321 CTCGCCACCCCAAGGGGACACTCTGTCACACGCGCAAGGAGGAGCCGCTGCGACGCC 1380
Db 1141 CTCGCCACCCCAAGGGGACACTCTGTCACACGCGCAAGGAGGAGCCGCTGCGACGCC 1200

Qy 1381 AACCCCAACCCCGCTCCAGCGCTCGGAGGGGTGCCCTGGAGGCGGCGGTCAAC 1440
Db 1201 AACCCCAACCCCGCTCCAGCGCTCGGAGGGGTGCCCTGGAGGCGGCGGTCAAC 1260

Qy 1441 TCCATCAAGAAACAGCTTTCTGGGCTACCCCGCTTCCACCGCGGAAACTGCAAGTTCCG 1500
Db 1261 TCCATCAAGAAACAGCTTTCTGGGCTACCCCGCTTCCACCGCGGAAACTGCAAGTTCCG 1320

Qy 1501 AGCGGAGGAGATGTCGAACCTGACACAGAGTCTGTCGCCAGAGCTGCGGAGGAGTCC 1560
Db 1321 AGCGGAGGAGATGTCGAACCTGACACAGAGTCTGTCGCCAGAGCTGCGGAGGAGTCC 1380

Qy 1561 TGGTTTGGGAACTTCATCAGCCTGGAGAGGAGGAGCAGATCTTCGTGTCTCATCAAGAC 1620
Db 1381 TGGTTTGGGAACTTCATCAGCCTGGAGAGGAGGAGCAGATCTTCGTGTCTCATCAAGAC 1440

Qy 1621 AAACCTCTGAGCTCCATCAAGGCTGACGCTGACGCGCTTCTGTCGATTCAGTCTC 1680
Db 1441 AAACCTCTGAGCTCCATCAAGGCTGACGCTGACGCGCTTCTGTCGATTCAGTCTC 1500

Qy 1681 AGCCACAGCTCATCTCCCAACGAGCTTCCCGGCGGAGTACAAGGCCACGCGGGGCCA 1740
Db 1501 AGCCACAGCTCATCTCCCAACGAGCTTCCCGGCGGAGTACAAGGCCACGCGGGGCCA 1560

Qy 1741 GCGGTCTTCCAGAGCGGCTCAAGTTCCAGGTTGATATCACCTACACGAGGTTGGGAG 1800
Db 1561 GCGGTCTTCCAGAGCGGCTCAAGTTCCAGGTTGATATCACCTACACGAGGTTGGGAG 1620

Qy 1801 GCGCAGAGGAGAACGGGATCTACTCCGTCACTTCACTTCACTTCACTTCACTTCACTT 1860
Db 1621 GCGCAGAGGAGAACGGGATCTACTCCGTCACTTCACTTCACTTCACTTCACTTCACTT 1680

Qy 1861 CGCTTCAAGAGGTTGGTGGAGACCATCCAGGCGGAGTCTGTCGAGCACACACGCGGCT 1920
Db 1681 CGCTTCAAGAGGTTGGTGGAGACCATCCAGGCGGAGTCTGTCGAGCACACACGCGGCT 1740

Qy 1921 GCGGCGGAGCAGCTTGTGAGACACCACTAACTGTATGAAATGATACGCGGCGGCTTTCC 1980
Db 1741 GCGGCGGAGCAGCTTGTGAGACACCACTAACTGTATGAAATGATACGCGGCGGCTTTCC 1800

Qy 1981 AAATGTGGAATATCCGAAAGTTAA 2007
Db 1801 AAATGTGGAATATCCGAAAGTTAA 1827

; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE OF INVENTION: THERBOF
; FILE REFERENCE: CL001304
; CURRENT APPLICATION NUMBER: US/10/283,247
; CURRENT FILING DATE: 2002-10-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1911
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-283-247-4

Query Match 84.0%; Score 1685.2; DB 14; Length 1911;
Best Local Similarity 96.2%; Pred. No. 0;
Matches 1763; Conservative 0; Mismatches 3; Indels 66; Gaps 1;

QY	181	ATGAAGGTGGAGCGGAGATCCGATCTCTGAAGCTCATATGAGCACCCCAAGTCTCTAAAG	240
DB	1	ATGAAGGTGGAGCGGAGATCCGATCTCTGAAGCTCATATGAGCACCCCAAGTCTCTAAAG	60
QY	241	CTGCACGAGCTTTATGAACAAAATAATTTGTACCTGGTCTAGAACAGTGTACAGT	300
DB	61	CTGCACGAGCTTTATGAACAAAATAATTTGTACCTGGTCTAGAACAGTGTACAGT	120
QY	301	GGTGAGCTCTTCGACTACCTCGTGTGAAGAGGGAGGCTGACGCCCTAAGAGGCTCGGAAG	360
DB	121	GGTGAGCTCTTCGACTACCTCGTGTGAAGAGGGAGGCTGACGCCCTAAGAGGCTCGGAAG	180
QY	361	TTCTCCCGCAGATCATCTCGCTGACATTTCTGCGACAGCACTCCATATGCCACAGG	420
DB	181	TTCTCCCGCAGATCATCTCGCTGACATTTCTGCGACAGCACTCCATATGCCACAGG	240
QY	421	GATCTGAACCTGAAACCTCTGCTGACGAGAGAGAACATCCGATCGCAGACTTT	480
DB	241	GATCTGAACCTGAAACCTCTGCTGACGAGAGAGAACATCCGATCGCAGACTTT	300
QY	481	GGCATGGCTCCCTCGAGTTTGGCAGACAGCTTTGGAGACAGCTGTGGGTCCCCCAC	540
DB	301	GGCATGGCTCCCTCGAGTTTGGCAGACAGCTTTGGAGACAGCTGTGGGTCCCCCAC	360
QY	541	TTAGCGCTGCCGAGGTGATCCGGGGGAGAGATGACGGCGGAGAGCGGAGCGGTGG	600
DB	361	TACGGCTTGCCCGAGGTGATCCGGGGGAGAGATGACGGCGGAGAGCGGAGCGGTGG	420
QY	601	AGCTCGGGGTCACTCTGTTCCCTTGTCTGTTGGGGGCTCTGCCCTTCGAGATGACAA	660
DB	421	AGCTCGGGGTCACTCTGTTCCCTTGTCTGTTGGGGGCTCTGCCCTTCGAGATGACAA	480
QY	661	TTTGACAGCTCTGCGAGAGGTGAAGCGGGCGGTGTTCCATGCGCGCACTTTATCCCG	720
DB	481	TTTGACAGCTCTGCGAGAGGTGAAGCGGGCGGTGTTCCATGCGCGCACTTTATCCCG	540
QY	721	CCCGATGCGCAGAGTCTGCTACGGGGCATGATCGAGGTGAGACCGCGCATCGCCCTCAG	780
DB	541	CCCGATGCGCAGAGTCTGCTACGGGGCATGATCGAGGTGAGACCGCGCATCGCCCTCAG	600
QY	781	CTAGAGCACATTCAGAACACATATGTTATAGGGGCGAAGATGAGCCCGAACAGAG	840
DB	601	CTAGAGCACATTCAGAACACATATGTTATAGGGGCGAAGATGAGCCCGAACAGAG	660
QY	841	CAGCCCATTCCTCGCAAGGTGAGATCCGCTCGCTGCCCGAGCTCGAGGACATCGACCCC	900
DB	661	CAGCCCATTCCTCGCAAGGTGAGATCCGCTCGCTGCCCGAGCTCGAGGACATCGACCCC	720
QY	901	GACGTGTGAGACAGATGACATCTGAGGTCTCTTCGAGACCGCAACAAGTGTGAG	960
DB	721	GACGTGTGAGACAGATGACATCTGAGGTCTCTTCGAGACCGCAACAAGTGTGAG	780
QY	961	GACCTGCTGTCGAGGAGAGAACAGAGAGATGATTTACTTCTCTCTCTGACCGG	1020
DB	781	GACCTGCTGTCGAGGAGAGAACAGAGAGATGATTTACTTCTCTCTCTGACCGG	840

RESULT 12

US-10-116-326-1
; Sequence 1, Application US/10116326
; Publication No. US2003016689A1

QY	1021	AAAGAAAGGTACCGAGCCAGGAGGATGAGACCTGCTCCCGCCGGAACGAGATAGACCT	1080
DB	841	AAAGAAAGGTACCGAGCCAGGAGGATGAGACCTGCTCCCGCCGGAACGAGATAGACCT	900
QY	1081	CCCGGAAGCGTGTGAGATCTCCCGATGCTGAACCGGCAACGGCAAGCGCGGCGCAAGACG	1140
DB	901	CCCGGAAGCGTGTGAGATCTCCCGATGCTGAACCGGCAACGGCAAGCGCGGCGCAAGACG	960
QY	1141	AAATCCATGAGGTGCTCAGCGTACCGAGCGGGCTCCCGGTGCTCGCGCGCGGGCC	1200
DB	961	AAATCCATGAGGTGCTCAGCGTACCGAGCGGGCTCCCGGTGCTCGCGCGCGGGCC	1020
QY	1201	ATTGAGATGGCCACGACGCGCCAG-----	1224
DB	1021	ATTGAGATGGCCACGACGCGCCAGAGTAAAGCAATGTTAGTAAAGCCTGGATATCGCT	1080
QY	1225	-----AGTCTCGTTCATCAGCGGTGCTCTCTCA	1254
DB	1081	GAGCCCATCCCAATTCAGCAAGAAAGACAGAGTCTCGTCCATCAGCGGTGCTCTCTCA	1140
QY	1255	GGCTTTTCCACCGCCCACTCAGCAGCCCGCGGTGACCTCACCCTCACCAGGGGC	1314
DB	1141	GGCTTTTCCACCGCCCACTCAGCAGCCCGCGGTGACCTCACCCTCACCAGGGGC	1200
QY	1315	AGTCCCTCCCGACCCCAAGGGGACACCTGTCCACACGCGCAAGAGAGAGCCCGCTGGC	1374
DB	1201	AGTCCCTCCCGACCCCAAGGGGACACCTGTCCACACGCGCAAGAGAGAGCCCGCTGGC	1260
QY	1375	ACGCCAAACCGCAGCCCGCTCAGCCCGCGGTGAGGGGTGCTTGGAGGGCGCGG	1434
DB	1261	ACGCCAAACCGCAGCCCGCTCAGCCCGCGGTGAGGGGTGCTTGGAGGGCGCGG	1320
QY	1435	CTCAACTCCATCAAGAAACAGCTTTCTGGGTTCACCCCGCTTCCACCGCGGAAACTCAA	1494
DB	1321	CTCAACTCCATCAAGAAACAGCTTTCTGGGTTCACCCCGCTTCCACCGCGGAAACTCAA	1380
QY	1495	GTTCCGACGCGGAGGAGATGTCCAACTGACACAGAGTGTCTCCAGAGCTGGCGAAG	1554
DB	1381	GTTCCGACGCGGAGGAGATGTCCAACTGACACAGAGTGTCTCCAGAGCTGGCGAAG	1440
QY	1555	AGTCTCGTGTGGAACTTCATCAGCTGAGAGGAGAGAGAGATCTTCTGTTGTCATC	1614
DB	1441	AGTCTCGTGTGGAACTTCATCAGCTGAGAGGAGAGAGATCTTCTGTTGTCATC	1500
QY	1615	AAAGCAAAACCTCTGAGCTCCATCAAGCGTGAACATGTCGACAGCTTCTCTCGATTCCC	1674
DB	1501	AAAGCAAAACCTCTGAGCTCCATCAAGCGTGAACATGTCGACAGCTTCTCTCGATTCCC	1560
QY	1675	AGTCTCAGCCACAGCGTCACTCTCCAAACGAGCTTCCGGGCGGAGTACAAGGCCACGGGG	1734
DB	1561	AGTCTCAGCCACAGCGTCACTCTCCAAACGAGCTTCCGGGCGGAGTACAAGGCCACGGGG	1620
QY	1735	GGGCGAGCGTGTTCAGAGACCGGTCAAGTTCAGGTTGATATACCTACACGAGGGGT	1794
DB	1621	GGGCGAGCGTGTTCAGAGACCGGTCAAGTTCAGGTTGATATACCTACACGAGGGGT	1680
QY	1795	GGGAGCGCAGAGAGAGAACCGCATCTCTCGTCACTTCCCTGCTCTCAGGGCCC	1854
DB	1681	GGGAGCGCAGAGAGAGAACCGCATCTCTCGTCACTTCCCTGCTCTCAGGGCCC	1740
QY	1855	AGCGTCTCGCTTCAAGAGGGTGTGAGACCATCCAGGCCCGAGCTGTGAGCACACGAC	1914
DB	1741	AGCGTCTCGCTTCAAGAGGGTGTGAGACCATCCAGGCCCGAGCTGTGAGCACACGAC	1800
QY	1915	CCGCTCGGGCCAGCACTTGTTCAGACACAC	1946
DB	1801	CCGCTCGGGCCAGCACTTGTTCAGAAACCCCC	1832

GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Brian
; APPLICANT: Friddle, Carl Johan
; TITLE OF INVENTION: No. US2003016689A1el Human Kinases and Polynucleotides Encoding
; FILE REFERENCE: LEX-0332-USA
; CURRENT APPLICATION NUMBER: US/10/116,326
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,036
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2337
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-116-326-1

Query Match 48.1%; Score 965; DB 12; Length 2337;
Best Local Similarity 70.0%; Pred. No. 3.1e-251;
Matches 1484; Conservative 0; Mismatches 440; Indels 195; Gaps 6;
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Db 74 CCCAGCAGCGCCAAATATGTTGGGCCCTATCGGCTGGAGAGACGCTGGGCGAGAGAGAGAG 133
Qy 89 CAGGTCTGTGAAGTGGGGGTTCACCTGCGTCACTGCCAGAGGTGGCCATCAAGATCG 148
Db 134 CAGGCTGTGAAGTGGGGGTTCACCTGCGTCACTGCCAGAGGTGGCCATCAAGATCG 193
Qy 149 TCAACCGGTGAGAAGTCAAGCAGTGGTGTGATGAAGGTGGAGCGGAGATCCGATCC 208
Db 194 TGAACCGGGAGAGAGTGTCCGAGTGGTGTGATGAAGGTGGAGCGGAGATCCGATCC 253
Qy 209 TGAAGCTATTTGAGCAGCCCAAGCTTCAAGCTGACAGAGCTTTATGAAGCAAAAT 268
Db 254 TGAAGCTATCGAAGCAGCCCAAGCTTCAAGCTGACAGAGCTTTATGAAGCAAAAT 313
Qy 269 ATTTGACTGTGTAGAACACGTGTGAGTGTGAGTCTTCAAGCTTACCTGAGTGAAGA 328
Db 314 ATTTGACTGTGTGAGAACACGTGTGAGTGTGAGTCTTCAAGCTTACCTGAGTGAAGA 373
Qy 329 AGGGAGGCTGACCGCTTAAGAGGCTCGGAAGTTCTTCCGAGAGATCATCTCTGCGTGG 388
Db 374 AGGGAGGCTGACCGCTTAAGAGGCTCGGAAGTTCTTCCGAGAGATCATCTCTGCGTGG 433
Qy 389 ACTTCTGCCAGCAGCTTCCATATGACAGAGGATCTGAAGCTTGAAGCTTGAAGCTTGG 448
Db 434 ACTTCTGCCAGCAGCTTCCATATGACAGAGGATCTGAAGCTTGAAGCTTGAAGCTTGG 493
Qy 449 ACGAAGAAACAACTCCGATCGCAGACTTTGGCATGGCGTCCCTGAGGTGGCGACA 508
Db 494 ATGAGAAACAACTCCGATCGCAGACTTTGGCATGGCGTCCCTGAGGTGGCGACA 553
Qy 509 GCCTTTGGAGACAGCTGTGGTTCCTCCCACTACGCTTGGCGGAGGTGATTCGGGGGG 568
Db 554 GCCTTTGGAGACAGCTGTGGTTCCTCCCACTACGCTTGGCGGAGGTGATTCGGGGGG 613
Qy 569 AGAAGTATGACGGCGGAGGAGGCTGTGGAGCTGGGGCTCATCTGTTCGCTTGC 628
Db 614 AAAAATAATGATGGCGCGGAGAGATGTGGAGCTGTGGAGCTCATCTGTTCGCTTGC 673
Qy 629 TGGTGGGGCTGTGCTTCCAGCATGACAACTTCCGACAGCTGTGGAGAGGTGAAGC 688
Db 674 TCGTGGGGCTGTGCTTCCAGCATGACAACTTCCGACAGCTGTGGAGAGGTGAAGC 733
Qy 689 GGGGCGGTTCACATGCGCACTTTATCCCGCCGACCTGCGCAGAGTCTGTACGGGGCA 748
Db 734 GGGGCGGTTCACATGCGCACTTTATCCCGCCGACCTGCGCAGAGTCTGTACGGGGCA 793
Qy 749 TGATCGAGGTGACGCGGAGGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCA 808
Db 794 TGATCGAGGTGACGCGGAGGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCA 853

Qy 809 ATATAGGGGGCAAGATGAGTCCGCAACC-----AGAGCAGCCCATTCCTCGAAGGTCC 862
Db 854 ACTAGGGGGGAAACACAGCCAGAGCCGCTGGAGCAGCCCTGCGCCCGGGGTAG 913
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Db 914 CCATGCGAGCCTGCCATCAACGGAGAGCTGGACCCCGACGCTCTTAGAGAGATGGCAT 973
Qy 923 CACTGGGCTGCTTCCGAGACCGCAACAGCTCTGCAGGACCTGTCTCCGAGGAGGAGA 982
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Qy 983 ACCAGGAGAGATGATTTACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1042
Db 1034 ACCAAGAAAGATATATATATCTGCTTTTGGATCGGAAGGAGCGGTATCCAGCTGTG 1093
Qy 1043 AGATGAGACCTGCCCCCGGAAACGAGATAGACCTCTCCCGGAAAGCTGTGGATCC 1102
Db 1094 AGGACGAGACCTGCT 1153
Qy 1103 CGATGCTGAACCGGACCGCAACGCGGCGCCAGAACGCAATCCATGGAGGTCTCTCAGCG 1162
Db 1154 CCATGCTGAGCCCTCACGGAAAGCGGACCGAGCGGAAGTCCATGGAAGTCTCTGAGCA 1213
Qy 1163 TGAC-----GGACGGCGGCTCTCCCGGTGCTTCCGCGGGCGGCAATTGAGATGGCCC 1213
Db 1214 TCACCGATGCGGGGGTGGTGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1273
Qy 1214 AGCAGGCGAGAGTCTGGTCCATCAGCGGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1273
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Qy 1274 TCAGCAGCCCCCGGT-----ACCCCAAGGGGACACCTGTCTCCACAGCGCAA 1357
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Db 1514 CCCCAGCTCCCGCGCTCTCTGCGGGGACCCCTTGTCACTCGCTCTGCAACGCGCCC 1573
Qy 1358 AGGAGAGCCCGGTGGCAGCCCAACCCCGAGCGCCCGCTCCAGCCCC-----AGCGTCG 1411
Db 1574 GGGCCAGTCCACCGGAGCCCGGGGACAAACACACCCCGAGCGCGCGGTGGCGTCG 1633
Qy 1412 GAGGGTGGCTGGAGGCGGGCTCAACTCCATCAAGACAGCTTCTGGGCTCACCCC 1471
Db 1634 GGGGAGCGCTGGAGGAGTCTCAACTCCATCCGCAACAGCTTCTGGGCTCCCTC 1693
Qy 1472 GCTTCCACCCCGGAAACTGCAAGTTCGAGCGCGGAGGAGATGTCCAACTGACACAG 1531
Db 1694 GCTTTCACCGGCGCAGATGAGTCCCTACCGCTGAGGAGATGTCCAGCTTGGCGCAG 1753
Qy 1532 AGTGTCTCCAGAGCTGGCGAAGAGTCTCTGTTTGGAACTTTCATCAGCGCTGGAGAGG 1591
Db 1754 AGTCTCTCCCGAGCTGGCAAAACGCTCTCTGTTTGGGAACTTTCATCTCTTGGACAAAG 1813
Qy 1592 AGGAGCAGATCTTCTGTTGTCATCAAGACAAACCTCTGAGCTCCATCAAGGCTGACATCG 1651
Db 1814 AAGAACAAATATTTCTCTGCTTAAAGGACAAACCTCTCAGCAGCATCAAGAGCAGATCG 1873
Qy 1652 TGACAGCTTCTCTGCTGATTTCCAGTCTCAGCAGCAGCGTCTCTCCCAACAGAGCTTCC 1711
Db 1874 TCCATGCTTCTGCTGATCTCCAGGCTCTGAGTCTCAGTGTCTGCTCAGACAGCTTCA 1933


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Db      |||||
QY 837 --AGAGAGCCATTCCTCGAAGGTGCAGATCGCTCGCTGCCAGCCTCGAGGACATC 894
Db      |||||
QY 661 CTGAGCCAGCCCTGGCGCGGTAGCCATCGGAGCCTGCCATCCAAAGGAGAGCTG 720
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QY 895 GACCCGACGTGTGAGACAGATGACATCACTGGGCTGCTTCGAGAGCCGCAACAAAGCTG 954
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QY 721 GACCCGACGTCTAGAGAGCATGATCATCACTGGGCTGCTTCAGGAGCCGCGAGAGGCTG 780
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QY 955 CTGAGGACCTGCTCTCGAGAGAGAGAACAGGAGAGATGATTTACTTCTCTCTCTG 1014
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QY 1015 GACCGAAAGAAAGTATCCCGAGCCAGGAGATGAGGACCTGCCCGCCGGAACGAGATA 1074
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QY 841 GATCGAAGAGCGGTATCCCAAGCTGTGAGAACAGGACCTGCCCGCGAATGATGTT 900
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QY 1075 GACCTTCCCGAAGCGTGTGACATCCCGATGCTGTAACCGGACGCGCAAGCGCGGCA 1134
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QY 901 GACCCCGCGGAGCGTGTGATTTCTCCATGCTGAGCGCTCACGGGAAGCGGACCA 960
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QY 1135 GNACGCAATCCATGAGGTGCTCAGCGTGACGGA-----CGGCGGTCCCGGTG 1185
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QY 961 GAGCGGAAGTCCATGGAAGTCTGAGCATCACGATGCCGGGGTGTGGCTCCCTCTGTA 1020
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QY 1303 TCACCAAGGGGAGTCCCTCTCCCT-----ACC 1329
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QY 1261 AGTGCCCGTCCACACCCCTGCGCGCCCCCAGGCTCCCGCGCTCCTCTGGGGGACC 1320
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QY 1624 CTTGAGCTCCATCAAGGCTGACATCGTGACGCTTCTCTGTGATTTCCAGTCTCAGC 1683
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RESULT 15

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US-10-116-326-3
; Sequence 3, Application US/10116326
; Publication No. US20030166889A1
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Brian
; APPLICANT: Fiddle, Carl Johan
; TITLE OF INVENTION: No. US20030166889A1 Human Kinases and Polynucleotides Encoding t
; FILE REFERENCE: LEX-0332-USA
; CURRENT APPLICATION NUMBER: US/10/116,326
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,036
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2289
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-116-326-3
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Query Match 38.7%; Score 777.2; DB 12; Length 2289;

Best Local Similarity 67.9%; Pred. No. 2.5e-200;

Matches 1277; Conservative 0; Mismatches 408; Indels 195; Gaps 6;

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Db      |||||
QY 325 AAGGGAGAGTGAAGCCCAAGGAGGCGCGAAAGTTCTTCGCCAGATTGTGTCTGCGCTG 384
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QY 388 GACTTCTGCCACAGCACTCCATATGCCACAGGATCTGAACCTGAAACCTCTCTGCTG 447
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QY 385 GACTTCTGCCACAGCACTCCATCTGCCACAGACCTTAAAGCCCGAGAACCTGCTTTTG 444
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QY 568 GAGAGATATGACGCCGGAAGGCGGAGCTGTGGAGCTGCGGCTCATCTGTTGCGCTTG 627
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QY 628 CTGCTGGGGGCTGCGCTTTCGACGATGACAACTTTCGACAGCTGCTGGAGAGGTGAAG 687
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QY 625 CTGCTGGGGGCTCTGCGCTTTGATGACGACAACTCTCGCAGAGCTGCTGGAGAGGTGAAA 684
Db      |||||
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 26, 2003, 12:01:57 ; Search time 28.2696 Seconds
(without alignments)
4358.326 Million cell updates/sec

Title: US-10-054-579-2

Perfect score: 3497

Sequence: 1 MTSTGKGGAHAQYGVPR.....TNCMMMTGRLSKGIIPKS 668

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 673684 seqs, 184443283 residues

Total number of hits satisfying chosen parameters: 673684

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

- Database : Published Applications AA:*
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 - 2: /cgn2_6/ptodata/2/pubpaa/FCT_NEW_PUB.pep.*
 - 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
 - 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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 - 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
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 - 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
 - 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
 - 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
 - 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
 - 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
 - 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3497	100.0	668	14	US-10-054-579-2
2	3497	100.0	668	15	US-10-195-072-2
3	3497	100.0	668	15	US-10-195-071-2
4	3423	97.9	664	12	US-10-288-798-18
5	3380	96.7	674	15	US-10-283-247-2
6	3374	96.5	674	10	US-09-842-582-2
7	3374	96.5	674	15	US-10-283-247-7
8	3374	96.5	674	15	US-10-283-247-8
9	3368	91.2	608	14	US-10-054-579-4
10	3065	87.6	614	15	US-10-283-247-9
11	3065	87.6	614	15	US-10-283-247-10
12	3050	87.2	636	15	US-10-283-247-5
13	3028	86.6	585	15	US-10-195-072-4
14	3028	86.6	585	15	US-10-195-071-4
15	3015	86.2	603	15	US-10-195-072-17

16	3015	86.2	603	15	US-10-195-071-17	Sequence 17, Appl
17	2799	80.0	778	12	US-10-354-358-92	Sequence 92, Appl
18	2799	80.0	778	12	US-10-116-326-2	Sequence 2, Appl
19	2545.5	72.8	703	12	US-10-116-326-6	Sequence 6, Appl
20	2386.5	68.2	762	12	US-10-116-326-4	Sequence 4, Appl
21	796.5	22.8	745	12	US-10-161-565-24	Sequence 24, Appl
22	796.5	22.8	745	15	US-10-195-101-36	Sequence 36, Appl
23	794.5	22.7	691	10	US-09-919-585-6	Sequence 6, Appl
24	794.5	22.7	724	10	US-09-919-585-9	Sequence 9, Appl
25	790.5	22.6	722	8	US-08-817-8328-32	Sequence 32, Appl
26	790	22.6	1518	10	US-09-801-368-152	Sequence 152, App
27	781	22.3	744	10	US-09-835-081-4	Sequence 4, Appl
28	779.5	22.3	752	10	US-09-835-081-2	Sequence 2, Appl
29	778.5	22.3	688	12	US-10-161-565-28	Sequence 28, Appl
30	778.5	22.3	688	12	US-10-161-565-29	Sequence 29, Appl
31	777.5	22.2	795	10	US-09-919-585-12	Sequence 12, Appl
32	777.5	22.2	795	12	US-10-161-565-25	Sequence 25, Appl
33	777.5	22.2	795	15	US-10-142-356-9	Sequence 9, Appl
34	771.5	22.1	783	9	US-09-815-915-2	Sequence 2, Appl
35	771.5	22.1	783	12	US-10-393-316-2	Sequence 7, Appl
36	769	22.0	1369	12	US-10-288-798-7	Sequence 26, Appl
37	768.5	22.0	729	12	US-10-161-565-26	Sequence 11, Appl
38	768.5	22.0	729	15	US-10-142-356-11	Sequence 33, Appl
39	768.5	22.0	729	15	US-10-195-101-33	Sequence 90, Appl
40	765.5	21.9	783	11	US-09-823-187-90	Sequence 32, Appl
41	764.5	21.9	793	15	US-10-195-101-32	Sequence 3, Appl
42	762.5	21.8	744	10	US-09-919-585-3	Sequence 91, Appl
43	759.5	21.7	713	12	US-10-161-565-27	Sequence 27, Appl
44	754	21.6	786	11	US-09-823-187-91	Sequence 92, Appl
45	749	21.4	776	11	US-09-823-187-92	

ALIGNMENTS

RESULT 1

US-10-054-579-2
; Sequence 2, Application US/10054579
; Publication No. US20020137913A1
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Brian
; TITLE OF INVENTION: No. US20020137913A1el Human Kinases and Polynucleotides Encoding t
; FILE REFERENCE: LEX-0300-USA
; CURRENT APPLICATION NUMBER: US/10/054,579
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/263,378
; PRIOR FILING DATE: 2001-01-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 668
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-054-579-2

Query Match	100.0%;	Score 3497;	DB 14;	Length 668;
Best Local Similarity	100.0%;	Pred. No. 2.8e-218;		
Matches	668;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
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Db	1	MTSTGKGGAHAQYGVPRLEKTLGQGLVKGHVCTCQKVAIKIVNREKLSVVL	60	
Qy	61	MKVERETAILKLIHHPVHLKLDVYENKYLVLVLEHVSGGELFDYLVKKGLTPKEARK	120	
Db	61	MKVERETAILKLIHHPVHLKLDVYENKYLVLVLEHVSGGELFDYLVKKGLTPKEARK	120	
Qy	121	FFRQIISALDFCHSHSICHRDLKPELNLLDEKKNIRIADFGMASIQVGDLSLETSCGSPH	180	
Db	121	FFRQIISALDFCHSHSICHRDLKPELNLLDEKKNIRIADFGMASIQVGDLSLETSCGSPH	180	
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Db 181 YACPEVIRGEKYDGRKADWVSCGVILFALLVGLPFDNDNLRQLLEKVRGVFHMHPFIP 240
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Db 241 PDCOSLARGMEVDAARLTLEHIQKHIWYIGGKNEPEPEQIPRKVQIIRSLPSLEIDIP 300
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Qy 361 PRKRVDSFMLNRHGKRRPERKSMELSVTDGGSVPARRAIEMAHQQRSRISGASSGL 420
Db 361 PRKRVDSFMLNRHGKRRPERKSMELSVTDGGSVPARRAIEMAHQQRSRISGASSGL 420
Qy 421 STSPLSSPRVTPHPSPRGSPPLTPKGTVPHTPKESPAGTNPPTPSSPSVGGVPMWRLN 480
Db 421 STSPLSSPRVTPHPSPRGSPPLTPKGTVPHTPKESPAGTNPPTPSSPSVGGVPMWRLN 480
Qy 481 SIKNSFLGSPRFRHRRKLQVPTPEMSNLTPSSPELAKKSWFGNFIISLEKEEQIFVVIKD 540
Db 481 SIKNSFLGSPRFRHRRKLQVPTPEMSNLTPSSPELAKKSWFGNFIISLEKEEQIFVVIKD 540
Qy 541 KPLSSIKADIIVHAFSLPSLSHVSISQTSFRAEYKATGGPAVFOKPVKFQVDITYTEGGE 600
Db 541 KPLSSIKADIIVHAFSLPSLSHVSISQTSFRAEYKATGGPAVFOKPVKFQVDITYTEGGE 600
Qy 601 AQKENGIVSYVFTLLSGSPRRFRKRVVETIOAQLLSTHDPAAQHLSDTTNCMENMTGRLS 660
Db 601 AQKENGIVSYVFTLLSGSPRRFRKRVVETIOAQLLSTHDPAAQHLSDTTNCMENMTGRLS 660
Qy 661 KCGIIPKS 668
Db 661 KCGIIPKS 668

RESULT 2
US-10-195-072-2
; Sequence 2, Application US/10195072
; Publication No. US20030092036A1
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies
; TITLE OF INVENTION: Full-Length Serine Protein Kinase in Brain and Pancreas
; FILE REFERENCE: 16U 101 C2
; CURRENT APPLICATION NUMBER: US/10/195,072
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: US 09/930,181
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2
; LENGTH: 668
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-195-072-2

Query Match 100.0%; Score 3497; DB 15; Length 668;
Best Local Similarity 100.0%; Pred. No. 2.8e-218;
Matches 668; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MTSTGKGGGAHQAYVGPYRLEKTLGKGTGLVKGVHCVTCQKVAIKIVNREKLSSEVL 60
Db 1 MTSTGKGGGAHQAYVGPYRLEKTLGKGTGLVKGVHCVTCQKVAIKIVNREKLSSEVL 60
Qy 61 MKVEREIALKLEIHPHVLKLDVYENKLYLVLEHVS GGELFDYLVKKGRLTPKEARK 120
Db 61 MKVEREIALKLEIHPHVLKLDVYENKLYLVLEHVS GGELFDYLVKKGRLTPKEARK 120
Qy 121 FFRQIISALDFCHSHSICHRLDKPENLLDEKNNIRIADFGWASIQVGDLSLETSCGSPH 180
Db 121 FFRQIISALDFCHSHSICHRLDKPENLLDEKNNIRIADFGWASIQVGDLSLETSCGSPH 180
Qy 181 YACPEVIRGEKYDGRKADWVSCGVILFALLVGLPFDNDNLRQLLEKVRGVFHMHPFIP 240

Db 181 YACPEVIRGEKYDGRKADWVSCGVILFALLVGLPFDNDNLRQLLEKVRGVFHMHPFIP 240
Qy 241 PDCOSLARGMEVDAARLTLEHIQKHIWYIGGKNEPEPEQIPRKVQIIRSLPSLEIDIP 300
Db 241 PDCOSLARGMEVDAARLTLEHIQKHIWYIGGKNEPEPEQIPRKVQIIRSLPSLEIDIP 300
Qy 301 DVLDSMHSGLGCFDRNRKLLQDLSSEENQEKMIYFLLLDKERYPSQDEDELPNRNEIDP 360
Db 301 DVLDSMHSGLGCFDRNRKLLQDLSSEENQEKMIYFLLLDKERYPSQDEDELPNRNEIDP 360
Qy 361 PRKRVDSFMLNRHGKRRPERKSMELSVTDGGSVPARRAIEMAHQQRSRISGASSGL 420
Db 361 PRKRVDSFMLNRHGKRRPERKSMELSVTDGGSVPARRAIEMAHQQRSRISGASSGL 420
Qy 421 STSPLSSPRVTPHPSPRGSPPLTPKGTVPHTPKESPAGTNPPTPSSPSVGGVPMWRLN 480
Db 421 STSPLSSPRVTPHPSPRGSPPLTPKGTVPHTPKESPAGTNPPTPSSPSVGGVPMWRLN 480
Qy 481 SIKNSFLGSPRFRHRRKLQVPTPEMSNLTPSSPELAKKSWFGNFIISLEKEEQIFVVIKD 540
Db 481 SIKNSFLGSPRFRHRRKLQVPTPEMSNLTPSSPELAKKSWFGNFIISLEKEEQIFVVIKD 540
Qy 541 KPLSSIKADIIVHAFSLPSLSHVSISQTSFRAEYKATGGPAVFOKPVKFQVDITYTEGGE 600
Db 541 KPLSSIKADIIVHAFSLPSLSHVSISQTSFRAEYKATGGPAVFOKPVKFQVDITYTEGGE 600
Qy 601 AQKENGIVSYVFTLLSGSPRRFRKRVVETIOAQLLSTHDPAAQHLSDTTNCMENMTGRLS 660
Db 601 AQKENGIVSYVFTLLSGSPRRFRKRVVETIOAQLLSTHDPAAQHLSDTTNCMENMTGRLS 660
Qy 661 KCGIIPKS 668
Db 661 KCGIIPKS 668

RESULT 3
US-10-195-071-2
; Sequence 2, Application US/10195071
; Publication No. US20030096271A1
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies
; TITLE OF INVENTION: Full-Length Serine Protein Kinase in Brain and Pancreas
; FILE REFERENCE: 16U 101 C1
; CURRENT APPLICATION NUMBER: US/10/195,071
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: US 09/930,181
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2
; LENGTH: 668
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-195-071-2

Query Match 100.0%; Score 3497; DB 15; Length 668;
Best Local Similarity 100.0%; Pred. No. 2.8e-218;
Matches 668; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MTSTGKGGGAHQAYVGPYRLEKTLGKGTGLVKGVHCVTCQKVAIKIVNREKLSSEVL 60
Db 1 MTSTGKGGGAHQAYVGPYRLEKTLGKGTGLVKGVHCVTCQKVAIKIVNREKLSSEVL 60
Qy 61 MKVEREIALKLEIHPHVLKLDVYENKLYLVLEHVS GGELFDYLVKKGRLTPKEARK 120
Db 61 MKVEREIALKLEIHPHVLKLDVYENKLYLVLEHVS GGELFDYLVKKGRLTPKEARK 120
Qy 121 FFRQIISALDFCHSHSICHRLDKPENLLDEKNNIRIADFGWASIQVGDLSLETSCGSPH 180
Db 121 FFRQIISALDFCHSHSICHRLDKPENLLDEKNNIRIADFGWASIQVGDLSLETSCGSPH 180
Qy 181 YACPEVIRGEKYDGRKADWVSCGVILFALLVGLPFDNDNLRQLLEKVRGVFHMHPFIP 240

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Db 181 YACPEVIREKDGKADVWSCGVILFALLVGLPDDNNLQLEKVKRGVFMHPHIP 240
QY 241 PDCQSLRGMIYDAARLTLEHIQKHIWYIGGKNEPEQIPRKVQIRSLPSLEDIDP 300
Db 241 PDCQSLRGMIYDAARLTLEHIQKHIWYIGGKNEPEQIPRKVQIRSLPSLEDIDP 300
QY 301 DVLDSHSLGCFRDRNKLQDLSSEENQEKMIYFLLDRKERYPSQDEDELPPENEIDP 360
Db 301 DVLDSHSLGCFRDRNKLQDLSSEENQEKMIYFLLDRKERYPSQDEDELPPENEIDP 360
QY 361 PRKRVDSPLNLRHGRKRPRKNEVLSVTDGSPVPARRAIEMAHQGRSISGASSGL 420
Db 361 PRKRVDSPLNLRHGRKRPRKNEVLSVTDGSPVPARRAIEMAHQGRSISGASSGL 420
QY 421 STSPSSPRVTHPSRPGSPLPTPKGTVPHTPKESPAGTNPPTPSSPSVGGVPMRRLN 480
Db 421 STSPSSPRVTHPSRPGSPLPTPKGTVPHTPKESPAGTNPPTPSSPSVGGVPMRRLN 480
QY 481 SIKNSFLGSPRHRRLQVPTPEMSNLTPSSPELAKKSWFNGFISLEKEQIFVVIKD 540
Db 481 SIKNSFLGSPRHRRLQVPTPEMSNLTPSSPELAKKSWFNGFISLEKEQIFVVIKD 540
QY 541 KPLSSIKADIVAFISIPLSHVSISQTSFRAEYKATGPAVFPKPVKFQVDITVTEGGE 600
Db 541 KPLSSIKADIVAFISIPLSHVSISQTSFRAEYKATGPAVFPKPVKFQVDITVTEGGE 600
QY 601 AQKENGIVSVTFLSGSPRRKRVRVETIQALLSTHDPAAQHLSDTTNCMEMTGRLS 660
Db 601 AQKENGIVSVTFLSGSPRRKRVRVETIQALLSTHDPAAQHLSDTTNCMEMTGRLS 660
QY 661 KCGIIPKS 668
Db 661 KCGIIPKS 668
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RESULT 4

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US-10-288-798-18
; Sequence 18, Application US/10288798
; Publication No. US20030207299A1
; GENERAL INFORMATION:
; APPLICANT: BANDMAN, Olga; NGUYEN, Danniell B.;
; APPLICANT: WALIA, Narinder K.; HAFALIA, April J.A.;
; APPLICANT: YAO, Monique G.; GANDHI, Ameena R.;
; APPLICANT: GURURAJAN, Rajagopal; DING, Li;
; APPLICANT: PATTERSON, Chandra; YUE, Henry;
; APPLICANT: BAUGHN, Mariah R.; TRIBOULEY, Catherine M.;
; APPLICANT: THORNTON, Michael; ELLIOTT, Vicki S.;
; APPLICANT: LU, Yan; ISON, Craig H.;
; APPLICANT: AU-YOUNG, Janice; TANG, Y. Tom;
; APPLICANT: AZIMZAI, Yalda; BURRILL, John D.;
; APPLICANT: MARCUS, Gregory A.; ZINGLER, Kurt A.;
; APPLICANT: LU, Dying Aina M.; LAL, Preeti G.;
; APPLICANT: RAMKUMAR, Jayalaxmi; WARREN, Bridget A.;
; APPLICANT: KEARNEY, Liam; POLICKY, Jennifer L.;
; APPLICANT: THANGAVELU, Kavitha; BURFORD, Neil
; TITLE OF INVENTION: HUMAN KINASES
; FILE REFERENCE: PI-0209 USA
; CURRENT APPLICATION NUMBER: US/10/288,798
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: PCT/US01/27219
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/240,542
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: US 60/238,389
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 60/236,499
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 60/234,902
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US 60/232,654
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US 60/231,357
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; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: US 60/229,873
; PRIOR FILING DATE: 2000-08-31
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PERL Program
; SEQ ID NO 18
; LENGTH: 664
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030207299A1 4022651CD1
US-10-288-798-18
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Query Match 97.9%; Score 3423; DB 12; Length 664;
Beat Local Similarity 100.0%; Pred. No. 1.7e-213;
Matches 654; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 15 YVGPVRLKTLGKGTGLVGLVHCVTCQKVAIKIVNREKLSVLMKVEREIALKLE 74
Db 11 YVGPVRLKTLGKGTGLVGLVHCVTCQKVAIKIVNREKLSVLMKVEREIALKLE 70
QY 75 HPHVLKLDVYENKYLVLVLEHVSGBELFDYLVKKGRLTPKEARKFFRQIISALDFCHS 134
Db 71 HPHVLKLDVYENKYLVLVLEHVSGBELFDYLVKKGRLTPKEARKFFRQIISALDFCHS 130
QY 135 HSIHRDLKPNLLDEKNIRIADFGWASIQVGSLSLETSCGSPHYACPEVIRGEKYDG 194
Db 131 HSIHRDLKPNLLDEKNIRIADFGWASIQVGSLSLETSCGSPHYACPEVIRGEKYDG 190
QY 195 RKADVMSCGVILFALLVGLPDDNNLQLEKVKRGVFMHPHIPPPCOSLLRGMIEVD 254
Db 191 RKADVMSCGVILFALLVGLPDDNNLQLEKVKRGVFMHPHIPPPCOSLLRGMIEVD 250
QY 255 AARLTLEHIQKHIWYIGGKNEPEQIPRKVQIRSLPSLEDIDPVDLDSHSLGCFRD 314
Db 251 AARLTLEHIQKHIWYIGGKNEPEQIPRKVQIRSLPSLEDIDPVDLDSHSLGCFRD 310
QY 315 RNKLQDLSSEENQEKMIYFLLDRKERYPSQDEDELPPENEIDPPKRVDSPMLNRHG 374
Db 311 RNKLQDLSSEENQEKMIYFLLDRKERYPSQDEDELPPENEIDPPKRVDSPMLNRHG 370
QY 375 KRRPERKSMEVLSVTDGSPVPARRAIEMAHQGRSISGASSGLSTSPSSPRVTHP 434
Db 371 KRRPERKSMEVLSVTDGSPVPARRAIEMAHQGRSISGASSGLSTSPSSPRVTHP 430
QY 435 SPRGSPLPTPKGTVPHTPKESPAGTNPPTPSSPSVGGVPMRRLNLSIKNSFLGSPRHR 494
Db 431 SPRGSPLPTPKGTVPHTPKESPAGTNPPTPSSPSVGGVPMRRLNLSIKNSFLGSPRHR 490
QY 495 RKLQVPTPEMSNLTPSSPELAKKSWFNGFISLEKEQIFVVIKDKPLSSIKADIVHAF 554
Db 491 RKLQVPTPEMSNLTPSSPELAKKSWFNGFISLEKEQIFVVIKDKPLSSIKADIVHAF 550
QY 555 LSIPSLSHSVISQTSFRAEYKATGPAVFPKPVKFQVDITVTEGGAOKENGIVSVTFL 614
Db 551 LSIPSLSHSVISQTSFRAEYKATGPAVFPKPVKFQVDITVTEGGAOKENGIVSVTFL 610
QY 615 LSGPSRRFRKRVVETIQALLSTHDPAAQHLSDTTNCMEMTGRLSKCGIIPKS 668
Db 611 LSGPSRRFRKRVVETIQALLSTHDPAAQHLSDTTNCMEMTGRLSKCGIIPKS 664
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RESULT 5

```
US-10-283-247-2
; Sequence 2, Application US/10283247
; Publication No. US20030119037A1
; GENERAL INFORMATION:
; APPLICANT: NEELAM, Beena et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001304
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; CURRENT APPLICATION NUMBER: US/10/283,247
; CURRENT FILING DATE: 2002-10-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 674
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-842-582-2

Query Match 96.7%; Score 3380; DB 15; Length 674;
Best Local Similarity 99.8%; Pred. No. 1.1e-210;
Matches 646; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MTSTGKGGAQAQYVGPYRLEKTLGKGTGLVKGVCVTCQKVAIKIVNREKLSV 60
Db 1 MTSTGKGGAQAQYVGPYRLEKTLGKGTGLVKGVCVTCQKVAIKIVNREKLSV 60
Qy 61 MKVEREIAILKLIIEHPHVLKLDVYENKKYLYLVLEHVS GGELFDYLVKGR LTPKEARK 120
Db 61 MKVEREIAILKLIIEHPHVLKLDVYENKKYLYLVLEHVS GGELFDYLVKGR LTPKEARK 120
Qy 121 FFRQIISALDFCHSHSICHRLKPNLLDDEKNIRIADFGMASLQVGDLSLETSCGSPH 180
Db 121 FFRQIISALDFCHSHSICHRLKPNLLDDEKNIRIADFGMASLQVGDLSLETSCGSPH 180
Qy 181 YACPEVIRGEKYDGRKADVWSCGVILFALLVGLPFD DDLNRLQLLEKVRGVFHPHFIP 240
Db 181 YACPEVIRGEKYDGRKADVWSCGVILFALLVGLPFD DDLNRLQLLEKVRGVFHPHFIP 240
Qy 241 PDCQSLLRGMIEVDAARLTLEHIQKHIWYIGGKNEPEPEQIPRKQVIRSLPSLEDIDP 300
Db 241 PDCQSLLRGMIEVDAARLTLEHIQKHIWYIGGKNEPEPEQIPRKQVIRSLPSLEDIDP 300
Qy 301 DVLDSMHSILGCFDRNKLQDLLSEBENQEKMIYFLLDRKERYPSQDEDLPPRNEIDP 360
Db 301 DVLDSMHSILGCFDRNKLQDLLSEBENQEKMIYFLLDRKERYPSQDEDLPPRNEIDP 360
Qy 361 PRKRVDSPLNHRGKRRPERKSMVLSVTDGSPVPARRAIEMAHQGQRSISGAS SGL 420
Db 361 PRKRVDSPLNHRGKRRPERKSMVLSVTDGSPVPARRAIEMAHQGQRSISGAS SGL 420
Qy 421 STSPLSSPRVTPHPSPRGSLPTPKGTPTVHTPKESPAGTNPPTPSSPSVGVPMRARN 480
Db 421 STSPLSSPRVTPHPSPRGSLPTPKGTPTVHTPKESPAGTNPPTPSSPSVGVPMRARN 480
Qy 481 SIKNSFLGSPRFRHRKLOVPTPEEMSNLTPSSPELAKKSWFGNFI SLEKEEQIFVVIKD 540
Db 481 SIKNSFLGSPRFRHRKLOVPTPEEMSNLTPSSPELAKKSWFGNFI SLEKEEQIFVVIKD 540
Qy 541 KPLSSIKADIVHAFSLSPSLSHSVISQTSFRAEYKATGGPAVFOKPVKFOVDIITYTGE 600
Db 541 KPLSSIKADIVHAFSLSPSLSHSVISQTSFRAEYKATGGPAVFOKPVKFOVDIITYTGE 600
Qy 601 AQKENGIVSVTFTLLSGSPRRFRKRVVETIOALLSTHDP PPAQHLS 647
Db 601 AQKENGIVSVTFTLLSGSPRRFRKRVVETIOALLSTHDP PPAQHLS 647

RESULT 6
US-09-842-582-2
; Sequence 2, Application US/09842582
; Patent No. US20020155570A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Meyers, Rachel
; TITLE OF INVENTION: 2246, NOVEL PROTEIN KINASE MOLECULES AND
; TITLE OF INVENTION: USES THEREFOR
; FILE REFERENCE: 38155-20054.00
; CURRENT APPLICATION NUMBER: US/09/842,582
; CURRENT FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 60/199,391
; PRIOR FILING DATE: 2000-04-25

; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 674
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-842-582-2

Query Match 96.5%; Score 3374; DB 10; Length 674;
Best Local Similarity 99.7%; Pred. No. 2.6e-210;
Matches 645; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MTSTGKGGAQAQYVGPYRLEKTLGKGTGLVKGVCVTCQKVAIKIVNREKLSV 60
Db 1 MTSTGKGGAQAQYVGPYRLEKTLGKGTGLVKGVCVTCQKVAIKIVNREKLSV 60
Qy 61 MKVEREIAILKLIIEHPHVLKLDVYENKKYLYLVLEHVS GGELFDYLVKGR LTPKEARK 120
Db 61 MKVEREIAILKLIIEHPHVLKLDVYENKKYLYLVLEHVS GGELFDYLVKGR LTPKEARK 120
Qy 121 FFRQIISALDFCHSHSICHRLKPNLLDDEKNIRIADFGMASLQVGDLSLETSCGSPH 180
Db 121 FFRQIISALDFCHSHSICHRLKPNLLDDEKNIRIADFGMASLQVGDLSLETSCGSPH 180
Qy 181 YACPEVIRGEKYDGRKADVWSCGVILFALLVGLPFD DDLNRLQLLEKVRGVFHPHFIP 240
Db 181 YACPEVIRGEKYDGRKADVWSCGVILFALLVGLPFD DDLNRLQLLEKVRGVFHPHFIP 240
Qy 241 PDCQSLLRGMIEVDAARLTLEHIQKHIWYIGGKNEPEPEQIPRKQVIRSLPSLEDIDP 300
Db 241 PDCQSLLRGMIEVDAARLTLEHIQKHIWYIGGKNEPEPEQIPRKQVIRSLPSLEDIDP 300
Qy 301 DVLDSMHSILGCFDRNKLQDLLSEBENQEKMIYFLLDRKERYPSQDEDLPPRNEIDP 360
Db 301 DVLDSMHSILGCFDRNKLQDLLSEBENQEKMIYFLLDRKERYPSQDEDLPPRNEIDP 360
Qy 361 PRKRVDSPLNHRGKRRPERKSMVLSVTDGSPVPARRAIEMAHQGQRSISGAS SGL 420
Db 361 PRKRVDSPLNHRGKRRPERKSMVLSVTDGSPVPARRAIEMAHQGQRSISGAS SGL 420
Qy 421 STSPLSSPRVTPHPSPRGSLPTPKGTPTVHTPKESPAGTNPPTPSSPSVGVPMRARN 480
Db 421 STSPLSSPRVTPHPSPRGSLPTPKGTPTVHTPKESPAGTNPPTPSSPSVGVPMRARN 480
Qy 481 SIKNSFLGSPRFRHRKLOVPTPEEMSNLTPSSPELAKKSWFGNFI SLEKEEQIFVVIKD 540
Db 481 SIKNSFLGSPRFRHRKLOVPTPEEMSNLTPSSPELAKKSWFGNFI SLEKEEQIFVVIKD 540
Qy 541 KPLSSIKADIVHAFSLSPSLSHSVISQTSFRAEYKATGGPAVFOKPVKFOVDIITYTGE 600
Db 541 KPLSSIKADIVHAFSLSPSLSHSVISQTSFRAEYKATGGPAVFOKPVKFOVDIITYTGE 600
Qy 601 AQKENGIVSVTFTLLSGSPRRFRKRVVETIOALLSTHDP PPAQHLS 647
Db 601 AQKENGIVSVTFTLLSGSPRRFRKRVVETIOALLSTHDP PPAQHLS 647

RESULT 7
US-10-283-247-7
; Sequence 7, Application US/10283247
; Publication No. US20030119037A1
; GENERAL INFORMATION:
; APPLICANT: NEELAM, Beena et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001304
; CURRENT APPLICATION NUMBER: US/10/283,247
; CURRENT FILING DATE: 2002-10-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 674

TYPE: PRT
ORGANISM: Homo sapiens
US-10-283-247-7

Query Match 96.5%; Score 3374; DB 15; Length 674;
Best Local Similarity 99.7%; Pred. No. 2.6e-210;
Matches 545; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MTSTGKGGGAQAQYVGPYRLEKTLGKQGLVGLGVHCVTCQKVAIKIVNREKLSVSL 60
Db 1 MTSTGKGGGAQAQYVGPYRLEKTLGKQGLVGLGVHCVTCQKVAIKIVNREKLSVSL 60
Qy 61 MKVEREAILKLEHPHVLLKLDVYENKYLVLVLEHVSQGLFDYLVKGRLLTPKEARK 120
Db 61 MKVEREAILKLEHPHVLLKLDVYENKYLVLVLEHVSQGLFDYLVKGRLLTPKEARK 120
Qy 121 FFRQIISALDFCHSHSICHRLDKPENLLDEKNNIRIADFGWASLQVDSLETSCGSPH 180
Db 121 FFRQIISALDFCHSHSICHRLDKPENLLDEKNNIRIADFGWASLQVDSLETSCGSPH 180
Qy 181 YACPEVIRGEKYDGRKADWSCGVILFALLVGLPFDNNLRQLLEKVKRGVFMHPHIP 240
Db 181 YACPEVIRGEKYDGRKADWSCGVILFALLVGLPFDNNLRQLLEKVKRGVFMHPHIP 240
Qy 241 PDCQSLLRGMIEVDAAARLTLEHIQKHITWYIGGKNEPEPEQIPRKQVIRSLPSLEDIDP 300
Db 241 PDCQSLLRGMIEVDAAARLTLEHIQKHITWYIGGKNEPEPEQIPRKQVIRSLPSLEDIDP 300
Qy 301 DVLDMSHSLGCFRDRNKLQDLLSEENQEKMIYFLLLDRKERYPSQDEDLPPRNEIDP 360
Db 301 DVLDMSHSLGCFRDRNKLQDLLSEENQEKMIYFLLLDRKERYPSQDEDLPPRNEIDP 360
Qy 361 PRKRVDSPLNRRHGKRRPERKSMELSVTDGSPVPARRAIEAQAQGRSISGASSGL 420
Db 361 PRKRVDSPLNRRHGKRRPERKSMELSVTDGSPVPARRAIEAQAQGRSISGASSGL 420
Qy 421 STSPLSSPRVTPHSPRSGPLTPKGTPTVHTPKESPAGTNPPTPPSSPSVGGVPMRRLN 480
Db 421 STSPLSSPRVTPHSPRSGPLTPKGTPTVHTPKESPAGTNPPTPPSSPSVGGVPMRRLN 480
Qy 481 SIKNSFLGSPFRHRRKLQVPTPEMSNLTPSSPELAKSWFGNFISLEKEQIFVVIKD 540
Db 481 SIKNSFLGSPFRHRRKLQVPTPEMSNLTPSSPELAKSWFGNFISLEKEQIFVVIKD 540
Qy 541 KPLSSIKADIVHAFSLPSLSHVSISQTSFRAEYKATGPAVFOKPVKFQVDITYTGE 600
Db 541 KPLSSIKADIVHAFSLPSLSHVSISQTSFRAEYKATGPAVFOKPVKFQVDITYTGE 600
Qy 601 AQKNGIYSVTFTLLSGPSRRFKRVVETIQALLSTHDPAAQHLSD 647
Db 601 AQKNGIYSVTFTLLSGPSRRFKRVVETIQALLSTHDPAAQHLSE 647

RESULT 8

US-10-283-247-8
Sequence 8, Application US/10283247
Publication No. US20030119037A1
GENERAL INFORMATION:
APPLICANT: NEELAM, Beena et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL001304
CURRENT APPLICATION NUMBER: US/10/283,247
CURRENT FILING DATE: 2002-10-30
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 674
TYPE: PRT
ORGANISM: Homo sapiens
US-10-283-247-8

Query Match 96.5%; Score 3374; DB 15; Length 674;
Best Local Similarity 99.7%; Pred. No. 2.6e-210;
Matches 645; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MTSTGKGGGAQAQYVGPYRLEKTLGKQGLVGLGVHCVTCQKVAIKIVNREKLSVSL 60
Db 1 MTSTGKGGGAQAQYVGPYRLEKTLGKQGLVGLGVHCVTCQKVAIKIVNREKLSVSL 60
Qy 61 MKVEREAILKLEHPHVLLKLDVYENKYLVLVLEHVSQGLFDYLVKGRLLTPKEARK 120
Db 61 MKVEREAILKLEHPHVLLKLDVYENKYLVLVLEHVSQGLFDYLVKGRLLTPKEARK 120
Qy 121 FFRQIISALDFCHSHSICHRLDKPENLLDEKNNIRIADFGWASLQVDSLETSCGSPH 180
Db 121 FFRQIISALDFCHSHSICHRLDKPENLLDEKNNIRIADFGWASLQVDSLETSCGSPH 180
Qy 181 YACPEVIRGEKYDGRKADWSCGVILFALLVGLPFDNNLRQLLEKVKRGVFMHPHIP 240
Db 181 YACPEVIRGEKYDGRKADWSCGVILFALLVGLPFDNNLRQLLEKVKRGVFMHPHIP 240
Qy 241 PDCQSLLRGMIEVDAAARLTLEHIQKHITWYIGGKNEPEPEQIPRKQVIRSLPSLEDIDP 300
Db 241 PDCQSLLRGMIEVDAAARLTLEHIQKHITWYIGGKNEPEPEQIPRKQVIRSLPSLEDIDP 300
Qy 301 DVLDMSHSLGCFRDRNKLQDLLSEENQEKMIYFLLLDRKERYPSQDEDLPPRNEIDP 360
Db 301 DVLDMSHSLGCFRDRNKLQDLLSEENQEKMIYFLLLDRKERYPSQDEDLPPRNEIDP 360
Qy 361 PRKRVDSPLNRRHGKRRPERKSMELSVTDGSPVPARRAIEAQAQGRSISGASSGL 420
Db 361 PRKRVDSPLNRRHGKRRPERKSMELSVTDGSPVPARRAIEAQAQGRSISGASSGL 420
Qy 421 STSPLSSPRVTPHSPRSGPLTPKGTPTVHTPKESPAGTNPPTPPSSPSVGGVPMRRLN 480
Db 421 STSPLSSPRVTPHSPRSGPLTPKGTPTVHTPKESPAGTNPPTPPSSPSVGGVPMRRLN 480
Qy 481 SIKNSFLGSPFRHRRKLQVPTPEMSNLTPSSPELAKSWFGNFISLEKEQIFVVIKD 540
Db 481 SIKNSFLGSPFRHRRKLQVPTPEMSNLTPSSPELAKSWFGNFISLEKEQIFVVIKD 540
Qy 541 KPLSSIKADIVHAFSLPSLSHVSISQTSFRAEYKATGPAVFOKPVKFQVDITYTGE 600
Db 541 KPLSSIKADIVHAFSLPSLSHVSISQTSFRAEYKATGPAVFOKPVKFQVDITYTGE 600
Qy 601 AQKNGIYSVTFTLLSGPSRRFKRVVETIQALLSTHDPAAQHLSD 647
Db 601 AQKNGIYSVTFTLLSGPSRRFKRVVETIQALLSTHDPAAQHLSE 647

RESULT 9

US-10-054-579-4
Sequence 4, Application US/10054579
Publication No. US20020137913A1
GENERAL INFORMATION:
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Mathur, Brian
TITLE OF INVENTION: No. US20020137913A1 Human Kinases and Polynucleotides Encoding t
FILE REFERENCE: LEX-0300-USA
CURRENT APPLICATION NUMBER: US/10/054,579
CURRENT FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: US 60/263,378
PRIOR FILING DATE: 2001-01-23
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 608
TYPE: PRT
ORGANISM: homo sapiens
US-10-054-579-4

Query Match 91.2%; Score 3188; DB 14; Length 608;
Best Local Similarity 100.0%; Pred. No. 2.5e-198;
Matches 608; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 MKVEREAILKLEHSHVHLKLDVYENKYLVLVLEHVSQGELEFDYLVKKGRITPKEARK 120
DB 1 MKVEREAILKLEHSHVHLKLDVYENKYLVLVLEHVSQGELEFDYLVKKGRITPKEARK 60

QY 121 FFRQIISALDFCHSHSICHRLDKPENLLDEKNNIRIADFGMASLQVGSLLTSCGSPH 180
DB 61 FFRQIISALDFCHSHSICHRLDKPENLLDEKNNIRIADFGMASLQVGSLLTSCGSPH 120

QY 181 YACPEVIRGEKYDGRKADVWSCGVILFALLVGVLPFDDNNLRQLLEKVKRGVFMHPHFIP 240
DB 121 YACPEVIRGEKYDGRKADVWSCGVILFALLVGVLPFDDNNLRQLLEKVKRGVFMHPHFIP 180

QY 241 PDCQSLLRGMIEVDAAARLTLEHIQKHIWYIGGKNEPEPEQIPRKVQIRSLPSLEDIDP 300
DB 181 PDCQSLLRGMIEVDAAARLTLEHIQKHIWYIGGKNEPEPEQIPRKVQIRSLPSLEDIDP 240

QY 301 DVLDMSHSLGCFRDRNKLQDILLSEENQEKMIYFLLDRKERYPSQDEDELPPENEIDP 360
DB 181 PDCQSLLRGMIEVDAAARLTLEHIQKHIWYIGGKNEPEPEQIPRKVQIRSLPSLEDIDP 240

QY 361 PRKRVDSPLNHRGKRPERKSMVLSVTDGSPVPARRAIEMAHQGQRSISGASSGL 420
DB 301 PRKRVDSPLNHRGKRPERKSMVLSVTDGSPVPARRAIEMAHQGQRSISGASSGL 360

QY 421 STSPLSSPRVTPHPSPRGSPPLTPKGTVPHTPKESPAGTNPPTPSSPSVGGVPMRRLN 480
DB 361 STSPLSSPRVTPHPSPRGSPPLTPKGTVPHTPKESPAGTNPPTPSSPSVGGVPMRRLN 420

QY 481 SIKNSFLGSPFRHRRKLQVTPPEMSNLTPSSPELAKKSWFGNFTSLEKEEQIFVVIKD 540
DB 421 SIKNSFLGSPFRHRRKLQVTPPEMSNLTPSSPELAKKSWFGNFTSLEKEEQIFVVIKD 480

QY 541 KPLSSIKADIVHAFSLPSLSHVSISQTSFRAEYKATGGPAVQKPKFQVDITYTEGGE 600
DB 481 KPLSSIKADIVHAFSLPSLSHVSISQTSFRAEYKATGGPAVQKPKFQVDITYTEGGE 540

QY 601 AQKENGIVSVTFTLLSGPSRRFRKRVETIIQAQLLSTHDPAAQHLSDTTNCMENMTGRLS 660
DB 541 AQKENGIVSVTFTLLSGPSRRFRKRVETIIQAQLLSTHDPAAQHLSDTTNCMENMTGRLS 600

QY 661 KCGIIPKS 668
DB 601 KCGIIPKS 608

RESULT 10
US-10-283-247-9
; Sequence 9, Application US/10283247
; Publication No. US20030119037A1
; GENERAL INFORMATION:
; APPLICANT: NEELAM, Beena et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001304
; CURRENT APPLICATION NUMBER: US/10/283.247
; CURRENT FILING DATE: 2002-10-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 614
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-283-247-9

Query Match 87.6%; Score 3065; DB 15; Length 614;
Best Local Similarity 99.7%; Pred. No. 2.3e-190;
Matches 585; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 61 MKVEREAILKLEHSHVHLKLDVYENKYLVLVLEHVSQGELEFDYLVKKGRITPKEARK 120
DB 1 MKVEREAILKLEHSHVHLKLDVYENKYLVLVLEHVSQGELEFDYLVKKGRITPKEARK 60

QY 121 FFRQIISALDFCHSHSICHRLDKPENLLDEKNNIRIADFGMASLQVGSLLTSCGSPH 180
DB 61 FFRQIISALDFCHSHSICHRLDKPENLLDEKNNIRIADFGMASLQVGSLLTSCGSPH 120

QY 181 YACPEVIRGEKYDGRKADVWSCGVILFALLVGVLPFDDNNLRQLLEKVKRGVFMHPHFIP 240
DB 121 YACPEVIRGEKYDGRKADVWSCGVILFALLVGVLPFDDNNLRQLLEKVKRGVFMHPHFIP 180

QY 241 PDCQSLLRGMIEVDAAARLTLEHIQKHIWYIGGKNEPEPEQIPRKVQIRSLPSLEDIDP 300
DB 181 PDCQSLLRGMIEVDAAARLTLEHIQKHIWYIGGKNEPEPEQIPRKVQIRSLPSLEDIDP 240

QY 301 DVLDMSHSLGCFRDRNKLQDILLSEENQEKMIYFLLDRKERYPSQDEDELPPENEIDP 360
DB 241 DVLDMSHSLGCFRDRNKLQDILLSEENQEKMIYFLLDRKERYPSQDEDELPPENEIDP 300

QY 361 PRKRVDSPLNHRGKRPERKSMVLSVTDGSPVPARRAIEMAHQGQRSISGASSGL 420
DB 301 PRKRVDSPLNHRGKRPERKSMVLSVTDGSPVPARRAIEMAHQGQRSISGASSGL 360

QY 421 STSPLSSPRVTPHPSPRGSPPLTPKGTVPHTPKESPAGTNPPTPSSPSVGGVPMRRLN 480
DB 361 STSPLSSPRVTPHPSPRGSPPLTPKGTVPHTPKESPAGTNPPTPSSPSVGGVPMRRLN 420

QY 481 SIKNSFLGSPFRHRRKLQVTPPEMSNLTPSSPELAKKSWFGNFTSLEKEEQIFVVIKD 540
DB 421 SIKNSFLGSPFRHRRKLQVTPPEMSNLTPSSPELAKKSWFGNFTSLEKEEQIFVVIKD 480

QY 541 KPLSSIKADIVHAFSLPSLSHVSISQTSFRAEYKATGGPAVQKPKFQVDITYTEGGE 600
DB 481 KPLSSIKADIVHAFSLPSLSHVSISQTSFRAEYKATGGPAVQKPKFQVDITYTEGGE 540

QY 601 AQKENGIVSVTFTLLSGPSRRFRKRVETIIQAQLLSTHDPAAQHLSD 647
DB 541 AQKENGIVSVTFTLLSGPSRRFRKRVETIIQAQLLSTHDPAAQHLSE 587

RESULT 11
US-10-283-247-10
; Sequence 10, Application US/10283247
; Publication No. US20030119037A1
; GENERAL INFORMATION:
; APPLICANT: NEELAM, Beena et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001304
; CURRENT APPLICATION NUMBER: US/10/283.247
; CURRENT FILING DATE: 2002-10-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 614
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-283-247-10

Query Match 87.6%; Score 3065; DB 15; Length 614;
Best Local Similarity 99.7%; Pred. No. 2.3e-190;
Matches 585; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 61 MKVEREAILKLEHSHVHLKLDVYENKYLVLVLEHVSQGELEFDYLVKKGRITPKEARK 120
DB 1 MKVEREAILKLEHSHVHLKLDVYENKYLVLVLEHVSQGELEFDYLVKKGRITPKEARK 60

QY 121 FFRQIISALDFCHSHSICHRLDKPENLLDEKNNIRIADFGMASLQVGSLLTSCGSPH 180
DB 61 FFRQIISALDFCHSHSICHRLDKPENLLDEKNNIRIADFGMASLQVGSLLTSCGSPH 120

QY 181 YACPEVIRGEKYDGRKADVWSCGVILFALLVGVLPFDDNNLRQLLEKVKRGVFMHPHFIP 240
DB 121 YACPEVIRGEKYDGRKADVWSCGVILFALLVGVLPFDDNNLRQLLEKVKRGVFMHPHFIP 180

QY 241 PDCOSLRGMIEVDAAARLTLEHTQKHIWYTGKNEPEPEQIPRKQIRSLPSLEIDP 300
DB 181 PDCOSLRGMIEVDAAARLTLEHTQKHIWYTGKNEPEPEQIPRKQIRSLPSLEIDP 240
QY 301 DVLDSMSLGCGRDRNKLQDLSSEENQEKMIYFLLLDRKERYPSQDEDLPRNEIDP 360
DB 241 DVLDSMSLGCGRDRNKLQDLSSEENQEKMIYFLLLDRKERYPSQDEDLPRNEIDP 300
QY 361 PRKRVDSPLNRHGRKRRPERKSMIEVSVTDGSPVPARRAIEMAHQQRSSISGASSGL 420
DB 301 PRKRVDSPLNRHGRKRRPERKSMIEVSVTDGSPVPARRAIEMAHQQRSSISGASSGL 360
QY 421 STSLSPSRVTPHPSGRGSLPTPKGTVPVHTPKESPAGTNPPTPPSPSVGGVPMRRLN 480
DB 361 STSLSPSRVTPHPSGRGSLPTPKGTVPVHTPKESPAGTNPPTPPSPSVGGVPMRRLN 420
QY 481 SIKNSFLGSPFRHRRKQVPTPEMSNLTPSSPELAKKSWFGNFIISLEKEEQIFVVIKD 540
DB 421 SIKNSFLGSPFRHRRKQVPTPEMSNLTPSSPELAKKSWFGNFIISLEKEEQIFVVIKD 480
QY 541 KPLSSIKADIHAFSLSPSLSHSVISQTSFRAEYKATGGAFFQKPVKQFVDITYTEGGE 600
DB 481 KPLSSIKADIHAFSLSPSLSHSVISQTSFRAEYKATGGAFFQKPVKQFVDITYTEGGE 540
QY 601 AKENGISYVTFLLSGPSRRFRKRVETIOAQLLSTHDPAAQHLSLSD 647
DB 541 AKENGISYVTFLLSGPSRRFRKRVETIOAQLLSTHDPAAQHLSLSD 587

RESULT 12

US-10-283-247-5
; Sequence 5, Application US/10283247
; Publication No. US20030119037A1
; GENERAL INFORMATION:
; APPLICANT: NEELAM, Bena et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001304
; CURRENT APPLICATION NUMBER: US/10/283,247
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 636
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-283-247-5

Query Match 87.2%; Score 3050; DB 15; Length 636;
Best Local Similarity 96.2%; Pred. No. 2.3e-189;
Matches 586; Conservative 1; Mismatches 0; Indels 22; Gaps 1;
QY 61 MKVERETAILKLEHPIVHLHDVYENKKYLYLVLEHVSQGELEFDYLVKKGRLTPKEARK 120
DB 1 MKVERETAILKLEHPIVHLHDVYENKKYLYLVLEHVSQGELEFDYLVKKGRLTPKEARK 60
QY 121 FFRQIIISALDFCHSHSICHRLDKPENLLLDKNNIRIADFGMASLQVDSLLSTSCGSPH 180
DB 61 FFRQIIISALDFCHSHSICHRLDKPENLLLDKNNIRIADFGMASLQVDSLLSTSCGSPH 120
QY 181 YACPEVIRGEKYDGRKADVWVSCGVILFALLVGLPFDNRLQLLEKVKRGVFMHPHFIP 240
DB 121 YACPEVIRGEKYDGRKADVWVSCGVILFALLVGLPFDNRLQLLEKVKRGVFMHPHFIP 180
QY 241 PDCOSLRGMIEVDAAARLTLEHTQKHIWYTGKNEPEPEQIPRKQIRSLPSLEIDP 300
DB 181 PDCOSLRGMIEVDAAARLTLEHTQKHIWYTGKNEPEPEQIPRKQIRSLPSLEIDP 240
QY 301 DVLDSMSLGCGRDRNKLQDLSSEENQEKMIYFLLLDRKERYPSQDEDLPRNEIDP 360
DB 241 DVLDSMSLGCGRDRNKLQDLSSEENQEKMIYFLLLDRKERYPSQDEDLPRNEIDP 300

QY 361 PRKRVDSPLNRHGRKRRPERKSMIEVSVTDGSPVPARRAIEMAHQHQ----- 408
DB 301 PRKRVDSPLNRHGRKRRPERKSMIEVSVTDGSPVPARRAIEMAHQHQSKAMFSSKSLDIA 360
QY 409 -----RSHSISGASSGLSTSLSPSRVTPHPSGRGSLPTPKGTVPVHTPKESPAG 458
DB 361 EAHQPSKEDRSISGASSGLSTSLSPSRVTPHPSGRGSLPTPKGTVPVHTPKESPAG 420
QY 459 TPNPTPPSPSVGGVPMRRLNLSIKNSFLGSPFRHRRKQVPTPEMSNLTPSSPELAK 518
DB 421 TPNPTPPSPSVGGVPMRRLNLSIKNSFLGSPFRHRRKQVPTPEMSNLTPSSPELAK 480
QY 519 KSWFGNFIISLEKEEQIFVVIKOKPLSSIADIVHAFSLSPSLSHSVISQTSFRAEYKATG 578
DB 481 KSWFGNFIISLEKEEQIFVVIKOKPLSSIADIVHAFSLSPSLSHSVISQTSFRAEYKATG 540
QY 579 GRAVFOKPVKQFVDITYTEGGEAKENGISYVTFLLSGPSRRFRKRVETIOAQLLSTH 638
DB 541 GRAVFOKPVKQFVDITYTEGGEAKENGISYVTFLLSGPSRRFRKRVETIOAQLLSTH 600
QY 639 PPAHQHLSLSD 647
DB 601 PPAHQHLSLSD 609

RESULT 13

US-10-195-072-4
; Sequence 4, Application US/10195072
; Publication No. US20030092036A1
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies
; TITLE OF INVENTION: Full-Length Serine Protein Kinase in Brain and Pancreas
; FILE REFERENCE: 16U 101 C2
; CURRENT APPLICATION NUMBER: US/10/195,072
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: US 09/930,181
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-195-072-4

Query Match 86.6%; Score 3028; DB 15; Length 585;
Best Local Similarity 100.0%; Pred. No. 5.5e-188;
Matches 577; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 92 YLVLEHVSQGELEFDYLVKKGRLTPKEARKFFRQIIISALDFCHSHSICHRLDKPENLLD 151
DB 9 YLVLEHVSQGELEFDYLVKKGRLTPKEARKFFRQIIISALDFCHSHSICHRLDKPENLLD 68
QY 152 KNNIRIADFGMASLQVDSLLSTSCGSPHYACPEVIRGEKYDGRKADVWVSCGVILFALL 211
DB 69 KNNIRIADFGMASLQVDSLLSTSCGSPHYACPEVIRGEKYDGRKADVWVSCGVILFALL 128
QY 212 GALPFDNRLQLLEKVKRGVFMHPHFIPDCCOSLRGMIEVDAAARLTLEHTQKHIWY 271
DB 129 GALPFDNRLQLLEKVKRGVFMHPHFIPDCCOSLRGMIEVDAAARLTLEHTQKHIWY 188
QY 272 GKNPEPEQIPRKQIRSLPSLEIDPDLDSMSHSLGCFDRNKLQDLSSEENQEK 331
DB 189 GKNPEPEQIPRKQIRSLPSLEIDPDLDSMSHSLGCFDRNKLQDLSSEENQEK 248
QY 332 MIYFLLLDRKERYPSQDEDLPRNEIDPDKVDSFPMNHRHGRKRRPERKSMIEVSVTDG 391
DB 249 MIYFLLLDRKERYPSQDEDLPRNEIDPDKVDSFPMNHRHGRKRRPERKSMIEVSVTDG 308
QY 392 GSPVPARRAIEMAHQQRSSISGASSGLSTSLSPSRVTPHPSGRGSLPTPKGTVPVHT 451
DB 309 GSPVPARRAIEMAHQQRSSISGASSGLSTSLSPSRVTPHPSGRGSLPTPKGTVPVHT 368

QY 452 PKSPAGTNPPTPPSPSVGVVWRLNLSIKNSFLGSPFRHRRKLVQVTPPEMSNLTP 511
DB 369 PKSPAGTNPPTPPSPSVGVVWRLNLSIKNSFLGSPFRHRRKLVQVTPPEMSNLTP 428
QY 512 SSPSLAKSWFGNFIISLEKEQIFVVIKDKPLSSIKADIVHAFSLSPSLSHSVISQTSFR 571
DB 429 SSPSLAKSWFGNFIISLEKEQIFVVIKDKPLSSIKADIVHAFSLSPSLSHSVISQTSFR 488
QY 572 AEYKATGGPAVFQKPVKFOVDITYTTEGGAQKENGIVSVTFTLLSGPSRRFRKRVVETIOA 631
DB 489 AEYKATGGPAVFQKPVKFOVDITYTTEGGAQKENGIVSVTFTLLSGPSRRFRKRVVETIOA 548
QY 632 QLLSTHDPAPAAHLSDTTNCMEMMTGRLSKCGIIPKS 668
DB 549 QLLSTHDPAPAAHLSDTTNCMEMMTGRLSKCGIIPKS 585
RESULT 14
US-10-195-071-4
; Sequence 4, Application US/10195071
; Publication No. US20030096271A1
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies
; TITLE OF INVENTION: Full-Length Serine Protein Kinase in Brain and Pancreas
; FILE REFERENCE: 16U 101 C1
; CURRENT APPLICATION NUMBER: US/10/195,071
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: US 09/930,181
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-195-071-4
Query Match 86.6%; Score 3028; DB 15; Length 585;
Best Local Similarity 100.0%; Pred. No. 5.5e-188;
Matches 577; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 92 YLVLEHVSQGLFDYLVKKGRLTPKEARKFRQIISALDFCHSHSICHRLDKPENLLIDE 151
DB 9 YLVLEHVSQGLFDYLVKKGRLTPKEARKFRQIISALDFCHSHSICHRLDKPENLLIDE 68
QY 152 KNNIRIADFGWASLQVGSLLTSCGSPHYACPEVIRGEKYDGRKADVWSCGVILFALLV 211
DB 69 KNNIRIADFGWASLQVGSLLTSCGSPHYACPEVIRGEKYDGRKADVWSCGVILFALLV 128
QY 212 GALPDDNNLRQLLEKVKRGVFMHPHFIPDQCQLLRGMI EVDAAARLTLLEHIQKHIWYI 271
DB 129 GALPDDNNLRQLLEKVKRGVFMHPHFIPDQCQLLRGMI EVDAAARLTLLEHIQKHIWYI 188
QY 272 GGNKEPEEQPIPRKVQIRSLPSLEDIDPDVLDMSHSLGCFRDRNKLQDILLSEENQEK 331
DB 189 GGNKEPEEQPIPRKVQIRSLPSLEDIDPDVLDMSHSLGCFRDRNKLQDILLSEENQEK 248
QY 332 MIYFLLDRKERYPSQEDDLPPRNEIDPPRKRVDSPMLNRHKKRRPERKSMEVLSVTDG 391
DB 249 MIYFLLDRKERYPSQEDDLPPRNEIDPPRKRVDSPMLNRHKKRRPERKSMEVLSVTDG 308
QY 392 GSPVPARRAIAEMAQGRSRSISGASGLSTSPRVTTPHPSPRGSPPLTPKGTPTVHT 451
DB 309 GSPVPARRAIAEMAQGRSRSISGASGLSTSPRVTTPHPSPRGSPPLTPKGTPTVHT 368
QY 452 PKSPAGTNPPTPPSPSVGVVWRLNLSIKNSFLGSPFRHRRKLVQVTPPEMSNLTP 511
DB 369 PKSPAGTNPPTPPSPSVGVVWRLNLSIKNSFLGSPFRHRRKLVQVTPPEMSNLTP 428
QY 512 SSPSLAKSWFGNFIISLEKEQIFVVIKDKPLSSIKADIVHAFSLSPSLSHSVISQTSFR 571
DB 429 SSPSLAKSWFGNFIISLEKEQIFVVIKDKPLSSIKADIVHAFSLSPSLSHSVISQTSFR 488

QY 572 AEYKATGGPAVFQKPVKFOVDITYTTEGGAQKENGIVSVTFTLLSGPSRRFRKRVVETIOA 631
DB 489 AEYKATGGPAVFQKPVKFOVDITYTTEGGAQKENGIVSVTFTLLSGPSRRFRKRVVETIOA 548
QY 632 QLLSTHDPAPAAHLSDTTNCMEMMTGRLSKCGIIPKS 668
DB 549 QLLSTHDPAPAAHLSDTTNCMEMMTGRLSKCGIIPKS 585
RESULT 15
US-10-195-072-17
; Sequence 17, Application US/10195072
; Publication No. US20030092036A1
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies
; TITLE OF INVENTION: Full-Length Serine Protein Kinase in Brain and Pancreas
; FILE REFERENCE: 16U 101 C2
; CURRENT APPLICATION NUMBER: US/10/195,072
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: US 09/930,181
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 17
; LENGTH: 603
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-195-072-17
Query Match 86.2%; Score 3015; DB 15; Length 603;
Best Local Similarity 99.7%; Pred. No. 3.9e-187;
Matches 574; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 72 LIEHPHVLKLDVYENKYLVLVLEHVSQGLFDYLVKKGRLTPKEARKFRQIISALDF 131
DB 1 LIEHPHVLKLDVYENKYLVLVLEHVSQGLFDYLVKKGRLTPKEARKFRQIISALDF 60
QY 132 CHSHSICHRLDKPENLLIDEKNNIRIADFGWASLQVGSLLTSCGSPHYACPEVIRGEK 191
DB 61 CHSHSICHRLDKPENLLIDEKNNIRIADFGWASLQVGSLLTSCGSPHYACPEVIRGEK 120
QY 192 YDGRKADVWSCGVILFALLVQALPFDNNLRQLLEKVKRGVFMHPHFIPDQCQLLRGMI 251
DB 121 YDGRKADVWSCGVILFALLVQALPFDNNLRQLLEKVKRGVFMHPHFIPDQCQLLRGMI 180
QY 252 EVDAARLTLLEHIQKHIWYIGGNKEPEEQPIPRKVQIRSLPSLEDIDPDVLDMSHSLG 311
DB 181 EVDAARLTLLEHIQKHIWYIGGNKEPEEQPIPRKVQIRSLPSLEDIDPDVLDMSHSLG 240
QY 312 FRDRNKLQDILLSEENQEKMIYFLLDRKERYPSQEDDLPPRNEIDPPRKRVDSPMLN 371
DB 241 FRDRNKLQDILLSEENQEKMIYFLLDRKERYPSQEDDLPPRNEIDPPRKRVDSPMLN 300
QY 372 RHGKRRPERKSMEVLSVTDGSGSPVPARRAIAEMAQGRSRSISGASGLSTSPSSPRVT 431
DB 301 RHGKRRPERKSMEVLSVTDGSGSPVPARRAIAEMAQGRSRSISGASGLSTSPSSPRVT 360
QY 432 PHPSPRGSPPLTPKGTPTVHTPKESPACTPNPTPPSPSVGVVWRLNLSIKNSFLGSPR 491
DB 361 PHPSPRGSPPLTPKGTPTVHTPKESPACTPNPTPPSPSVGVVWRLNLSIKNSFLGSPR 420
QY 492 FHRKLVQVTPPEMSNLTPPESSPELAKSWFGNFIISLEKEQIFVVIKDKPLSSIKADIV 551
DB 421 FHRKLVQVTPPEMSNLTPPESSPELAKSWFGNFIISLEKEQIFVVIKDKPLSSIKADIV 480
QY 552 HAFSLSPSLSHSVISQTSFRAEYKATGGPAVFQKPVKFOVDITYTTEGGAQKENGIVSVT 611
DB 481 HAFSLSPSLSHSVISQTSFRAEYKATGGPAVFQKPVKFOVDITYTTEGGAQKENGIVSVT 540
QY 612 FTLLSGPSRRFRKRVVETIOALLSTHDPAPAAHLSD 647
DB 541 FTLLSGPSRRFRKRVVETIOALLSTHDPAPAAHLSD 576

Search completed: November 26, 2003, 12:11:01
Job time : 29.2696 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 26, 2003, 11:49:36 ; Search time 40.3103 Seconds
(without alignments)
2630.326 Million cell updates/sec

Title: US-10-054-579-2

Perfect score: 3497

Sequence: 1 MTSTGKGGAQAQVGYR.....TNCMEMTGRLSKGLIPKS 668

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Genesec 19Jun03.*

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1: /SIDS1/gcgdata/genesec/genesecp-emb1/AA1980.DAT.*
2: /SIDS1/gcgdata/genesec/genesecp-emb1/AA1981.DAT.*
3: /SIDS1/gcgdata/genesec/genesecp-emb1/AA1982.DAT.*
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23: /SIDS1/gcgdata/genesec/genesecp-emb1/AA2002.DAT.*
24: /SIDS1/gcgdata/genesec/genesecp-emb1/AA2003.DAT.*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3497	100.0	668	23	Human kinase NHP #
2	3497	100.0	668	24	Human serine prote
3	3423	97.9	664	23	Human PKIN-18 prot
4	3374	96.5	674	23	Human protein kina
5	3188	91.2	608	23	Human kinase NHP #
6	3028	86.6	585	24	Human serine prote
7	2799	80.0	778	24	Human kinase #1.
8	2785.5	79.7	794	22	Human protein kina
9	2785.5	79.7	794	23	Human kinase PKIN-

10	2768	79.2	754	24	AA016604	Human cell cycle-r
11	2545.5	72.8	703	24	ABB98745	Human kinase #3.
12	2386.5	68.2	762	24	ABB98744	Human kinase #2.
13	1974	56.4	851	22	ABG62061	Drosophila melanog
14	1275.5	36.5	301	22	ABBI1052	Human HrPOPK-1 hom
15	872.5	24.9	1349	22	AA070854	C albicans apoptos
16	797	22.8	768	22	AA078349	Human protein SEQ
17	796.5	22.8	745	24	AAE33550	Human microtubule
18	796.5	22.8	796	24	ABU11830	Human MDDT polyep
19	794.5	22.7	691	23	AAE19050	Human PAR-1B alpha
20	794.5	22.7	724	23	AAE19051	Human PAR-1B beta
21	793.5	22.7	724	24	ABU08527	Human serine/threo
22	790.5	22.6	514	21	AA030420	Soybean putative c
23	790.5	22.6	514	24	ABR40714	Glycine max oil tr
24	790.5	22.6	722	17	AA098227	Rat neuronal prote
25	788	22.5	769	23	ABP62966	Human polypeptide
26	784.5	22.4	514	24	ABR40816	Glycine max oil tr
27	784.5	22.4	515	21	ABR03422	Soybean putative c
28	784.5	22.4	515	24	ABR40716	Glycine max oil tr
29	784	22.4	505	24	ABR40810	Oryza sativa oil t
30	781	22.3	744	24	ABG73795	Murine MARK protei
31	779.5	22.3	761	24	ABP96068	Human kinase (PKIN
32	779.5	22.3	752	22	AAE11782	Human polypeptide,
33	779.5	22.3	752	22	AA093956	Human neuronal ser
34	779.5	22.3	752	23	ABO44433	Human MARK protein
35	779.5	22.3	752	24	ABG73794	Human microtubule
36	778.5	22.3	688	24	AAE33554	Human microtubule
37	778.5	22.3	688	24	AAE33555	Human microtubule
38	777.5	22.2	795	23	AAE19052	Human PAR-1C prote
39	777.5	22.2	795	23	AAE16258	Human kinase PKIN-
40	777.5	22.2	795	24	AAE33551	Human microtubule
41	776.5	22.2	804	22	AA079333	Human protein SEQ
42	775.5	22.2	688	23	ABO4434	Human neuronal ser
43	774.5	22.1	579	21	AA030417	Corn putative carb
44	774.5	22.1	579	24	ABR40709	Zea mays oil trait
45	774.5	22.1	823	21	AA090879	Human keratinocyte

ALIGNMENTS

RESULT 1

ABB09557

ID ABB09557 standard; Protein; 668 AA.

AC ABB09557;

XX

XX

DT 21-OCT-2002 (first entry)

XX

DE Human kinase NHP #1, SEQ ID NO:2.

XX

XX

XX

XX

KW Human; kinase; NHP; chromosome 11; signal transduction; cytoplasmic;

KW nuclear; brain; pituitary; hypothalamus; adipose; cerebellum;

KW adrenal gland; foetal lung; foetal brain; cancer; drug screening;

KW mental disorder; diagnostic reagent; clinical trial monitoring;

KW nutraceutical; mutation detection; gene expression analysis;

KW chromosome mapping; transgenic animal; cytostatic; gene therapy;

XX enzyme.

XX Homo sapiens.

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

[illegible]

OS	Homo sapiens.
XX	
Key	Location/Qualifiers
PH	Domain
FT	15..266
FT	/note= "Eukaryotic protein kinase domain"
FT	16..257
FT	/note= "Protein kinase domain"
FT	17..257
FT	/note= "Protein kinase domain"
FT	36..256
FT	/note= "Protein kinase domain"
XX	
PN	W0200218557-A2.
XX	
PD	07-MAR-2002.
XX	
PP	31-AUG-2001; 2001WO-US27219.
XX	
PR	31-AUG-2000; 2000US-229873P.
PR	08-SEP-2000; 2000US-231357P.
PR	14-SEP-2000; 2000US-232654P.
PR	22-SEP-2000; 2000US-234902P.
PR	29-SEP-2000; 2000US-236499P.
PR	06-OCT-2000; 2000US-238389P.
PR	13-OCT-2000; 2000US-240542P.
XX	
PA	(INCY-) INCYTE GENOMICS INC.
XX	
PI	Bandnan O, Nguyen DB, Wallia NK, Hafalia AJA, Yao MG, Gandhi AR;
PI	Gururajan R, Ding L, Patterson C, Yue H, Baughn MR, Tribouley CM;
PI	Thornton M, Elliott VS, Lu Y, Ison CH, Au-Young J, Tang YT;
PI	Azimzai Y, Burrill JB, Marcus GA, Zingler KA, Lu DAM, Lal PG;
PI	Ramkumar J, Warren BA, Kearney L, Policky JL, Thangavelu K;
PI	Burford N;
XX	
DR	WPI; 2002-329769/36.
DR	N-PSDB; AAD34315.
XX	
PT	New human kinases, useful for diagnosing, treating or preventing immune
PT	system disorders (e.g. Crohn's disease), neurological disorders (e.g.
PT	epilepsy), or cell proliferative disorders (e.g. cancers such as
PT	leukemia or lymphoma)
XX	
XX	Claim 73; Page 181-183; 218pp; English.
XX	
CC	The present invention relates to human kinases (PKIN) and polynucleotides
CC	encoding such proteins. PKIN sequences of the invention are useful for
CC	diagnosing, treating or preventing disorders associated with aberrant
CC	expression of PKIN, particularly immune system disorders (e.g. acquired
CC	immune deficiency syndrome (AIDS), thymic hypoplasia, Crohn's disease,
CC	anaemia, asthma), neurological disorders (e.g. epilepsy, Charcot-Marie-
CC	Tooth disease or seizures), cell proliferative disorders (e.g. cancers
CC	such as adenocarcinoma, leukaemia, lymphoma, melanoma, myeloma, sarcoma),
CC	and developmental disorders (e.g. Down's syndrome). They are also used
CC	in gene therapy and protein therapy. The present sequence is human
CC	PKIN-18 protein.
XX	
SQ	Sequence '664 AA;
Query Match	97.9%; Score 3423; DB 23; Length 664;
Best Local Similarity	100.0%; Pred. NO. 4.5e-244;
Matches 654; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Qy	15 YVGYRLEKTLKGQTGLVKVLGVHCVTCQVAIKIVNREKLSSEVLMMKVVERETAILKLIE 74
Dd	11 YVGYRLEKTLKGQTGLVKVLGVHCVTCQVAIKIVNREKLSSEVLMMKVVERETAILKLIE 70
Qy	75 HPYVLKLDHYENKNKYLYLVLEHVSGGELFDYLAVKKGRLLTPKEARKEFRQIIISALDFCHS 134
Dd	71 HPYVLKLDHYENKNKYLYLVLEHVSGGELFDYLAVKKGRLLTPKEARKEFRQIIISALDFCHS 130
Qy	135 HSICHRDLKPENLLLDEKNRIADFGMASLQVGDSILLETSCGSPHYACPEVTIRGEKYDG 194

Db 131 HSIHRDLKPNLLDKNRIRADFGWASLQVGSLLSTSCGSPHYACPEVIRGEKYDG 190
QY 195 RKADVWSCGVILFALLVGCALPFDDNLLQLLEKVKRGVFMHPHPIPPDCQSLLRGMIEVD 254
Db 191 RKADVWSCGVILFALLVGCALPFDDNLLQLLEKVKRGVFMHPHPIPPDCQSLLRGMIEVD 250
QY 255 AARLTLEHIQKHIWYIGGKNEPEPEQIPRKVOIRSLPSLEDDPVDLSDMHSILGCFRD 314
Db 251 AARLTLEHIQKHIWYIGGKNEPEPEQIPRKVOIRSLPSLEDDPVDLSDMHSILGCFRD 310
QY 315 RNKLLQDLSSEENQEKMIYFLLDRKERYPSQDEDLPPRNEIDPPRKRVDSPMLNRHG 374
Db 311 RNKLLQDLSSEENQEKMIYFLLDRKERYPSQDEDLPPRNEIDPPRKRVDSPMLNRHG 370
QY 375 KRRPERKMEVLSTVGGSPVPARRAIEAQAQSGORSRISGASGLSTSPSSPRVTPHP 434
Db 371 KRRPERKMEVLSTVGGSPVPARRAIEAQAQSGORSRISGASGLSTSPSSPRVTPHP 430
QY 435 SPRGSPPLTPKGTVPHTPKESPAGTNPPTPSSVGVGVPWRRLNSIKNSFLGSPRFRH 494
Db 431 SPRGSPPLTPKGTVPHTPKESPAGTNPPTPSSVGVGVPWRRLNSIKNSFLGSPRFRH 490
QY 495 RKLQVTPTEEMSNLTPSSPELAKKSWFGNFIISLEKEQIIFVWIKDKPLSIKADIVHAF 554
Db 491 RKLQVTPTEEMSNLTPSSPELAKKSWFGNFIISLEKEQIIFVWIKDKPLSIKADIVHAF 550
QY 555 LSIPSLSHSVISQTSFRAEYKATGGPAVFOKPVQFVDITYTEGGAQKENGISVTFLL 614
Db 551 LSIPSLSHSVISQTSFRAEYKATGGPAVFOKPVQFVDITYTEGGAQKENGISVTFLL 610
QY 615 LSGPSRRFRKRVVETIQALLSTHDPAAQHLSDTTNCMEMMTGRLSKGIIIPKS 668
Db 611 LSGPSRRFRKRVVETIQALLSTHDPAAQHLSDTTNCMEMMTGRLSKGIIIPKS 664

RESULT 4
AAM47830
ID AAM47830 standard; Protein; 674 AA.
AC AAM47830;
XX
DT 19-FEB-2002 (first entry)
XX
DE Human protein kinase 2246 SEQ ID NO 2.
KW Human; protein kinase 2246; cytosolic; immunomodulator; carcinoma;
KW anti-inflammatory; analgesic; cardiovascular; cancer; sarcoma;
KW cellular proliferation disorder; cellular differentiation disorder;
KW metastatic; haematopoietic disorder; leukaemia; immune disorder;
KW inflammatory disorder; arthritis; autoimmune disease; diabetes mellitus;
KW psoriasis; Crohn's disease; cardiovascular disease; virus; pain;
KW gene therapy.
XX
OS Homo sapiens.
XX
FN WO200181588-A2.
XX
PD 01-NOV-2001.
XX
PF 25-APR-2001; 2001WO-US13784.
XX
PR 25-APR-2000; 2000US-199391P.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Meyers R;
XX
DR WPI; 2002-049281/06.
XX
NR N-PSDB; ABA02994, ABA02995.
XX
PT New protein kinase nucleic acid and polypeptide molecules, designated
PT 2246, useful for diagnosing, preventing or treating cancer or a
PT cellular proliferation/differentiation disorders, e.g. carcinoma,

PT sarcoma or leukaemias -
XX Claim 4; Fig 1; 11pp; English.
XX
CC The invention relates to the human protein kinase 2246 gene and the
CC the isolated encoded polypeptide with cytosolic, immunomodulator,
CC anti-inflammatory, analgesic and cardiovascular activity. The 2246
CC nucleic acid and polypeptide are useful for diagnosing, preventing or
CC treating a subject having cancer or a cellular proliferation and/or
CC differentiation disorder or at risk of developing cancer or a cellular
CC proliferation and/or differentiation disorder. In particular, the
CC disorder includes carcinoma, sarcoma, metastatic or haematopoietic
CC disorders (e.g. leukaemias) or cancers of the lung, breast, thyroid, head
CC neck, prostate or genito-urinary tract. The 2246 nucleic acid and
CC polypeptide are also useful for treating immune disorders, e.g.
CC inflammatory (e.g. respiratory inflammation or arthritis), autoimmune
CC disease (e.g. diabetes mellitus, psoriasis, Wegener's granulomatosis,
CC Crohn's disease or Grave's disease), for treating cardiovascular
CC diseases, endothelial cell disorder, viral diseases or pain. The nucleic
CC acid and polypeptide are also useful for evaluating the efficacy of a
CC treatment of cancer or a cellular proliferation and/or differentiation
CC disorder. The nucleic acid is useful for gene therapy. The present
CC sequence is that of the 2246 protein kinase.
XX
SQ Sequence 674 AA;
Query Match 96.5%; Score 3374; DB 23; Length 674;
Best Local Similarity 99.7%; Pred. No. 1.9e-240;
Matches 645; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MTSTGDKGGAQAQYVGYPRLEKTLGKGQTLGKVLGVHCVTCOKVAIKVNRKLSVSL 60
Db 1 MTSTGDKGGAQAQYVGYPRLEKTLGKGQTLGKVLGVHCVTCOKVAIKVNRKLSVSL 60
QY 61 MKVERETAILKLEHPIVHLKLDVYENKYLVLVLEHVSQGLPFDYLVKGRLLTPKEARK 120
Db 61 MKVERETAILKLEHPIVHLKLDVYENKYLVLVLEHVSQGLPFDYLVKGRLLTPKEARK 120
QY 121 FFRQIISALDFCHSHSICHRLDKPENLLDEKKNIRIADFGWASLQVGSLLSTSCGSPH 180
Db 121 FFRQIISALDFCHSHSICHRLDKPENLLDEKKNIRIADFGWASLQVGSLLSTSCGSPH 180
QY 181 YACPEVIRGEKYDGRKADVWSCGVILFALLVGCALPFDDNLLQLLEKVKRGVFMHPHPI 240
Db 181 YACPEVIRGEKYDGRKADVWSCGVILFALLVGCALPFDDNLLQLLEKVKRGVFMHPHPI 240
QY 241 PDCQSLLRGMIEVDAAARLTLEHIQKHIWYIGGKNEPEPEQIPRKVOIRSLPSLEDDP 300
Db 241 PDCQSLLRGMIEVDAAARLTLEHIQKHIWYIGGKNEPEPEQIPRKVOIRSLPSLEDDP 300
QY 301 DVLDSMHSILGCFRDNRKLLQDLSSEENQEKMIYFLLDRKERYPSQDEDLPPRNEIDP 360
Db 301 DVLDSMHSILGCFRDNRKLLQDLSSEENQEKMIYFLLDRKERYPSQDEDLPPRNEIDP 360
QY 361 PRKRVDSFPLNRHGRKRRPERKSMESVLSVTDGSPVPARRAIEAQAQSGORSRISGASGL 420
Db 361 PRKRVDSFPLNRHGRKRRPERKSMESVLSVTDGSPVPARRAIEAQAQSGORSRISGASGL 420
QY 421 STSPSSPRVTPHPSPRGSPPLTPKGTVPHTPKESPAGTNPPTPSSVGVGVPWRRLN 480
Db 421 STSPSSPRVTPHPSPRGSPPLTPKGTVPHTPKESPAGTNPPTPSSVGVGVPWRRLN 480
QY 481 SIKNSFLGSPRFRHGRKRRKLOVTPPEMSNLTPESSPELAKKSWFGNFIISLEKEQIFVWIKD 540
Db 481 SIKNSFLGSPRFRHGRKRRKLOVTPPEMSNLTPESSPELAKKSWFGNFIISLEKEQIFVWIKD 540
QY 541 KPLSSIKADIVHAFPLSIPLSHSVISQTSFRAEYKATGGPAVFOKPVQFVDITYTEGGE 600
Db 541 KPLSSIKADIVHAFPLSIPLSHSVISQTSFRAEYKATGGPAVFOKPVQFVDITYTEGGE 600
QY 601 AQKENGISVTFLLSGPSRRFRKRVVETIQALLSTHDPAAQHLSD 647
Db 601 AQKENGISVTFLLSGPSRRFRKRVVETIQALLSTHDPAAQHLSD 647

RESULT 5
ID ABB09558 standard; Protein; 608 AA.
XX AC ABB09558;
XX DT 21-OCT-2002 (first entry)
XX DE Human kinase NHP #2, SEQ ID NO:4.
XX KW Human; kinase; NHP; chromosome 11; signal transduction; cytoplasmic;
KW nuclear; brain; pituitary; hypothalamus; adipose; cerebellum;
KW adrenal gland; foetal lung; foetal brain; cancer; drug screening;
KW mental disorder; diagnostic reagent; clinical trial monitoring; cosmetic;
KW nutraceutical; mutation detection; gene expression analysis;
KW chromosome mapping; transgenic animal; cytostatic; gene therapy;
KW enzyme.
XX OS Homo sapiens.
XX PN W0200259287-A2.
XX PD 01-AUG-2002.
XX PF 22-JAN-2002; 2002WO-US01818.
XX PR 23-JAN-2001; 2001US-263378P.
XX PA (LEXI-) LEXICON GENETICS INC.
XX PI Turner CA, Mathur B;
XX DR WPI; 2002-599780/64.
XX DR N-PSDB; ABQ77626.
XX PT Novel polynucleotide encoding human proteins sharing sequence
PT similarity with animal kinases, useful for drug screening, diagnosis,
PT in gene therapy of disorders and diseases e.g. cancer -
XX PS Claim 4; Page 39-40; 40pp; English.
XX CC The invention relates to novel human kinases (ABB09557, AAB09558),
CC referred to as NHPs, and to nucleic acids encoding them (ABQ77625,
CC ABQ77626). The NHPs have structural similarity with animal kinases
CC including serine-threonine kinases, carbon catabolite repressing kinases,
CC calcium/calmodulin-dependent protein kinases, and CAMP-dependent protein
CC kinases. The NHPs do not contain consensus signal sequences, indicating
CC that they may be cytoplasmic or nuclear proteins, and are thought to be
CC involved in signal transduction. Polynucleotides encoding NHPs were
CC obtained using human brain, pituitary, hypothalamus, adipose, cerebellum,
CC adrenal gland, foetal lung, and foetal brain cDNAs and primers derived
CC from human genomic DNA. The gene encoding the NHPs is located on
CC chromosome 11. NHP nucleotides and proteins are useful for treating
CC mental, biological or medical disorders including cancer, and for
CC screening compounds useful in the treatment of such conditions. They can
CC also be used as diagnostic reagents, in clinical trial monitoring and in
CC cosmetic and nutraceutical applications. NHP nucleotides can additionally
CC be used in the detection of disease-associated mutations, in the analysis
CC of gene expression, for mapping chromosome 11, for the recombinant
CC expression of NHPs, to generate transgenic animals, in gene therapy,
CC and as part of ribozyme and/or triple helix sequences useful in the
CC modulation of NHP gene expression. The present sequence represents a
CC 608 amino acid NHP (#2).
XX SQ Sequence 608 AA;
Query Match 91.2%; Score 3188; DB 23; Length 608;
Best Local Similarity 100.0%; Pred. No. 9e-227;
Matches 608; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
91 MKVERETAILKLIIEHPHVLKLDVYENKYLVLVLEHVS GGELFDYLVKKGR LTPKEARK 120

1 MKVERETAILKLIIEHPHVLKLDVYENKYLVLVLEHVS GGELFDYLVKKGR LTPKEARK 60
121 FFRQIIISALDFCHSHSICHRLDKPENLLLEKKNIRIADFGMASLQVDSLLTSCGSPH 180
61 FFRQIIISALDFCHSHSICHRLDKPENLLLEKKNIRIADFGMASLQVDSLLTSCGSPH 120
181 YACPEVIRGEKDYGRKADVWSCGVILFALLVGLALPDNDNLRQLLEKVKRGVFMHPHFIP 240
121 YACPEVIRGEKDYGRKADVWSCGVILFALLVGLALPDNDNLRQLLEKVKRGVFMHPHFIP 180
241 PDCQSLLRGMIEVDAARRLTLEHIQKHIWYIGGKNEPEPEQIPRKVQIRSLSPLEIDP 300
181 PDCQSLLRGMIEVDAARRLTLEHIQKHIWYIGGKNEPEPEQIPRKVQIRSLSPLEIDP 240
301 DVLDMSHSLGCFDRNKLQDLLESEENQEKMIYFLLDKERYPSQEDDLPPRNEIDP 360
241 DVLDMSHSLGCFDRNKLQDLLESEENQEKMIYFLLDKERYPSQEDDLPPRNEIDP 300
361 PRKRVDSPLNLRHGKRRPERKSMELSVTDGGSVPARRAIEMAHQGRSRSISGASSGL 420
301 PRKRVDSPLNLRHGKRRPERKSMELSVTDGGSVPARRAIEMAHQGRSRSISGASSGL 360
421 STSPLSSPRVTPHPSPRGSPPLTPKGTVPVHTPKESPAGTPNPPTSPSPSVGGVPMWRARLN 480
361 STSPLSSPRVTPHPSPRGSPPLTPKGTVPVHTPKESPAGTPNPPTSPSPSVGGVPMWRARLN 420
481 SIKNSFLGSPRHRKLOVPTPEEMNLTPESPPELAKKSWFNGFISLEKEQIFVVIKD 540
421 SIKNSFLGSPRHRKLOVPTPEEMNLTPESPPELAKKSWFNGFISLEKEQIFVVIKD 480
541 KPLSSIKADIVHAFLSIPSLSHSVISQTSFRABYKATGGPAVFQKPKFQVDITYTEGGE 600
481 KPLSSIKADIVHAFLSIPSLSHSVISQTSFRABYKATGGPAVFQKPKFQVDITYTEGGE 540
601 AQKNGIYSVTFTLLSGPSRRFRKRVVETIIQAQLLSTHDPAAQHLSDTTNCMEMMTGRLS 660
541 AQKNGIYSVTFTLLSGPSRRFRKRVVETIIQAQLLSTHDPAAQHLSDTTNCMEMMTGRLS 600
661 KCGIIPKS 668
601 KCGIIPKS 608
RESULT 6
ID ABG72383 standard; Protein; 585 AA.
XX AC ABG72383;
XX DT 10-FEB-2003 (first entry)
XX DE Human serine protein kinase KSE336-2.
XX KW Human; enzyme; chromosome 11p15.5-pter; astrocytoma; meningioma;
KW pancreatic adenocarcinoma; insulin-dependent diabetes mellitus 2;
KW helicoid peripapillary chorioretinal degeneration; brain; pancreas;
KW Beckwith-Wiedemann syndrome; congenital hyperinsulinism; KSE336.
XX OS Homo sapiens.
XX PN US6455292-B1.
XX PD 24-SEP-2002.
XX PF 16-AUG-2001; 2001US-0930181.
XX PR 16-AUG-2001; 2001US-0930181.
XX PA (ORIG-) ORIGENE TECHNOLOGIES INC.
XX PI Shu Y, Fan W, Kovacs KF, Zidanic M, Jay G;

DR WPI: 2003-066233/06.
DR N-PSDB; ABX13584.
XX New isolated polynucleotide coding without interruption for a human
PT KSE336 polypeptide useful for preventing or treating
PT diseases/conditions relating to brain and pancreas, e.g. meningioma,
PT insulin-dependent diabetes mellitus 2
XX
PS Claim 1; Fig 2; 34pp; English.
XX
CC The invention relates to an isolated polynucleotide (its complement
CC or a sequence 99% similar to it) coding without interruption for a human
CC KSE336 polypeptide, a serine protein kinase, comprising the KSE336-1 and
CC KSE336-2 splice variants appearing as ABG72382 and ABG72383. Also
CC included is a method of identifying an agent that modulates the
CC expression of KSE336 in brain, pancreas, brain progenitor or pancreas
CC progenitor cells comprising: (a) contacting a cell population comprising
CC the cells with a test agent under conditions effective for the test agent
CC to modulate the expression of KSE336; and (b) determining if the test
CC agent modulates the expression of KSE336. The polynucleotides are useful
CC as molecular targets of drug targets, and for detecting, diagnosing,
CC staging, monitoring, prognosticating, preventing or treating diseases or
CC conditions relating to brain and pancreas, such as astrocytoma,
CC meningioma, pancreatic adenocarcinoma, insulin-dependent diabetes
CC mellitus 2, heliocoid peripapillary chorioretinal degeneration, Beckwith-
CC Wiedemann syndrome or congenital hyperinsulinism. The method and
CC polynucleotides are useful in research, diagnosis, drug discovery,
CC therapy, clinical medicine, forensic science and pathology.
CC The gene for KSE336 is located on chromosome 1p15.5-pter.
CC The present sequence represents the KSE366 variant KSE366-2.
XX
SQ Sequence 585 AA;

Query Match 86.6%; Score 3028; DB 24; Length 585;
Best Local Similarity 100.0%; Pred. No. 5.6e-215;
Matches 577; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 92 YLVLEHVSGLGELFDYLVKGRTPKARKEFRQIISALDFCHSHSICHRDLKPENLLDE 151
DB 9 YLVLEHVSGLGELFDYLVKGRTPKARKEFRQIISALDFCHSHSICHRDLKPENLLDE 68

QY 152 KNNIRIADFGWASIQVDSLETSCGSPHYACPEVIRGEKYDGRKADVWSCGVILFALLV 211
DB 69 KNNIRIADFGWASIQVDSLETSCGSPHYACPEVIRGEKYDGRKADVWSCGVILFALLV 128

QY 212 GALPDDDDNLRQLLEKVRGVFHPHPIPPDCQSLRGMIEVDAAARELTLEHIQKHIWYI 271
DB 129 GALPDDDDNLRQLLEKVRGVFHPHPIPPDCQSLRGMIEVDAAARELTLEHIQKHIWYI 188

QY 272 GGNKEPEPEQIPKRVQIRSLPSLEDDDPVLDSDMSHSLGCFRDRNKLQDLLSEENQEK 331
DB 189 GGNKEPEPEQIPKRVQIRSLPSLEDDDPVLDSDMSHSLGCFRDRNKLQDLLSEENQEK 248

QY 332 MIYFLLDRKERYPSQDEDLPPRNEIDPPRKRVDSPMLNRHGKRRPERKSMVLSVTDG 391
DB 249 MIYFLLDRKERYPSQDEDLPPRNEIDPPRKRVDSPMLNRHGKRRPERKSMVLSVTDG 308

QY 392 GSPVPARRATEMAHQGORSISGASGLSTSPSSPRVTPHPSRGSPLTPKGTVPVHT 451
DB 309 GSPVPARRATEMAHQGORSISGASGLSTSPSSPRVTPHPSRGSPLTPKGTVPVHT 368

QY 452 PKESPAGTNPPTPSSVGVVPRARLNSIKNSFLGSPFRHRKLOVPTPEEMSNLTPE 511
DB 369 PKESPAGTNPPTPSSVGVVPRARLNSIKNSFLGSPFRHRKLOVPTPEEMSNLTPE 428

QY 512 SSPELAKSWFGNFISLEKEQIFVWIKOKPLPSIKADIVHAFISPSLSHSVTSQTSFR 571
DB 429 SSPELAKSWFGNFISLEKEQIFVWIKOKPLPSIKADIVHAFISPSLSHSVTSQTSFR 488

QY 572 AYEYKATGCPAVFQKPVKFOVDITTEGEAQKENGIVSVTFTLLSGSPRRPRKRVETIOA 631
DB 489 AYEYKATGCPAVFQKPVKFOVDITTEGEAQKENGIVSVTFTLLSGSPRRPRKRVETIOA 548

QY 632 QLLSTHDPAPAAQHLSDDTTNCMEMMTGRLSKCGIIPKS 668
DB 549 QLLSTHDPAPAAQHLSDDTTNCMEMMTGRLSKCGIIPKS 585

RESULT 7
ID ABB98743
XX ABB98743 standard; Protein; 778 AA.
AC ABB98743;
XX
XX 20-JAN-2003 (first entry)
DT Human kinase #1.
DE Human kinase #1.
XX Human; kinase; chromosome 19.
XX Homo sapiens.
OS
XX WO200281670-A1.
PN
PD 17-OCT-2002.
XX
XX 04-APR-2002; 2002WO-US10786.
PF
PR 06-APR-2001; 2001US-282036P.
XX (LEXI-) LEXICON GENETICS INC.
PA
XX Turner CA, Mathur B, Friddle CJ;
PI
XX WPI: 2003-058538/05.
DR N-PSDB; ABV74557.
XX
PT New human kinase proteins useful for diagnosis, drug screening, and
PT clinical trial monitoring, treatment of disorders and diseases, and
PT cosmetic and nutritional applications
XX
PS Claim 5; Page 40-41; 47pp; English.
XX
CC The present sequence is a novel human kinase. The genomic locus encoding
CC the kinase is thought to be on human chromosome 19. The kinase and its
CC coding sequence are useful for diagnosis, drug screening, clinical trial
CC monitoring, treatment of disorders and diseases, and cosmetic and
CC nutritional applications.
XX
SQ Sequence 778 AA;

Query Match 80.0%; Score 2799; DB 24; Length 778;
Best Local Similarity 75.1%; Pred. No. 6.5e-198;
Matches 548; Conservative 54; Mismatches 48; Indels 80; Gaps 8;

QY 1 MISTGKDGGA-----QHAQVGPYRLEKTLGKGTGLVKGVLVHCITGQKV 45
DB 1 MMSGAGEGGGSPAYLPHPHPPHQAQVGPYRLEKTLGKGTGLVKGVLVHCITGQKV 60

QY 46 AIKIVNREKLSVLMKVERETAILKLEHPPHVLKLDVYENKYLVLVLEHVSGLGELFD 105
DB 61 AIKIVNREKLSVLMKVERETAILKLEHPPHVLKLDVYENKYLVLVLEHVSGLGELFD 120

QY 106 YLVKGRTPKARKEFRQIISALDFCHSHSICHRDLKPENLLDKNNIRIADFGWASL 165
DB 121 YLVKGRTPKARKEFRQIISALDFCHSHSICHRDLKPENLLDKNNIRIADFGWASL 180

QY 166 QVGDLSLETSCGSPHYACPEVIRGEKYDGRKADVWSCGVILFALLVGLPDDNLRQLL 225
DB 181 QVGDLSLETSCGSPHYACPEVIRGEKYDGRKADVWSCGVILFALLVGLPDDNLRQLL 240

QY 226 EKVRGVFHPHPIPPDCQSLRGMIEVDAAARELTLEHIQKHIWYIGKNEPEP-EQIP 284
DB 241 EKVRGVFHPHPIPPDCQSLRGMIEVDAAARELTLEHIQKHIWYIGKNEPEP-EQIP 300

QY 285 -RKVQIRSLPSLEDDDPVLDSDMSHSLGCFRDRNKLQDLLSEENQEKMIYFLLDRKER 343

Db 301 GRVAMRLSPNGELDPDVLSEMASLGCFRDRRLHRLSEENQEKMIYVLLDRKER 360
 QY 344 YPSQDEDLPPNETDPRKRVDSPLNHRGKRRPERKSMVLSVTD---CGSPVPARRA 400
 Db 361 YPSCEDQDLPPNDVDPKRVDSPLNHRGKRRPERKSMVLSITDAGGGGSPVPTERRA 420
 QY 401 IEMAQHGQRSRISGASSGLSTSPSSPR----- 429
 Db 421 LEMAHQSQRSRVSGASTGLSSPLSSPRSPVFSFSPGAGDEARGGSPSTKTQTLPS 480
 QY 430 -----VTPHPSRGSPLPTPKG-----TPVHTPKESPAGTNPPTPPSP 468
 Db 481 RGRGGGAGEQPPPSARSSTPLPGPPGPRSSGGTPLHSPHTPRASPTGTPPTPPSP 540
 QY 469 --SVGVPWRARLNSIKNSFLGSPFRHKLQVPTPEMSNLTPESSPELAKSWFGNFI 526
 Db 541 GGGVGAARSLNSIRNSFLGSPFRHKLQVPTPEMSNLTPESSPELAKSWFGNFI 600
 QY 527 SLEKEEQIFVVIKDKPLSSIKADIHAFSLIPSLSHSVISQTSFRAEYKATGCPAVFOKP 586
 Db 601 SLDKEEQIFVVIKDKPLSSIKADIHAFSLIPSLSHSVISQTSFRAEYKATGCPAVFOKP 660
 QY 587 VKFQVDITVTEGEQAQKE-----NGIYSVTFLLSGPSRRRFRKRVVETIQALLSTHDP 640
 Db 661 VRFQVDISSEGPEPSRRDGGGGGIYSVTFLLSGPSRRRFRKRVVETIQALLSTHDP 720
 QY 641 AAQHLSDDTN 650
 Db 721 SVQALADEKN 730

RESULT 8
 AAU03517
 ID AAU03517 standard; Protein; 794 AA.
 AC AAU03517;
 XX

DT 12-SEP-2001 (first entry)
 DE Human protein kinase #17.
 XX Human; protein kinase; PTK; STK; cancer; cardiovascular disease;
 KW metabolic disorder; immune related disease; neurological disorder;
 KW neurodegenerative disorder; inflammatory disorder; infectious disease;
 KW reproductive disorder.

XX Homo sapiens.
 OS
 FN WO200138503-A2.
 PD
 PD 31-MAY-2001.

PF 22-NOV-2000; 2000WO-US32085.

XX 24-NOV-1999; 99US-0167482.

XX (SUCG-) SUGEN INC.

PI Plowman GD, Whyte D, Manning G, Sudarsanam S, Martinez R;
 PI Flanagan P, Clary D;
 XX

DR WPI; 2001-343950/36.
 DR N-PSDB; AAS06717.

XX Nucleic acids encoding human kinase polypeptides, useful for preventing
 PT diagnosing and/or treating e.g. cancer, immune, cardiovascular and
 PT neuronal-associated diseases, and microbial infections -

XX Claim 7; Figure 2; 433pp; English.

XX AAU03501-AAU03557 represent novel human protein kinases #1-57. The
 CC novel protein kinases have been identified as members of the tyrosine

CC or serine/threonine kinase (PTK and STK) families. The polynucleotides
 CC encoding protein kinases and the polypeptides may be used in the
 CC prevention, diagnosis and treatment of diseases associated with
 CC cancers (especially cancers of haematopoietic origin), cardiovascular
 CC disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes),
 CC immune related diseases (e.g. rheumatoid arthritis), neurological
 CC disorders (e.g. schizophrenia), neurodegenerative disorders (e.g.
 CC Parkinson's disease), inflammatory disorders (e.g. asthma), infectious
 CC disease (e.g. HIV) and reproductive disorders (e.g. infertility).
 CC Additionally, polynucleotides encoding protein kinases may be
 CC used for gene therapy and as DNA probes in diagnostic assays.
 CC The protein kinase polypeptides may be used as antigens in the production
 CC of antibodies against the protein kinases and in assays to identify
 CC modulators of protein kinase expression and activity.

XX Sequence 794 AA;

Query Match 79.7%; Score 2785.5; DB 22; Length 794;
 Best Local Similarity 76.9%; Pred. No. 6.7e-197;
 Matches 542; Conservative 53; Mismatches 45; Indels 65; Gaps 7;
 QY 11 QHAYVGYRLEKTLGKQTLGVLKGVHCVTCQKVAIKIVNREKLSBVLKMKVEREAIL 70
 Db 42 RHAQYVGYRLEKTLGKQTLGVLKGVHCVTCQKVAIKIVNREKLSBVLKMKVEREAIL 101
 QY 71 KLIHHPHVLKLDVYENKYLVLVLEHVSGLGELFDYLVKKGRLTPKARKFROIISALD 130
 Db 102 KLIHHPHVLKLDVYENKYLVLVLEHVSGLGELFDYLVKKGRLTPKARKFROIISALD 161
 QY 131 FCHSHSICHRDLKPENLLDEKNNIRIADFGMASLQVGDLSLETSCGSPHYACPEVIRGE 190
 Db 162 FCHSYISICHRDLKPENLLDEKNNIRIADFGMASLQVGDLSLETSCGSPHYACPEVIRGE 221
 QY 191 KYDGRKADWMSGCVILFALLVIGALPDDNMLRQLLEKVKGVGFHMFHIPPDCQSLRGM 250
 Db 222 KYDGRADWMSGCVILFALLVIGALPDDNMLRQLLEKVKGVGFHMFHIPPDCQSLRGM 281
 QY 251 IEVDAARRLTLEHTQKHIWYIGKNEPEP-EQTPP-RKQVIRSLPSLEDIDPDVLDMSHS 308
 Db 282 IEVEPERKLSLEQIQKHPWYIGGKHEPDCLEPAGRRVAMRSLPSNGELDPDVLSENAS 341
 QY 309 LGCFRDRNKLIDLLSEENQEKMIYVLLDRKERYPSQEDDLPFRNEIDPPKRVDS 368
 Db 342 LGCFRDRERLHRLSEENQEKMIYVLLDRKERYPSCEDQDLPPNDVDPKRVDS 401
 QY 369 MLNRHGKRRPERKSMVLSVTD---GGSPVPARRAEMAQHGQRSRISGASSGLSTSP 425
 Db 402 MLSRHGKRRPERKSMVLSITDAGGGSPVPTRRALEMAQHGQRSRISGASTGLSSPL 461
 QY 426 SSPP-----VTPHPSRGSPLPTP 444
 Db 462 SSPPSPVFSFSPGAGDEARGGSPSTKTQTLPSRGRGGGAGEQPPPSARSSTPTLPG 521
 QY 445 KG-----TPVHTPKESPAGTNPPTPPSP--SVGVPWRARLNSIKNSFLGSP 491
 Db 522 PGSPRSSGGTPLHSPHTPRASPTGTPPTPPSPGCVGGAARSLNSIRNSFLGSP 581
 QY 492 FHRRLQVPTPEMSNLTPESSPELAKSWFGNFIISLEKEEQIFVVIKDKPLSIKADIV 551
 Db 582 FHRKMQVPTAEENSLTPESSPELAKSWFGNFIISLDKEEQIFVVIKDKPLSIKADIV 641
 QY 552 HAFSLIPSLSHSVISQTSFRAEYKATGCPAVFOKPVKFOVDITVTEGEQAQKE-----N 605
 Db 642 HAFSLIPSLSHSVISQTSFRAEYKATGCPAVFOKPVKFOVDITVTEGEQAQKE-----N 701
 QY 606 GIYSVTFLLSGPSRRRFRKRVVETIQALLSTHDPAAQHLSDDTN 850
 Db 702 GIYSVTFLLSGPSRRRFRKRVVETIQALLSTHDPAAQHLSDDTN 850

RESULT 9
 AAU16271

ID AAE16271 standard; Protein; 794 AA.
 AC AAE16271;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Human kinase PKIN-17 protein.
 XX
 KW Human; kinase; PKIN-17; cancer; leukaemia; adenocarcinoma; osteoporosis;
 KW immune disorder; atherosclerosis; Crohn's disease; Hodgkin's disease;
 KW Acquired Immune Deficiency Syndrome; AIDS; Addison's disease; anaemia;
 KW allergy; asthma; adult respiratory distress syndrome; multiple sclerosis;
 KW autoimmune thyroiditis; bronchitis; diabetes mellitus; osteoarthritis;
 KW Good pasture's syndrome; Graves' disease; pancreatitis; psoriasis;
 KW rheumatoid arthritis; ulcerative colitis; cirrhosis; Cushing's syndrome;
 KW hepatitis; hypothyroidism; cerebral palsy; cataract; angina pectoris;
 KW cardiovascular disease; hypertension; vasculitis; myocarditis; obesity;
 KW congestive heart failure; ischaemic heart disease; lung tumour; gout;
 KW fatty liver; Niemann-Pick's disease; gene therapy.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 50..301
 FT Domain /note= "Eukaryotic protein kinase domain"
 FT Domain 51..292
 FT Domain /label= Protein_kinase_domain
 FT Domain 52..292
 FT Domain /label= Protein_kinase_domain
 FT Domain 71..292
 FT Domain /label= Protein_kinase_domain
 XX
 WO200196547-A2.
 XX
 PD 20-DEC-2001.
 XX
 PF 14-JUN-2001; 2001WO-US19444.
 XX
 PR 15-JUN-2000; 2000US-212073P.
 PR 23-JUN-2000; 2000US-213467P.
 PR 30-JUN-2000; 2000US-215651P.
 PR 07-JUL-2000; 2000US-216805P.
 PR 13-JUL-2000; 2000US-218372P.
 PR 25-AUG-2000; 2000US-228056P.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX
 PI Yue H, Lal P, Bandman O, Borowsky ML, Au-Young J, Lu Y;
 PI Gandhi AR, Tribouley CM, Walia NK, Yao MG, Lu DAM, Greenwald SR;
 PI Ramkumar J, Griffin JA, Kearney L, Burford N, Nguyen DB, Tang YT;
 PI Baughn MR, He A, Thornton M, Hafalia A, Patterson C, Gururajan R;
 PI Lo TP, Khan F, Recipon SA, Azimzai Y, Policky JL, Ding L;
 PI Grether M, Elliott VS, Thangavelu K, Batra S, Ison CH;
 XX
 DR WPI; 2002-090207/12.
 DR N-PSDB; AAD26464.
 XX
 PT New polypeptides, useful for diagnosing, treating or preventing
 PT disorders of growth and development, cardiovascular and lipid, and
 PT diseases such as cancer, comprise human kinase polypeptides -
 XX
 PS Claim 1; Page 159-161; 197pp; English.
 XX
 CC The invention relates to human kinase PKIN proteins and their
 CC corresponding cDNAs. A composition containing PKIN agonist is useful for
 CC treating a disease or condition associated with decreased expression of
 CC PKIN and a composition comprising PKIN antagonist is useful for treating
 CC a disease or condition associated with overexpression of PKIN. The
 CC disorders include cancer (leukaemia, adenocarcinoma, lymphoma, melanoma,
 CC myeloma, sarcoma, teratocarcinoma, Hodgkin's disease); immune disorder
 CC (Acquired Immune Deficiency Syndrome (AIDS), asthma, Addison's disease,
 CC atherosclerosis, anaemia, allergies, adult respiratory distress syndrome,
 CC autoimmune thyroiditis, gout, bronchitis, Crohn's disease, diabetes

CC mellitus, multiple sclerosis, Good pasture's syndrome, Graves' disease,
 CC osteoarthritis, osteoporosis, pancreatitis, psoriasis, Reiter's syndrome,
 CC rheumatoid arthritis, Sjogren's syndrome, uveitis, ulcerative colitis,
 CC bacterial, parasitic, fungal, viral, protozoal and helminthic infections)
 CC growth and development disorders (arteriosclerosis, cirrhosis, hepatitis,
 CC Cushing's syndrome, hypothyroidism, cerebral palsy, vasculitis;
 CC vascular disease (arteriovenous fistula, hypertension, myocarditis,
 CC aneurysms, congestive heart failure, angina pectoris, myocardiitis,
 CC ischaemic heart disease, chronic bronchitis, lung tumours); lipid
 CC disorder (fatty liver, Fabry's disease, Niemann-Pick's disease,
 CC hypocholeraemia, obesity). PKIN DNA is useful for assessing
 CC toxicity of a test compound and in gene therapy. The present sequence
 CC is human PKIN-17 protein.
 XX
 SQ Sequence 794 AA;
 Query Match 79.7%; Score 2785.5; DB 23; Length 794;
 Best Local Similarity 76.9%; Pred. No. 6.7e-197;
 Matches 542; Conservative 53; Mismatches 45; Indels 65; Gaps 7;
 QY 11 QHAQYVGPYRLEKTLGKGTGLVKGVCVTQKVAIKIVNREKLSVLMKVERIAIL 70
 DB 42 RHAQYVGPYRLEKTLGKGTGLVKGVCITGQKVAIKIVNREKLSVLMKVERIAIL 101
 QY 71 KLIEHPHVLKLDVYENKKYLYLVLEHVS GGELFDYLVKKGR LTPKEARKPFRQIISALD 130
 DB 102 KLIEHPHVLKLDVYENKKYLYLVLEHVS GGELFDYLVKKGR LTPKEARKPFRQIISALD 161
 QY 131 FCHSHSICHRLDKPENLLDDEKNIRIADFGWASLOVGSLLTSCGSHYACPEVIRGE 190
 DB 162 FCHSYISICHRLDKPENLLDDEKNIRIADFGWASLOVGSLLTSCGSHYACPEVIRGE 221
 QY 191 KYDGRKADVMSCGVILFALLVGA LPPDDNRLLEKVKRGVFMHPHFIPPCQSLRGM 250
 DB 222 KYDGRADVMSCGVILFALLVGA LPPDDNRLLEKVKRGVFMHPHFIPPCQSLRGM 281
 QY 251 IEVDAARLTLEHIQKHWIYGKNEPEP-EQIP-RKVQIRSLPLEDIDPPVLSMHS 308
 DB 282 IEVEPEKRLSLEIQIKHPWYLGKHEPDPCLPEAPGRRVAMRSLPNSGELDPDVLSEMAS 341
 QY 309 LGCFDRNKLQDLLSEENQERMIYFLLLDRKERYPSQDEDLPPRNEIDPPKRVDS 368
 DB 342 LGCFDRERLHRELSEENQERMIYFLLLDRKERYPSQDEDLPPRNDVDPKRVDS 401
 QY 369 MLNRHGKRRPERKSMELVSVTD---CGSPVPARRAIEAQAQGRSRSISGASGLTSPL 425
 DB 402 MLSRHGKRRPERKSMELVSVTDAGGGSPVPTTRALEMAQHSQSRSVSGASTGLSSPL 461
 QY 426 SSPR-----VTPHPSPRGSPLPTP 444
 DB 462 SSPRSPVFSFSPFGAGDEARGGSGTSKTQTLPSRPGGGGAGEQPPPSARSTPLPGP 521
 QY 445 KG-----TPVHTPKESPAGTNPPTPPSSP--SVGGVPWRARLNSIKNSFLGSPR 491
 DB 522 PGSPRSSGGTPLHSP LHTPRASPTGTPPTPPSPGGVGGAAWRKLNIRNSFLGSPR 581
 QY 492 FHRKLVQPTPEEMSNLTPESSPELAKSWFGNFISLEKEEIFVWIKDKLSIKADIV 551
 DB 582 FHRKLVQPTAEEMSNLTPESSPELAKSWFGNFISLDEKEIFLVLDKFLSIKADIV 641
 QY 552 HAFSLSPSLSHSVISQTSFRAEYKATGCPAVFOKPVKFQVDITYTTEGGAQKE-----N 605
 DB 642 HAFSLSPSLSHSVISQTSFRAEYKATGCPAVFOKPVKFQVDITYTTEGGAQKE-----N 701
 QY 606 GIYSVTFTLLSGSPRRPKRVVETIQALLSTHDPAPAAQHLSDTTN 650
 DB 702 GIYSVTFTLLSGSPRRPKRVVETIQALLSTHDPAPAAQHLSDTTN 746
 RESULT 10
 AAO16604
 ID AAO16604 standard; protein; 754 AA.
 XX

AC AAO1604;
XX 08-MAY-2003 (first entry)
XX Human cell cycle-regulatory factor Cdr2.
XX Human; cell cycle-regulatory factor; Cdr2; kinase; proliferative disease;
KW anticancer agent; wound-healing drug.
XX Homo sapiens.
XX WO200299110-A1.
XX 12-DEC-2002.
XX 03-JUN-2002; 2002WO-JP05411.
XX 04-JUN-2001; 2001JP-0168792.
XX (TAIH) TAIHO PHARM CO LTD.
XX (NAKA/) NAKANISHI M.
XX Nakanishi M;
XX WPI; 2003-156857/15.
XX N-PSDB; AAL51889.
XX Cell cycle-regulatory factor Cdr2 with kinase activity and encoded
PT gene, applicable in diagnosis of and screening drugs for proliferative
PT diseases e.g. anticancer agents and wound-healing drugs -
XX Claim 1; Fig 2 A-C; 63pp; Japanese.
XX The invention comprises the amino acid and coding sequence of the human
CC cell cycle-regulatory factor Cdr2 (with kinase activity). The DNA and
CC protein sequences of the invention are useful in diagnosing and screening
CC drugs for proliferative diseases (e.g. anticancer agents and wound-
CC healing drugs). The present amino acid sequence represents the human cell
CC cycle-regulatory factor Cdr2 protein.
XX Sequence 754 AA;
Query Match 79.2%; Score 2768; DB 24; Length 754;
Best Local Similarity 78.9%; Pred. No. 1.2e-195;
Matches 537; Conservative 52; Mismatches 51; Indels 41; Gaps 8;
QY 11 QHAYVGPYRLKLETKGQOTGLVGLGVHCVTCOKVAIKIVNREKLSVLMKVERETAIL 70
DB 26 QHAYVGPYRLKLETKGQOTGLVGLGVHCVTCOKVAIKIVNREKLSVLMKVERETAIL 85
QY 71 KLIHHPVHLKLDVYENKYYLYLVLEHVS GGGELFDYLVKKGRLTPKEARKPFROIISALD 130
DB 86 KLIHHPVHLKLDVYENKYYLYLVLEHVS GGGELFDYLVKKGRLTPKEARKPFROIIVCAG 145
QY 131 FCHSHSICHRDLKPNLLLDKNNIRIADFQVWASLQVGSLLLETSCGSPHYACPEVIRGE 190
DB 146 LCHSYISICHRDLKPNLLLDKNNIRIADFQVWASLQVGSLLLETSCGSPHYACPEVIKGE 205
QY 191 KYDGRKADVWCGVITFALLVGLPFDNDNLRLLEKVKRGVFMHPHPIPDCCSLLRGM 250
DB 206 KYDGRADWCGVITFALLVGLPFDNDNLRLLEKVKRGVFMHPHPIPDCCSLLRGM 265
QY 251 IEVDAARLTLEHIOKHWIYGGKNEPEP-EQIP-RKVQIRSLPSLEDDIPDVLDSMHS 308
DB 266 IEVEPEKLSLEQIKHPYILGGKHEPFCLEPAPGRVAMRSLPSNGELDPDVLDSWAS 325
QY 309 LGCFDRNKLLODLLSEENQKMYIFLLDRKERYPSQEDLPPRNEIDPPRKRVDSP 368
DB 326 LGCFDRERLRELSEENQKMYIFLLDRKERYPSQEDLPPRNDVPPRKRVDSP 385
QY 369 MLNRHGKRPKRKSNVLSVTD--CGSPVAPARRAEMAQHQRSRISGASSGLSTSP 425
DB 386 MLSRHGKRPKRKSNVLSITDAGGGGSPVPTRRALEMAQHQRSRISVSGASTGLSSSP 445

QY 426 SSPP-----VTPH-----PSRGSPLP-----TPKGPVHTPKESPA 457
DB 446 SSPPSPVFSFSPGAGDEARGGSGTSTKTQTLPGPPGSPRSGGTPLHSPHTPRASPT 505
QY 458 GTNPPTPPSP--SVGGVWRLNLSIKNSFLGSPRHRRLKQVPTPEMSNLTPESSPE 515
DB 506 GTPGTTTPPSPGCGVGAARSLNIRNSFLGSPRHRRLKQVPTPEMSNLTPESSPE 565
QY 516 LAKKSWFGNFIKKEEQIFWIKDKPLSSIKADIVHAFISPSLSHVSISQTSFRAEYK 575
DB 566 LAKKSWFGNFIKKEEQIFWIKDKPLSSIKADIVHAFISPSLSHVSISQTSFRAEYK 625
QY 576 ATGGPAVFOKPVKQVDITVTEGGEAQKE-----NGIYSVTFTLLSGPGRFRKRVVETI 629
DB 626 ASGGPSVFOKPVKQVDITVTEGGEAQKE-----NGIYSVTFTLLSGPGRFRKRVVETI 685
QY 630 QAQLLSTHDPAAQHLSDTTN 650
DB 686 QAQLLSTHDPQSVQALADEKN 706

RESULT 11

ABB98745
ID ABB98745 standard; Protein; 703 AA.

XX AC ABB98745;

XX DT 20-JAN-2003 (first entry)

XX DE Human kinase #3.

XX KW Human; kinase; chromosome 19.

XX OS Homo sapiens.

XX PN WO200281670-A1.

XX PD 17-OCT-2002.

XX PF 04-APR-2002; 2002WO-US10786.

XX PR 06-APR-2001; 2001US-282036P.

XX PA (LEXI-) LEXICON GENETICS INC.

XX PI Turner CA, Mathur B, Friddle CJ;

XX DR WPI; 2003-058538/05.

XX DR N-PSDB; ABV74559.

XX PT New human kinase proteins useful for diagnosis, drug screening, and
PT clinical trial monitoring, treatment of disorders and diseases, and
PT cosmetic and nutritional applications -

XX PS Claim 5; Page 44-46; 47pp; English.

XX CC The present sequence is a novel human kinase. The genomic locus encoding
CC the kinase is thought to be on human chromosome 19. The kinase and its
CC coding sequence are useful for diagnosis, drug screening, clinical trial
CC monitoring, treatment of disorders and diseases, and cosmetic and
CC nutritional applications.

XX SQ Sequence 703 AA;

Query Match 72.8%; Score 2545.5; DB 24; Length 703;

Best Local Similarity 75.6%; Pred. No. 3e-179;

Matches 495; Conservative 51; Mismatches 44; Indels 65; Gaps 7;

QY 61 MKVERETAILKLIHHPVHLKLDVYENKYYLYLVLEHVS GGGELFDYLVKKGRLTPKEARK 120

DB 1 MKVERETAILKLIHHPVHLKLDVYENKYYLYLVLEHVS GGGELFDYLVKKGRLTPKEARK 60

OS Drosophila melanogaster.

PN WO200171042-A2.

XX 27-SEP-2001.

PD 23-MAR-2001; 2001WO-US09231.

XX 23-MAR-2000; 2000US-191637P.

PR 11-JUL-2000; 2000US-0614150.

XX (PEKE) PE CORP NY.

XX Venter JC, Adams M, Li PWD, Myers EW;

PI WPI; 2001-656860/75.

XX N-PSDB; ABL06164.

XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -

XX Disclosure; SEQ ID NO 12975; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (AB16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (ABB57737-ABB72072).

CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 851 AA;

Query Match 56.4%; Score 1974; DB 22; Length 851;
Best Local Similarity 54.7%; Pred. No. 5.9e-137;
Matches 424; Conservative 85; Mismatches 134; Indels 132; Gaps 20;

QY 10 AQAQYGVGYRLEKTLGKQGTGLVKLGVCVTCQKVAIKIVNREKLSVLMKVEREIAI 69

DB 9 AENCQFVGYRLEKTLGKQGTGLVKLGVCVTCQKVAIKIVNREKLSVLMKVEREIAI 68

QY 70 LKLIHSHVILKHDYENKYLVLVLEHVSGELFDYLVKKGRITPKARKFQQIISAL 129

DB 69 MKLIDHSHVILKHDYENKYLVLVLEHVSGELFDYLVKKGRITPKARKFQQIISAL 128

QY 130 DFCHSHSICHRLDKPENLLDKNNIRIADFGMASLQVDSLETSCGSPHYACPEVIRG 189

DB 129 DFCHSHSICHRLDKPENLLDKNNIKIADFGMASLQVDSLETSCGSPHYACPEVIRG 188

QY 190 EKYDGRKADVWSCGVLVALLVGLPFDNRLQLLEKVRGVFHPHFIPDQCQLRG 249

DB 189 EKYDGRKADVWSCGVLVALLVGLPFDNRLQLLEKVRGVFHPHFIPDQCQLRG 248

QY 250 MIEVDAAARLLTLEHIQHIWY-IGGKNEPEPEQIPKRVQIRSLPSLEDIPDVLDSMHS 308

DB 249 MIEVNPORRLTLEINHPWVTAGGGELELEPMVEVQTHVPTATAVDPDVNAICS 308

QY 309 LGCFRDRNKLQDLLSEBENCKMYIFLLDRKERYPSQDEED--LPPRNE---IDPPR 362

DB 309 LGCFEKEKLIQELLSSHNTEKVIYFLLERKRRPALEDDDDIAKSRSELDVADPPR 368

QY 363 KRVDSPMLN-----RHGKRPERKSEMEVLVSVD 390

DB 369 KRLDTCRINGTNAPYQGISSEGPLTPRQAFNFRSYSTRNHQRRPTTIVTSVRS--SS 427

QY 391 GGSVPARRALEMAQ-----HGQSRISIGASGLSTSPSS--- 427

DB 428 YHSFTRCNPSMSSAQQAANAIKSRPSPAAGTRHSTYGRDR--SCHHSVSRTSPSHSQK 485

QY 428 -----PRVTPHSPR-----GSP-----LPTPKGTP-----VHTPX 453
DB 486 SIEGDVVVREPRIERRDSLQERGGSGPRDGCIPPGSPGSGNSGTSASPSVHHRA 545
QY 454 ES-----PAGTP-----NPTPPSSP--SVGGVPMRRLNSIKNSFLGSPFRHRRKL 497
DB 546 NSGPTTIIIVNPNNGSPMNNSSPGMFGSPCNTPGGQMKTLTNIKNSFLGSPFRHRRKM 605
QY 498 QVTPPEMSNLTPESSPELAKSWFNGFNISLEKEQIFVVIKPKLSSIIKADIVHAPLSI 557
DB 606 QVSADE--VHLTPESSPELTKRSWFNGFNITTEDEFTTILVKGKIATVKAHLIHAFLSM 663
QY 558 PSLSHVISQTSFRAEYKATG-GPAVFQKPVKQVDIT--YTEGGEAQKENGIVSVTFTL 614
DB 664 AELSHSVVSTPSFVRYKRNNGNPFVNFQRHVKQVDLSAICKQGDADM--FALFTFTL 720
QY 615 LSGSPRRFRKRVETIIQAALLSTH-----DPP-----AAQHLSDTTNCMEMMTGRIS 660
DB 721 LSGNIRFRICEHIQSVCKSRFGPGSPPTVTSVQAVSESSCGSVSSERLS 775

RESULT 14

ABBI1052

XX ID ABB11052 standard; peptide; 301 AA.

AC ABB11052;

XX 11-JAN-2002 (first entry)

DE Human HrPOPK-1 homologue, SEQ ID NO:1422.

XX Human; cytokine; cell proliferation; cell differentiation; growth factor;
KW haematopoiesis regulation; tissue growth; immunomodulator; activin;
KW inhibin; chemotaxis; chemokinesis; thrombolytic; oncogenesis;
KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
KW chronic inflammatory condition; proliferative retinopathy;
KW atherosclerosis; coronary heart disease; arterial ischaemia;
KW bone disorder; osteoporosis; vascular growth disorder;
KW tissue regeneration; wound healing; infection; immune disorder;
KW cell culture; drug screening; gene therapy; antiinflammatory;
KW antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
KW cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
KW antifungal; vulnetary; antiulcer.

XX Homo sapiens.

OS WO200157188-A2.

XX 09-AUG-2001.

PD 05-FEB-2001; 2001WO-US03800.

XX 03-FEB-2000; 2000US-0496914.

PR 27-APR-2000; 2000US-0560875.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT;

PI WPI; 2001-457740/49.

XX N-PSDB; ABA08296.

DR Human proteins and DNA encoding sequences useful for preventing,
XX treating or ameliorating a medical condition in a mammalian subject
XX e.g. arthritis and cancer -

PS Claim 20; Page 140; 1963pp; English.

XX Sequences ABB10981-ABB12130 represent 1350 novel human polypeptides, and
CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
CC invention also relates to vectors and recombinant host cells comprising a

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 26, 2003, 11:51:21 ; Search time 35.5987 Seconds
(without alignments)
4842.281 Million cell updates/sec

Title: US-10-054-579-2

Perfect score: 3497

Sequence: 1 MTSTGDKGGAHQAGYGVYPR.....TNCMEMTGRSLKCGIIPKS 668

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3491	99.8	668	Q81WQ3	Q81WQ3 homo sapien
2	3015	86.2	603	O60843	O60843 homo sapien
3	2799	80.0	778	Q8TDC2	Q8TDC2 homo sapien
4	2785.5	79.7	794	Q8TDC3	Q8TDC3 homo sapien
5	2736.5	78.3	768	Q8NDD0	Q8NDD0 homo sapien
6	2599.5	74.3	715	Q8GJL4	Q8GJL4 homo sapien
7	1812.5	51.8	698	O61298	O61298 halocynthia
8	1743	49.8	914	Q19469	Q19469 caenorhabdi
9	1712	49.0	793	Q9VUV4	Q9VUV4 drosophila
10	1439.5	41.2	473	Q96AV4	Q96AV4 homo sapien
11	1248	35.7	701	Q95T82	Q95T82 drosophila
12	870.5	24.9	833	Q8SSX5	Q8SSX5 dictyosteli
13	796.5	22.8	745	Q15524	Q15524 homo sapien
14	796.5	22.8	755	Q96HB3	Q96HB3 homo sapien
15	794.5	22.7	691	Q96RG0	Q96RG0 homo sapien
16	792.5	22.7	722	11	O08679 rattus norv

ALIGNMENTS

RESULT 1

Q81WQ3 ID Q81WQ3 PRELIMINARY; PRT; 668 AA.

AC Q81WQ3; 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Serine/threonine protein kinase isoform.

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain tumor;

RA Guo J.H., Yu L.;

RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY166857; AAN87839.1; -

KW Kinase.

SQ SEQUENCE 668 AA; 74714 MW; 6AF8CB84FC48C07 CRC64;

Query Match 99.8%; Score 3491; DB 4; Length 668;

Best Local Similarity 99.8%; Pred. No. 1.9e-248;

Matches 667; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MTSTGDKGGAHQAGYGVYPRLEKTLGKGTGLVGLVHVSGELFDYLVKGRLLTPKARK 120

Db 1 MTSTGDKGGAHQAGYGVYPRLEKTLGKGTGLVGLVHVSGELFDYLVKGRLLTPKARK 120

Qy 61 MKVERETAILKLEHPHVLKLDVYENKYLVLVLEHVSGELFDYLVKGRLLTPKARK 120

Db 61 MKVERETAILKLEHPHVLKLDVYENKYLVLVLEHVSGELFDYLVKGRLLTPKARK 120

Qy 121 FFRQIISALDFCHSHSICHRLDPENLLDEKKNIRIADFGMASLQVDSLETSCSPH 180

Db 121 FFRQIISALDFCHSHSICHRLDPENLLDEKKNIRIADFGMASLQVDSLETSCSPH 180

Qy 181 YACEVIRGEKYDGRKADVWSCGVILFALLVGLPFDNRLQLLEKVKRGVFMHPFIP 240

Db 181 YACEVIRGEKYDGRKADVWSCGVILFALLVGLPFDNRLQLLEKVKRGVFMHPFIP 240

Qy 181 YACEVIRGEKYDGRKADVWSCGVILFALLVGLPFDNRLQLLEKVKRGVFMHPFIP 240

Db 181 YACEVIRGEKYDGRKADVWSCGVILFALLVGLPFDNRLQLLEKVKRGVFMHPFIP 240

Qy 181 YACEVIRGEKYDGRKADVWSCGVILFALLVGLPFDNRLQLLEKVKRGVFMHPFIP 240

Db 181 YACEVIRGEKYDGRKADVWSCGVILFALLVGLPFDNRLQLLEKVKRGVFMHPFIP 240

Qy 181 YACEVIRGEKYDGRKADVWSCGVILFALLVGLPFDNRLQLLEKVKRGVFMHPFIP 240

Db 181 YACEVIRGEKYDGRKADVWSCGVILFALLVGLPFDNRLQLLEKVKRGVFMHPFIP 240

Qy 181 YACEVIRGEKYDGRKADVWSCGVILFALLVGLPFDNRLQLLEKVKRGVFMHPFIP 240

Db 181 YACEVIRGEKYDGRKADVWSCGVILFALLVGLPFDNRLQLLEKVKRGVFMHPFIP 240

Qy 181 YACEVIRGEKYDGRKADVWSCGVILFALLVGLPFDNRLQLLEKVKRGVFMHPFIP 240

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Db 181 YACPEVIRGEKYDGRKADVMSCGVILFALLVGLALPFDNLLRQLLEKVKRGVPHMPHFIP 240
Qy 241 PDCOSLIRGMIEVDAAARLTLEHQHIWYIGGKNEPEPEQPIPRKVQIRSLPSLEDDIP 300
Db 241 PDCOSLIRGMSEVDAARLTLEHQHIWYIGGKNEPEPEQPIPRKVQIRSLPSLEDDIP 300
Qy 301 DVLDSMHSLSGCFDRNKLQDLSEENQEKMIYFLLDRKERYPSQDEDDLPPENEIDP 360
Db 301 DVLDSMHSLSGCFDRNKLQDLSEENQEKMIYFLLDRKERYPSQDEDDLPPENEIDP 360
Qy 361 PRKRVDSPLNLRHGRKRPERSMEVLVSDTGGSPVPARRAIEAQAQGRSISGASSGL 420
Db 361 PRKRVDSPLNLRHGRKRPERSMEVLVSDTGGSPVPARRAIEAQAQGRSISGASSGL 420
Qy 421 STSPLSSPRVTPHPSRGSLPTPKGTVPVHTPKESPAQTNPPTSPSSVGGVPMRARN 480
Db 421 STSPLSSPRVTPHPSRGSLPTPKGTVPVHTPKESPAQTNPPTSPSSVGGVPMRARN 480
Qy 481 SIKNSFLGSRFRHRRKLQVPTPEMSNLTPESSPELAKKSWFGNFISLEKEEQIFVVIKD 540
Db 481 SIKNSFLGSRFRHRRKLQVPTPEMSNLTPESSPELAKKSWFGNFISLEKEEQIFVVIKD 540
Qy 541 KPLSSIKADIVHAFSLPSLSHVSISQTSFRAEYKATGGPAVQKPVKFOVDITYTEGGE 600
Db 541 KPLSSIKADIVHAFSLPSLSHVSISQTSFRAEYKATGGPAVQKPVKFOVDITYTEGGE 600
Qy 601 AQKENGIVSYVTFTLLSGPSRRFRKRVETIOAQLLSTHDPAAQHLSDTTNCMEWMTCRLS 660
Db 601 AQKENGIVSYVTFTLLSGPSRRFRKRVETIOAQLLSTHDPAAQHLSDTTNCMEWMTCRLS 660
Qy 661 KCGIIPKS 668
Db 661 KCGIIPKS 668

RESULT 2
O60843
ID O60843 PRELIMINARY; PRT; 603 AA.
AC O60843;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Putative serine/threonine protein kinase (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Brain;
RX MEDLINE=21064499; PubMed=11124703;
RA Stanchi F., Bertocco E., Toppo S., Dioguardi R., Simonati B.,
RA Cannata N., Zimbello R., Lanfranchi G., Valle G.;
RT "Characterization of 16 novel human genes showing high similarity to
RT yeast sequences."
RL Yeast 18:69-80(2001).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AJ006701; CAA07196.1; -.
DR HSSP; Q63450; 1A06.
DR Genew; HGNC:11405; STK29.
DR InterPro; IPR000719; Prot_kinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
FT NON_TER
SQ SEQUENCE 603 AA; 67401 MW; B02C5D678F8E96 CRC64;
```

Query Match 86.2%; Score 3015; DB 4; Length 603;
Best Local Similarity 99.7%; Pred. No. 1.8e-213;
Matches 574; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy 72 LLEHSHVLKLDHVENKKVLYLVLEHVSGLGFDYLKKGRLLTPKEARKFFRQIISALDF 131
Db 1 LLEHSHVLKLDHVENKKVLYLVLEHVSGLGFDYLKKGRLLTPKEARKFFRQIISALDF 60
Qy 132 CHSHSICHRLDKPENLLDEKNNIRIADFGMASLQVSDLSLETSCGSHYACPEVIRGEK 191
Db 61 CHSHSICHRLDKPENLLDEKNNIRIADFGMASLQVSDLSLETSCGSHYACPEVIRGEK 120
Qy 192 YDGRKADVMSCGVILFALLVGLALPFDNLLRQLLEKVKRGVPHMPHFIPDQCOSLIRGM 251
Db 121 YDGRKADVMSCGVILFALLVGLALPFDNLLRQLLEKVKRGVPHMPHFIPDQCOSLIRGM 180
Qy 252 EYDAARRLTLEHQHIWYIGGKNEPEPEQPIPRKVQIRSLPSLEDDIPDVLDSMHSLSG 311
Db 181 EYDAARRLTLEHQHIWYIGGKNEPEPEQPIPRKVQIRSLPSLEDDIPDVLDSMHSLSG 240
Qy 312 FRDRNKLQDLSEENQEKMIYFLLDRKERYPSQDEDDLPPENEIDPPEKRVDSPLN 371
Db 241 FRDRNKLQDLSEENQEKMIYFLLDRKERYPSQDEDDLPPENEIDPPEKRVDSPLN 300
Qy 372 RHGRKRPERSMEVLVSDTGGSPVPARRAIEAQAQGRSISGASSGLSTSPSSPRVT 431
Db 301 RHGRKRPERSMEVLVSDTGGSPVPARRAIEAQAQGRSISGASSGLSTSPSSPRVT 360
Qy 432 PHPSRGSLPTPKGTVPVHTPKESPAQTNPPTSPSSVGGVPMRARNLSIKNSFLGSR 491
Db 361 PHPSRGSLPTPKGTVPVHTPKESPAQTNPPTSPSSVGGVPMRARNLSIKNSFLGSR 420
Qy 492 FHRRKLQVPTPEMSNLTPESSPELAKKSWFGNFISLEKEEQIFVVIKDKPLSSIKADIV 551
Db 421 FHRRKLQVPTPEMSNLTPESSPELAKKSWFGNFISLEKEEQIFVVIKDKPLSSIKADIV 480
Qy 552 HAFSLPSLSHVSISQTSFRAEYKATGGPAVQKPVKFOVDITYTEGGAQKENGIVSYVT 611
Db 481 HAFSLPSLSHVSISQTSFRAEYKATGGPAVQKPVKFOVDITYTEGGAQKENGIVSYVT 540
Qy 612 FTLLSGPSRRFRKRVETIOAQLLSTHDPAAQHLSD 647
Db 541 FTLLSGPSRRFRKRVETIOAQLLSTHDPAAQHLSE 576

RESULT 3
Q8TDC2
ID Q8TDC2 PRELIMINARY; PRT; 778 AA.
AC Q8TDC2;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Protein kinase-like protein.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA She X.Y., Yu L., Guo J.H.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AF479827; AAL87698.1; -.
DR HSSP; P24941; 1BUH.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR000449; UBA_domain.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TK; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 778 AA; 85086 MW; 8D1818D4E34398BB CRC64;
```


DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein (fragment).
GN DXFZP54781613.
OS Homo sapiens (Human).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Koehrer K., Beyer A., Mewes H.W., Weil B., Wiemann S.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL834275; CAB38950.1; -
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR000449; UBA domain.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW Hypothetical protein; ATP-binding; Transferase.
FT NON_TER 1
SQ SEQUENCE 768 AA; 83962 MW; 1P954ADF62B889A CRC64;
Query Match 76.3%; Score 2736.5; DB 4; Length 768;
Best Local Similarity 76.7%; Pred. No. 8e-193;
Matches 534; Conservative 52; Mismatches 45; Indels 65; Gaps 7;
QY 20 RLEKTLGKGTGLVGLVGHVCTQKVAIKIVNREKLSVLMKVERIAIKLIEHPHVL 79
DB 1 RLEKTLGKGTGLVGLVGHVCTQKVAIKIVNREKLSVLMKVERIAIKLIEHPHVL 60
QY 80 KLHDVYENKYLVLVLEHVSGLGFLDYLVKGRITPKAEKFPQIISALDFCHSHSICH 139
DB 61 KLHDVYENKYLVLVLEHVSGLGFLDYLVKGRITPKAEKFPQIISALDFCHSHSICH 120
QY 140 RDLKPNLLDEKNNIRIADFGMASLQVDSLLTSCGSPHYACPEVIRGEKDGKADV 199
DB 121 RDLKPNLLDEKNNIRIADFGMASLQVDSLLTSCGSPHYACPEVIRGEKDGKADV 180
QY 200 WSCGVILFALLVGLPFDNDNLRLLEKVRGVFPMHPHFIPDQCQLLRGMIEVDAARL 259
DB 181 WSCGVILFALLVGLPFDNDNLRLLEKVRGVFPMHPHFIPDQCQLLRGMIEVDAARL 240
QY 260 TLEHIQKHIWYIGKNEPEP-EQIP-RKVOIRSLPSLEDIDPDVLSMHSGLGCFRDRN 317
DB 241 SLEQIQKHPWYLGKHPDPCLEFAPARRVAMRSLPSNGELDPDVLSEMASLGCFRDR 300
QY 318 LLODLLSEENQEKMIYFLLDLDRKERYPSQDEDLPPRNEIDPPRKRVDSPMLNRHGKR 377
DB 301 LHRELSEENQEKMIYFLLDLDRKERYPSQDEDLPPRNDVDPKRKVDSPMLSRHGKR 360
QY 378 PERKSMELSVTD---GGSPVARRAEMAQHGQRSSISGASSGLTSLPSR----- 429
DB 361 PERKSMELSVTDAGGGGSPVTRALEMAQHSQRSSVSGASTGLSSPLSSPSRPFVS 420
QY 430 -----VTPHSPRSGSLPTPKG----- 446
DB 421 FSPFPGADGEARGGSPSTKQTQLPSRPGROGGAGEQPPPSARSTPLPGPSRSGG 480
QY 447 ----TPVHTPKESPAGTNPPTPSSP--SVGVPMARALNSIKNSFLGSPRFRHKLQVP 500
DB 481 TPLHSLPTPRASPTGTPPTPSPGGVGAARSLNSIRNSFLGSPRFRHKKQVP 540
QY 501 TPEMSNIPTPSSPELAKSHFGNFIISLEKEQFVVIKDFPLSIKADIIVHAFSLPSL 560
DB 541 TAEEMSSLTSPSSPELAKRSWFGNFIISLDKEQIFVLKDKPLSLSIKADIIVHAFSLPSL 600

QY 561 SHSVISQTSFRAEYKATGPAVQKPAVKFOVDITYTEGGAQKE-----NGIYSVTFTL 614
DB 601 SHSVISQTSFRAEYKASGPSVQKPAVQVDFVDSISSEGGPEPSRRDGGGGGYSVITFL 660
QY 615 LSGPSRRRKRVVETITQALLSTHDPAPAAQHLSDTTN 650
DB 661 ISGPSRRRKRVVETITQALLSTHDPAPAAQHLSDTTN 696
RESULT 6
Q96JL4 PRELIMINARY; PRT; 715 AA.
AC Q96JL4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein KIAA1811 (fragment).
GN KIAA1811.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Nagase T., Nakayama M., Nakajima D., Kikuno R., Ohara O.;
RL MEDLINE=21245130; PubMed=11347906;
RT "Prediction of the coding sequences of unidentified human genes. XX.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro."
RL DNA Res. 8:85-95(2001).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AS058714; BAB47440.1; -
DR HSSP; P24941; IBUH.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR000449; UBA domain.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW Hypothetical protein; ATP-binding; Kinase;
KW Serine/threonine-protein kinase; Transferase.
FT NON_TER 1
SQ SEQUENCE 715 AA; 78499 MW; B90F6EE115C418A5 CRC64;
Query Match 74.3%; Score 2599.5; DB 4; Length 715;
Best Local Similarity 76.0%; Pred. No. 8.9e-183;
Matches 507; Conservative 51; Mismatches 44; Indels 65; Gaps 7;
QY 49 IVNREKLSVLMKVERIAIKLIEHPHVLKLDVYENKYLVLVLEHVSGLGFLDYLV 108
DB 1 IVNREKLSVLMKVERIAIKLIEHPHVLKLDVYENKYLVLVLEHVSGLGFLDYLV 60
QY 109 KKGRLTPKARFPFROIISALDFCHSHSICHRLDKPENLLDEKNNIRIADFGMASLQV 168
DB 61 KKGRLTPKARFPFROIISALDFCHSHSICHRLDKPENLLDEKNNIRIADFGMASLQV 120
QY 169 DSLETSCGSPHYACPEVIRGEKYGKADVMSGCVILFALLVGLPFDNDNLRLLEKV 228
DB 121 DSLETSCGSPHYACPEVIRGEKYGKADVMSGCVILFALLVGLPFDNDNLRLLEKV 180
QY 229 KRGVFMHPHFIPDCCSLLRGMIEVDPKRLSLEQIQKHPWYLGKHPDPCLEFAPARR 286
DB 181 KRGVFMHPHFIPDCCSLLRGMIEVDPKRLSLEQIQKHPWYLGKHPDPCLEFAPARR 240
QY 287 VOIRSLPSLEDIDPDVLSMHSGLGCFRDRNKLQDLLSEENQEKMIYFLLDLDRKERYPS 346
DB 241 VAMRSLPSNGELDPDVLSEMASLGCFCFRDRERLHRELSEENQEKMIYFLLDLDRKERYPS 300
QY 347 QEDEDLPFRNEIDPPRKRVDSPMLNRHGKRPERKSMELSVTD---GGSPVARRAIE 403

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Db 301 CEDQDLPPNDVDPPKRVDSFVMSLRRGKRRPRKSMELVLSITDAGGGSPVPTRRALM 360
Qy 404 AOHQORSRISGASSGLSTPLSSPR----- 429
Db 361 AOHQORSRISGASTGLSSLSPPRSFVSFPSPGAGDEARGGGSPSTKOTLPSRGP 420
Qy 430 -----VTPHPSRPGSLPTPKG-----TPVHTPKESPAGTTPNTPPSSP--S 469
Db 421 RGGGAGGQPPPSARSFTLPFPSPSPRSSGGTPLHSLPLHTRASPTGTPTTPPSPGGG 480
Qy 470 VGVFWNARLINSIKNSFLGSPFRHRRKQVPTPEMSNLTPESSPELAKSWFGNFTSLE 529
Db 481 VGGAAWRSRLNSIRNSFLGSPFRHRRKQVPTAEEMSLTPESSPELAKSWFGNFTSLD 540
Qy 530 KEEQIFVVKDKPLSSITKADIVHAFSLTPSLSHSVISQTSFRAEYKATGGPAVFKQKVPK 589
Db 541 KEEQIFVVKDKPLSSITKADIVHAFSLTPSLSHSVISQTSFRAEYKATGGPAVFKQKVPK 600
Qy 590 QVDITYTTEGGEAQKE-----NGIYSVTFTLLSGSPRRFRKRVVETIOALLSTHDPAAQ 643
Db 601 QVDISSSEGEPPSRDDSGGGGIYSVTFTLLSGSPRRFRKRVVETIOALLSTHDPAAQ 660
Qy 644 HLSDTTN 650
Db 661 ALADEKN 667

RESULT 7
O61298 PRELIMINARY; PRT; 698 AA.
ID AC O61298;
AC O61298;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE HRPPOK-1 protein.
GN HRPPOK-1.
OS Halocynthia roretzi (Sea squirt).
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
OC Stolidobranchia; Pyrosidae; Halocynthia.
OX NCBI_TaxID=7729;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Egg;
RX MEDLINE=98440280; PubMed=97671157;
RA Sasakura Y., Ogasawara M., Makabe K.W.;
RT "Maternally localized RNA encoding a serine/threonine protein kinase
in the ascidian, Halocynthia roretzi.";
RL Mech. Dev. 76:161-163(1998).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AB014885; BAA28663.1; -.
DR HSSP; O63450; 1A06
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_Thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00069; Pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 698 AA; 78607 MW; B29B1751E83200BF CRC64;

Query Match 51.8%; Score 1812.5; DB 5; Length 698;
Best Local Similarity 55.7%; Pred. No. 7.2e-125;
Matches 371; Conservative 103; Mismatches 125; Indels 67; Gaps 16;

Qy 11 QHQAQVGPYRLEKTLGKQGTGLVGLGVCVTCQVAKIVNREKLSVLMKVERETAIL 70
Db 6 QPGQVGPYKLEKTLGKQGTGLVGLGVCVTCQVAKIVNREKLSVLMKVERETAIL 65
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Qy 71 KLIEHPHVLKHDVYENKKYLVILVLEHVSGLFDYLVKKGLRTPKEARKFRQIISALD 130
Db 66 KLIEHPHILGLHDVYENKKYLVILVLEHVSGLFDYLVKKGLRTPKEARKFRQIISAVD 125
Qy 131 FCHSHSICHRLDKPENLLDEKNNIRIADFGMASLQVGDLSLETSCGSPHYACPEVIRGE 190
Db 126 YCHNHNVCHRLDKPENLLDEKNNIKVADFGLMASLQVGDLSLETSCGSPHYACPEVIRGE 185
Qy 191 KYDGRADVWSCGVILFALLVGNLPDDNNLRQLLEKVKRGVHFHMFIPDDCQSLRGM 250
Db 186 RYDGRADVWSCGVILFALLVGNLPDDNNLRQLLEKVKRGVYHIFHVFPPDQAQLRGM 245
Qy 251 IEYDAARRLTLEHIOKHIVIGGKNE-----PEPEQIPRKVQIRSLPSLEIDDPDL 303
Db 246 IDVPPDKRLSLQOVQLGHPWMPGGSNSVEGVITPDPVPV-----IDCVPLPEESVDPDL 302
Qy 304 DSMHSLGCFRDRNKLQDLLESEENQEKMIYFLLDRKERYPS-QBEDLPPRNEIDPPR 362
Db 303 ASMTSLGCFNCKEKLKLNLTTEQNTKVVYVYMLLRKKRYPSPFDDADSLPCKHPDAPR 362
Qy 363 KRVD--SPMLNRHG-----KRPERK-SMEVLVSTGGSPVPARRAIEAQAHQQRSSIS 414
Db 363 KRVDSTSLSSNGDDWCYNPIPQRKMSAESLCLTSSSPSLSRK--KSTETHQRSQSLT 420
Qy 415 GASSEL-----STSPLSRPRVTPHPSRGSPLTPKGTPEVH--TPKESPACTPNPTPP 465
Db 421 GESNRLVCNISDTKAESKRI-----NGTPVRGTTCSNQVPQINTP 466
Qy 466 SPSPGVGVPWRAPLNSIKNSFLGSPFRHRRKQVPTPEMSNLTPESSPELAKSWFGNF 525
Db 467 ASDN-----PWRQRLASLKNFTMGSPFRHRRKQAPSSDEVEN-QGNSSSELSKRSWFGNF 521
Qy 526 ISLE-----KEEQIFVVKOKPLSSIADIVHAFSLTPSLSHSVISQTSFRAEYKATG 578
Db 522 MSSRYSSTEHCDELPAIYAIYKNTLSVKSELVHAFSLTPSLSHSVISQTSFRAEYKATG 591
Qy 579 --GPVVF-QKPVKQFVDITVTEGGEAQKEN-----GIYSVTFTLLSGSPRRFRKRVVE 627
Db 582 TSTTSVFHQRSEIKFQVDIIQHSLDRQENGKPKSSQTSVTFIAFSLISGPIRRYKRVLE 641
Qy 628 TIOAQL 633
Db 642 LLQMQM 647

RESULT 8
Q19469 PRELIMINARY; PRT; 914 AA.
ID AC Q19469; Q9BMN6;
DC 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE F15A2.6 protein (Serine/threonine kinase SAD-1).
GN F15A2.6.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Gregory J.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
investigating biology.";
RL Science 282:2012-2018(1998).
RN [3]
RP SEQUENCE FROM N.A.
RA Crump J.G., Zhen M., Jin Y., Bargmann C.;
RT "The SAD-1 kinase regulates presynaptic vesicle clustering.";
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Db 361 DISSEGEPEPRRDGSGGGIYVTFLLISGSPRRFRKRVETIQALLSTHDQPSVAL 420
Qy 646 SDTTN 650
Db 421 ADEKN 425

RESULT 11
Q5782
ID Q5782 PRELIMINARY; PRT; 701 AA.
AC Q5782
DT 01-DEC-2001 (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DE 01-MAR-2003 (TREMELrel. 23, Last annotation update)
DE GH13047P.
GN CG6114.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkely;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nunco J., Pacleb J., Paragae V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celnikier S.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY060288; AAL25327.1; -.
DR FlyBase; FBgn0036544; CG6114.
DR InterPro; IPR000719; Prot_kinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Transferase.
SQ SEQUENCE 701 AA; 76973 MW; 87B30879883B2425 CRC64;

Query Match 35.7%; Score 1248; DB 5; Length 701;
Best Local Similarity 44.9%; Pred. No. 2.6e-83;
Matches 284; Conservative 76; Mismatches 131; Indels 142; Gaps 19;

Qy 162 MASLQVGSLLTSCGSPHYACPEVIRGEKYDKRKYDVCVILFALLVGVLPDDNL 221
Db 1 MASLQVAGSMLETSCGSPHYACPEVIRGEKYDKRKYDVCVILFALLVGVLPDDNL 60

Qy 222 ROLLEKVRGVPHFIPPPDCQSLLRGMIEVDAAARLTLEHIQHIWY-IGKNEPEPE 280
Db 61 ROLLEKVRGVPHFIPPPDCQSLLRGMIEVDAAARLTLEHIQHIWY-IGKNEPEPE 120

Qy 281 QPIPRKQIRSLPSLEDIDPDVLDMSHISGCPDRNKLLODLSEENQEKWIYFLILDR 340
Db 121 LPMMEVQTHVPTATVPDVLNACISGCGKEKEKLIQELLSSHNTEKVIYFELLER 180

Qy 341 KERYPSQEDD---LPPRNE---IDPPRKVRDPSMLN----- 371
Db 181 KERRALEDDDDIAQKRSSELDAVPPKRLTCTCRINGTNAPSQISEGSLTPRRQAF 240

Qy 372 -----RHKKRPERKSMELVSVTDGGSVPARRAEMAQ----- 405
Db 241 NFRSYSTRNHQRRSPPTVTSSRS-SSYHSPTRCNSPMSSAQQAQANAISSPSSPAAGTR 299

Qy 406 ---HGORSSISGASGLSTSLSS-----PRVTPHPSR---GSP--- 440
Db 300 HSTYGDGRD--SGHSSVSRTPSHSQKSIIEGVVVVREPRERDSLRQEGGSGPRDR 357

Qy 441 --LPTPKGTP-----VHTKESPAGTNPPTP----- 464
Db 358 GDCGIPPGSGPGSGSGSTASPSVHHRANSPTIALSMFHDPSNVNPNNGSPMWNSS 417

Qy 465 ---PSP--SVGVPMWRALNISKNSFLGSPFRHKKIQVTPPEMSNLTPESSPELAKK 519
Db 1
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Db 418 PCMPGSPCNTPGQQLWKTRLTNIKNSFLGSPFRHRRKMQVSADE--VHLTPESSPELTKR 475
Qy 520 SWFGNFISLEKEBQIFVVIKDPKLSIKADIWAFLSIFSLSHSVISQTSFRAEYKATG- 578
Db 476 SWFGNLTTEKDETFTILVKGPATVKAHLIHAFLSMAELSHSVSPTSFRVEYKRGNG 535
Qy 579 GRAVFOKPVKFOVDIT--YTEGGAQKENGIVYVTFLLSGPSRRFRKRVETIQALLST 636
Db 536 GPVNFQGHVKFQVDISAICKQGDIDM---LFAITFTLLSGNIRFRICEHIQSQCCK 592
Qy 637 H-----DPP-----AAQHLSDTNCMEMMTGRLS 660
Db 593 RFPGPSPTVTSVTQAVSESSCGSVSSERLS 625

RESULT 12
Q8SSX5
ID Q8SSX5 PRELIMINARY; PRT; 833 AA.
AC Q8SSX5;
DT 01-JUN-2002 (TREMELrel. 21, Created)
DT 01-JUN-2002 (TREMELrel. 21, Last sequence update)
DE 01-MAR-2003 (TREMELrel. 23, Last annotation update)
DE Putative serine/threonine protein kinase.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RA Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P.,
RA Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,
RA Tungal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;
RT "Sequence and Analysis of Chromosome 2 of Dictyostelium.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AC115685; AAL92711.1; -.
DR HSP; P24941; 1BUH.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_Thr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 833 AA; 93467 MW; 51E64036C90C0F94 CRC64;

Query Match 24.9%; Score 870.5; DB 5; Length 833;
Best Local Similarity 31.1%; Pred. No. 2e-55;
Matches 215; Conservative 94; Mismatches 169; Indels 213; Gaps 16;

Qy 16 VGPVRLKTLKGGTGLVGLGVHCVTCQKVAIKIVNREKL--SSVLMMKYRETAIKLI 73
Db 6 VGPVRLKTLKGGTGLVGLGVHCVTCQKVAIKIVNREKL--SSVLMMKYRETAIKLI 65

Qy 74 EHPHVLKHDVYENKYLVLVLEHVSGLFVLEHVSGLFVLEHVSGLFVLEHVSGLFVLEHVS 133
Db 66 DHPNMMKYREYETSKYFLILEVEGGLFVLEHVSGLFVLEHVSGLFVLEHVSGLFVLEHVS 125

Qy 134 SHSTCHRDLPENLLLEKNNIRIADFGMASLQVGDLSLETSCGSPHYACPEVIRGEKYD 193
Db 126 SRNICHRDLAPENLLSGDKRIKIADFGMGSIVRKMLLHTSCGSPHYASPEVVSIGDYD 185

Qy 194 GRKADVSCGVILFALLVGVLPDDNLRLLEKVRGVHFMHFIIPDCQSLLRGMIEV 253
Db 186 GQKADVSCGVILFALLVGVLPDDNLRLLEKVRGVHFMHFIIPDCQSLLRGMIEV 245

Qy 254 DAARLTLEHIQHIWYIGKNEPEPEQIPRKQIRSLPSLEDIDPDVLDMSHISGCPDR 313
Db 246 DPKSRISIKELKEHPWFVSNFQKATPV-EEINAEPLVDYSQIDEDIFRSLMALG-VG 303

Qy 314 DRNKLQDLSEENQEKWIYFLLDRKERY----- 344
Db 1
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Db 304 TIDEVQQLVSNQKS-ATLIYYRLLEERKKFSDVNVKYGKPKETRRNSLSDMSLKIFPS 362
QY 345 ----- 344
Db 363 GSNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 422
QY 345 -----PSQEDDLPPRNEIDPPRKRV 365
Db 423 NNNNNNNNNNSAVGKSDSSSQPPHIQQPHSQQIPSNSTQESMQISPSNGAN--NMAI 480
QY 366 DSPMLNRHCKRPP-----ERKSMEVLVSTDGSPVPARRAIEAQAHQ 408
Db 481 QQPIINNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 536
QY 409 RERSISG-----ASSGLSTSPSPRVTPHPSPRGSPLPKGPVHTPKE 454
Db 537 QQQQFNNGNNNNNTMVQPLTMSASSSSSSSTPSLSPNSSTSTSTSPQLSAIKPDHY 596
QY 455 SPAG--TPNPTPPSPSVGVGVPWRARLNSIKNSFLGSPFRHRKLQVP-----T 501
Db 597 QRRGSMTASTNPATSPMS-----HRGKTSPTTEITSKVRKLKI 635
QY 502 PEEMSLTPE-----SSPELAKSMFGNFIS 527
Db 636 SSSQSN-TPNSPIIGSSP---KXSWFSYFFS 662

RESULT 13
Q15524
ID Q15524 PRELIMINARY; PRT; 745 AA.
AC Q15524;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Serine/threonine protein kinase.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RX MEDLINE=98399868; PubMed=9730619;
RA Espinosa L.; Navarro E.;
RT "Human serine/threonine protein kinase EMK1: genome structure and cDNA
cloning of isoforms produced by alternative splicing.";
RL Cytogenet. Cell Genet. 81:278-278(1998)
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
Db EMBL; X97630; CAA66229.1; --
Db HSSP; Q63450; 1A06.
Dr InterPro; IPR001772; Kinase Cterm.
Dr InterPro; IPR000719; Prot_kinase.
Dr InterPro; IPR002290; Ser_Thr_kinase.
Dr InterPro; IPR001245; Tyr_kinase.
Dr InterPro; IPR000449; UBA_domain.
Dr Pfam; PF02149; KAI; 1.
Dr Pfam; PF00069; pkinase; 1.
Dr Pfam; PF00627; UBA; 1.
Dr PRINTS; PR00109; TYRKINASE.
Dr ProDom; PD000001; Prot_kinase; 1.
Dr SMART; SM00220; S_TKc; 1.
Dr SMART; SM00165; UBA; 1.
Dr PROSITE; PS00107; PROTEIN KINASE ATP; 1.
Dr PROSITE; PS00111; PROTEIN KINASE DOM; 1.
Dr PROSITE; PS00108; PROTEIN KINASE-ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 745 AA; 83204 MW; CEEA02EE762EC5DF CRC64;

Query Match 22.8%; Score 796.5; DB 4; Length 745;
Best Local Similarity 29.1%; Pred. No. 4.8e-50;
Matches 224; Conservative 120; Mismatches 243; Indels 183; Gaps 21;
QY 10 AQHAQTVGVPYRLEKTLGKGQTLGLVGVHCVTCQKVAIKVNRKLSVLMKVEREIAI 69

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Db 11 ADEQPHIGNYELLKTIIGKGNFAKVKLARHILTKGEVAVKIIDKTQLNSSSLQKLFREVRI 70
QY 70 LKLEHPEVLKLDVYENKKYLYLVLEHVSGGELFDYLVKKGRLLTPKEARFPQIISAL 129
Db 71 MKVLNHPNIVKLFVETETKTLYLMEYASGEVFDYLVVAHRMKKEARAKFRQIVSAV 130
QY 130 DFCSHSICHRLDKPENLLLDKKNIRIADFGMASLQVGDLSLLETSCGSPHYACPEVIRG 189
Db 131 QYCHQKFLVHRDLKAENLLLDADNWKIADGFNEFTFGNKLDTFCGSPYAPAELEFG 190
QY 190 EKYDGRKADVWSCGVILFALLVGLALPDDDLNRLLEKVGKGVFHPHFIPDPQCSLLRG 249
Db 191 KKYDGPVDMVSLGVILYTLVSGSLPFDQGNLKELRERVLGRKYRIPYMTGDCENLLKK 250
QY 250 MIEVDAARLLEHIOKHIWYIGGKNBEPPEQIPRKVQIRSLPSLEDDIDPDVLDMSHL 309
Db 251 FLILNPSKRGTLQIMKDRMNVGHEDDE-----LKPVEFLPDYK--DPRRTELMYSM 302
QY 310 GCFRDNKLLQDLASEENQEMKIYFLLDRKERYPSOEDEDLPPRNEID----- 359
Db 303 CYTREE-----IQDSLVGQRYNEWMATYLLLYGYSSELEGDITLXPRPSADLTNSAQFPS 359
QY 360 -----PPRKRVDS-----PMLNRHOK-----RRPE-----RKSM----- 383
Db 360 HKVQSVSANPKQRRFSDQAGPAIPTSNYSYKTKQSNNAENKRPEDRESGRKASSTAKV 419
QY 384 -----EVLSTVDG-----GSPVPARRAIEMA--OHQGRSRISG--A 416
Db 420 PASPLPGLERKKTTPSTNSVLSTSTNRSNPLLERASLGQASIQNGKSLTPGSGRA 479
QY 417 SSGLSLSTPLSSPRVTPH-----PSPRGSLPTPKGTPVHTPKESPA-- 457
Db 480 STASASAAVSAARPRQHKMSASVHPNKAAGSLPFTESNCEVPRPSTAPQRPVVASPSAH 539
QY 458 -----GPNPT-----PSSPSVGVGVPWRARLNS 481
Db 540 NISSGGAPDRTNFPRGVSSRSTFHAGQLRQVRDQGNLPYGVTPASPSPGHSQGRGASGS 599
QY 482 IKNSFLGSPFRHRKLQVP--TPEEMSLTP-----ESSPELAKSM--FG 523
Db 600 IFSKP--TSKVVRRNLNPEPKDRVETLRPHVVGSGNDKKEEFREAKRPSLRFTWSMK 657
QY 524 NFISLEKEEFVVIKDKPLSSIKADIVHAFSLPSLSHVSISQTSFRAEYKATGGPAVF 583
Db 658 TTSSMEPNEMREIRKVLDA NSCQSELHEKYMLL--CMHGTPGHEDF----- 702
QY 584 QKPVKQVDITVYTBGGEAKENGISYVTFLLSGSPSRFRKRVETIQAL 633
Db 703 ---VQWEMEVC-----KLPRLSLNGVRFKRISGTSMAPKFNIAKIANEL 743

RESULT 14
Q96HB3
ID Q96HB3 PRELIMINARY; PRT; 755 AA.
AC Q96HB3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Similar to ELKI motif kinase.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Strausberg R.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
Db EMBL; BC008771; AAH08771.1; --
Db HSSP; P24941; 1BUH.
Db Genew; HGNC:3332; MARK2.

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OM protein - protein search, using sw model

Run on: November 26, 2003, 11:50:16 ; Search time 10.9937 Seconds
(without alignments)
2857.432 Million cell updates/sec

Title: US-10-054-579-2

Perfect score: 3497

Sequence: 1 MTSTGDKGGAHQVGVYR.....TNCMEMTGRLSKCGIIPKS 668

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	790	22.6	1518	1 KKK1_YEAST	P34244 saccharomyc
2	785.5	22.5	512	1 KI10_ARATH	Q38997 arabidopsis
3	779.5	22.3	752	1 MKR4_HUMAN	Q96134 homo sapien
4	769.5	22.0	774	1 MKR2_MOUSE	Q05512 mus musculu
5	764	21.8	576	1 SNF1_SCHPO	O74536 schizosacch
6	754	21.6	786	1 SNF1_HUMAN	P57059 homo sapien
7	749	21.4	776	1 SN1L_RAT	Q91155 rattus norv
8	742	21.2	776	1 MKR3_HUMAN	P27448 homo sapien
9	738	21.1	779	1 SN1L_MOUSE	Q60670 mus musculu
10	734	21.0	775	1 CDR2_SCHPO	P87050 schizosacch
11	729.5	20.9	552	1 AAK2_RAT	Q09137 rattus norv
12	729.5	20.9	915	1 KCC4_YEAST	P25389 saccharomyc
13	729	20.8	1142	1 GIN4_YEAST	Q12263 saccharomyc
14	726	20.8	619	1 SNF1_CANTR	O94168 candida tro
15	725.5	20.7	552	1 AAK2_HUMAN	P54646 homo sapien
16	723	20.7	548	1 AAK1_RAT	P54645 rattus norv
17	720.5	20.6	633	1 SNF1_YEAST	Q06782 saccharomyc
18	719	20.6	550	1 AAK1_HUMAN	Q13131 homo sapien
19	707	20.2	611	1 SNF1_CANGA	Q00372 candida gla
20	706	20.2	620	1 SNF1_CANAL	P52497 candida alb
21	688	19.7	502	1 RK11_SECCO	Q02723 secale cere
22	647	18.5	891	1 KIN1_SCHPO	P22987 schizosacch
23	634	18.1	622	1 YNA3_CABEL	P45894 caenorhabdi
24	609.5	17.4	661	1 Y537_HUMAN	O60285 homo sapien
25	606	17.3	1064	1 KIN1_YEAST	P13185 saccharomyc
26	601	17.2	593	1 CDR1_SCHPO	P07334 schizosacch
27	558	16.0	800	1 KIN4_YEAST	Q01919 saccharomyc
28	551	15.8	1147	1 KIN2_YEAST	P13186 saccharomyc
29	522.5	14.9	714	1 HUNK_HUMAN	P57058 homo sapien
30	521	14.9	714	1 HUNK_MOUSE	O88866 mus musculu
31	504	14.4	353	1 ASK2_ARATH	P43292 arabidopsis
32	492.5	14.1	664	1 KCCB_HUMAN	Q13554 homo sapien
33	490	14.0	363	1 ASK1_ARATH	P43291 arabidopsis

RESULT 1
ID KKK1_YEAST STANDARD; PRT; 1518 AA.
AC P34244; 486 13.9 472 1 KCCG_HUMAN
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Probable serine/threonine-protein kinase YKL101W (EC 2.7.1.-).
GN YKL101W OR YKL453.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetaceae; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxId=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=S288c;
RC MEDLINE=94078677; PubMed=8256524;
RA Pallier C., Valens M., Puzos V., Fukuhara H., Cheret G., Sor F.,
RA Bolotin-Fukuhara M.;
RT "DNA sequence analysis of a 17 kb fragment of yeast chromosome XI
physically localizes the MRB1 gene and reveals eight new open reading
frames, including a homologue of the KIN1/KIN2 and SNF1 protein
kinases.";
RL Yeast 9:1149-1155(1993).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC -!- SIMILARITY: BELONGS TO THE NIM1 SUBFAMILY.

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or send an email to license@isb-sib.ch).

EMBL; X71133; CAA50456.1; --
EMBL; Z28101; CAA81941.1; --
PIR; S37928; S37928.
HSSP; Q63450; 1A06.
SGD; S0001584; HSL1.
GO; GO:0005935; C:bud neck; IDA.
GO; GO:0005940; C:septin ring; IDA.
GO; GO:0000086; P:G2/M transition of mitotic cell cycle; IGI.
GO; GO:0006468; P:protein amino acid phosphorylation; IDA.
GO; GO:0000074; P:regulation of cell cycle; IMP.
GO; GO:0000135; P:septin checkpoint; IGI.
InterPro; IPR000719; Prot_kinase.
InterPro; IPR002290; Ser_thr_kinase.
InterPro; IPR001245; Tyr_kinase.
Pfam; PF00069; pkinase; 1.
PRINTS; PR00109; TYRKINASE.
ProDom; PD000001; Prot_kinase; 1.
SMART; SM00220; S_TKc_1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR

ALIGNMENTS

KW Hypothetical protein; Transferase; Serine/threonine-protein kinase;
KX ATP-binding. 81 369 PROTEIN KINASE.
FT NP BIND 87 95 ATP (BY SIMILARITY).
FT BINDING 110 110 ATP (BY SIMILARITY).
FT ACT SITE 239 239 BY SIMILARITY.
SQ SEQUENCE 1518 AA; 169592 MW; 803F84F7531241DD CRC64;

Query Match 22.6%; Score 790; DB 1; Length 1518;
Best Local Similarity 30.1%; Pred. No. 1.3e-26;
Matches 239; Conservative 107; Mismatches 32; Indels 182; Gaps 21;
QY 16 VGPYRLKTLGKGTGLVGLGVHCVTCQKVAIKVNRKLE----- 55
DB 78 VGPWKLGKTLGKSGGVRVLAKNMTQGLAAIKIVPKKAFVHCSSNGTVPNSSYSSMT 137
QY 56 -----SSSVLMK-----VEREIAIKLIEHPHVLKLDVYENKYLVLVLEHVS 99
DB 138 SNVSSPSIASREHNSHNSQTPYGIERIEIVIMKLSHTNVNVALFEVWENKSELYLVLEYVD 197
QY 100 GGELEFDLVKKGRLTPKEARKFPTQIISALDFCHSHSICHRDLKPNLLIDKGN-NIRIA 158
DB 198 GGELEFDLVKKGRLTPKEARKFPTQIISALDFCHSHSICHRDLKPNLLIDKGN-NIRIA 257
QY 159 DFGWASLQVGDLSLETSCGSPHYACPEVIRGEKYDGRKADVWSCGVILFALLVGLPFD 218
DB 258 DFGWAALELKNLLKLTSCGSPHYASPIVNGRPHVGGPSDVWSCGIVLFPALLTGHLPFD 317
QY 219 DNLRLLEKVKRGVFMHPHFPDQCGLLGMIEVDAAARLTLEHTQKHWYGGKNEPE 278
DB 318 DNIKLLLVQSGKYQMPNSLSEARDLSKILVIDPEKRTTQEILKH-PLIKKYDDL 375
QY 279 PEQPIREPQVQ-----IRSLPSLEDIDPDVLDMSHSLGCFDRN 316
DB 376 PVNKLVRKMDKNWARKNSDHLNANVSPSIVTLHSGKEIDSLRSQILWHGVSR 435
QY 317 KLLQDLISEENOKMYIFLLDLRKERY-----PSQDEDLPRNETDPPKRVDSFPLN 371
DB 436 LIITAKLLQKPMSEKLFYLLQYKQHSISLSSSENKKSATESVNEPIEVASKTAN 495
QY 372 RHGKRPER-KMEVLVS-TDGGSPVPARRAE-----MAHQGRSRS----- 412
DB 496 NTGLRSENNDVTLHSLHSEIDTSTVQNNAITGVNTEINAPVLAQKSFINTLSQPE 555
QY 413 -----TSGASSG-----LSTSPSLSPRYTPHPSPR 437
DB 556 SDKABEAVALPPAIPFNASSRIFRNSYTSISRRSRRLSLNSLSASTSRETWH 615
QY 438 GSPLPKPGTPVHTPKESPAGTPNTPPSGVSQGVPMWRLNLSKNSFLGSPFRHRRKL 497
DB 616 DNEMPLPQ-LPKSPSYSLSRRAIHASPSKSIH-----KSLSRKNIAATVAARRTL 666
QY 498 QVPTPEMSNLTPSSPELAKSHFGNFISLEKEQIFVVIKPLSSIKADIVHAFLSI 557
DB 667 Q-----NSASKRSYLSQISKRS-----LNLDN-----LLVFDPLSPKPSASENVKSE 712
QY 558 PSLSHSVISOTSFR-----EYKATGPAVFOKPVKFOVDITYTE 597
DB 713 P-----HSLESDFEILCDQILFGNALDRILEEEDNEKERDTQORQNDTKSSADTTIS 769
QY 598 GGEAKEN-----GIYSVFTLLSGPSRFRKV-----VETIOAQLLSTHDPAA 642
DB 770 GVSTNKENGEYPTKIEKNFNMSYKPSENNWSGLSPFPIPEKENTLSSYLEBQKPKRA 829
QY 643 QHLSDTNCMEMM 655
DB 830 A-LSDDITNSFNKM 841

RESULT 2

K110_ARATH

ID K110_ARATH STANDARD; PRT; 512 AA.

AC Q38997; 004728; Q39076;

DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE SNF1-related protein kinase KIN10 (RC 2.7.1.-) (AKIN10).
GN KIN10 OR SKIN10 OR ATG301090 OR T4P13.22.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eudicots II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_taxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93013041; PubMed=1339373;
RA le Guen L., Thomas M., Bianchi M., Halford N.G., Kreis M.;
RT "Structure and expression of a gene from Arabidopsis thaliana
RT encoding a protein related to SNF1 protein kinase.";
RL Gene 120:249-254(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=cv. Columbia;
RA Lessard P., Kreis M., Thomas M.;
RT Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=cv. Columbia;
RL MEDLINE=21016720; PubMed=11130713;
RA Salanoubat M., Lemcke K., Bloeker H., Perez-Alonso M., Obermaier B.,
RA Fartmann B., Boutry M., Griwell L.A., Mache R., Puigdomenech P.,
RA Deisenroth V., Choise N., Artiguenave F., Robert C., Brottier P.,
RA De Simone V., Cattolico L., Weissbach J., Saurin W., Quetier F.,
RA Winkler P., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
RA Schaefer M., Drzonek H., Erfle H., Jordan N., Bangert S.,
RA Wurmbach E., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
RA Wiedemann R., d'Angelo M., Pallavicini A., Toppo S., Simonati B.,
RA Vezzi A., Hornischer K., Kauer G., Loehner T.-H., Nordstiek G.,
RA Reichelt J., Schafie M., Schoen O., Barges M., Terol J., Climent J.,
RA Navarro R., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,
RA Cooke R., Laudie M., Berger-Llauro C., Ornelles B., Masuy D.,
RA de Haan M., Maere A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,
RA Montfort A., Argirou A., Flores M., Liguori R., Vitale D.,
RA Manthaupt G., Haase D., Floore H., Rudd S., Zaccaria P., Mewes H.-W.,
RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
RA Rooney T., Rizzo M., Waits A., Utterback T., Fujii C.Y., Shea T.P.,
RA Creasy T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S.,
RA Pai G., Miltscher J., Sellers P., Gill J.E., Feldblyum T.V.,
RA Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,
RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
RA Sasamoto S., Kimura T., Ideasa K., Kawashima K., Kishida Y.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T.,
RA Watanabe A., Yamada M., Yasuda M., Tabata S.;
RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis
RT thaliana.";
RL Nature 408:820-822(2000).
RN [4]
RP SEQUENCE OF 1-19 FROM N.A.
RX STRAIN=cv. Columbia;
RL MEDLINE=95115691; PubMed=7816049;
RA le Guen L., Thomas M., Kreis M.;
RT "Gene density and organization in a small region of the Arabidopsis
RT thaliana genome.";
RL Mol. Gen. Genet. 245:390-396(1994).
CC -I- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN A SIGNAL TRANSDUCTION IN
CC CASCADE REGULATING GENE EXPRESSION AND CARBOHYDRATE METABOLISM IN
CC HIGHER PLANTS.
CC -I- TISSUE SPECIFICITY: EXPRESSED IN ROOTS, SHOOTS AND LEAVES.
CC -I- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC SNF1 SUBFAMILY.
CC -I- SIMILARITY: Contains 1 UBA domain.
CC -----
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CC DR EMBL; AY057448; AAL23583.1; -
CC DR EMBL; AB049127; BAB39380.1; -
CC DR EMBL; AY120867; AAM55491.1; -
CC DR EMBL; AK075272; BAC11510.1; -
CC DR EMBL; AB058763; BAB47489.1; ALT_INIT.
CC DR HSSP; Q63450; 1A06.
CC Genew; HGNC.13538; MARK4.
CC MIM; 606495; -.
CC InterPro; IPR001772; Kinase Cterm.
CC InterPro; IPR000719; Prot_kinase.
CC InterPro; IPR002290; Ser Thr_pkinase.
CC InterPro; IPR001245; Tyr_pkinase.
CC InterPro; IPR000449; UBA_domain.
CC Pfam; PF02149; KAI; 1.
CC Pfam; PF00069; pkinase; 1.
CC Pfam; PF00627; UBA; 1.
CC PRINTS; PR00109; TYRKINASE.
CC ProDom; PD000001; Prot_kinase; 1.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
CC PROSITE; PS00030; UBA; 1.
CC Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Alternative splicing.
FT DOMAIN 59 310 PROTEIN_KINASE.
FT DOMAIN 324 368 UBA.
FT NP_BIND 703 752 KAI.
FT BINDING 65 73 ATP (BY SIMILARITY).
FT BINDING 88 88 ATP (BY SIMILARITY).
FT ACT_SITE 181 181 BY SIMILARITY.
FT VARSPIC 628 752
FT ADEPERIGGEVTSCHLPWDQETAPRLLPFMSVKLTSSR
FT SHEVEVCQLPRLGRLFRVAGTALAFKTLVTRISNDL
FT EL -> TLDPKRNQNRCSGASLPQGSIKRQTNLRSG
FT DLRSQVAIYLGIKKRPPPGSDSPGV (in isoform
FT 2).
FT FTId=VSP 004946.
FT CONFLICT 70 70 F -> S (IN REF. 2).
FT SEQUENCE 752 AA; 82519 MW; 48430FFD2B150E7A CRC64;
Query Match 22.3%; Score 779.5; DB 1; Length 752;
Best Local Similarity 30.4%; Pred. No. 2e-32;
Matches 227; Conservative 105; Mismatches 237; Indels 177; Gaps 22;
Qy 15 YGVGYRLEKTLGKGTGLVKGVCVTCQKVAIKIVNREKLSBVLNKKVERETAILKIE 74
Db 55 HVGNVRLRLTGTGKGNFAKVKVLAHILTGREVAIKIIDKTQLNPSSLOKLFREVRIMKGLN 114
Qy 75 HPHVYKLHDVYENKYLVLVLEHVSGLPDLVYKGLRTPKEARKEPFRQIISALDFCHS 134
Db 115 HPNIVKLFVETETKTLVWMEYASAGEVFDYLVSHGMKEKEARAKFRQIVSAVHYCHQ 174
Qy 135 HSIChRDLKPNLLLDKNNIRIADFGMASLQVSDLSLETSCGSPHYACPEVIRGEKYDG 194
Db 175 KNIIVHRLDKAENLLDAEANIADFGSPNEFTLGSKLDTCGSPPYAAPELFGKKYDG 234
Qy 195 RKADVWCGVILFALLVLCALPDDNLLQLLEKVRGVFHFPHIPDPQCQLLRGMLEVD 254
Db 235 PEVDIMSLGVITLVSGSLPFDGHNKELRVLRGKYRVFPFTYMSTDCESILRRFLVLN 294
Qy 255 AARLTLEHIOKHTW---YTGKNEP--EPEQIPRKVQIRSLPSLEDI--DPDVLDSMH 307
Db 295 PAKCTLEQIMKDKWINIGYGEELKPYTEP-----EDFGDTKRIEVMV 339
Qy 308 SLGCFRDRNKLQDLLSEENQEKMIYELLDDRKYRVPQDEDLPPRNEIDPPRKRVD 367
Db 340 GMGYTREEIK--ESLTSQKNEVTATY--LLGRK----TEEGGD---RGAPGLALARVRA 389
Qy 368 PMLNRHG---KRPERKSMELSVT-----DGSPVPARRALEMAHQHQ----- 408
Db 390 PSDTTNGTSSSGKGTSHSGQRSSSTYHRRQRHSDFCGSPAPLHPKRPSTSTGEALKE 449
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RESULT 4

```
MRK2_MOUSE
ID MRK2_MOUSE STANDARD; PRT; 774 AA.
AC Q05512;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE MAP/microtubule affinity-regulating kinase 2 (EC 2.7.1.27)
DE (Serine/threonine-protein kinase Emk).
GN MARK2 OR EMK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=93364122; PubMed=8358177;
RA Inglis J.D., Lee M., Hill R.E.;
RT "Emk, a protein kinase with homologs in yeast maps to mouse
RT chromosome 19.";
RL Mamm. Genome 4:401-403 (1993).
CC -|- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -|- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC MARK SUBFAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC
CC EMBL; X70764; CAA50040.1; -.
CC PIR; I48609; I48609.
CC HSSP; Q63450; 1A06.
CC MGD; MGI.99638; Mark2.
CC InterPro; IPR001772; Kinase Cterm.
CC InterPro; IPR000719; Prot_kinase.
CC InterPro; IPR002290; Ser Thr_pkinase.
CC InterPro; IPR001245; Tyr_pkinase.
CC Pfam; PF02149; KAI; 1.
CC Pfam; PF00069; pkinase; 1.
CC PRINTS; PR00109; TYRKINASE.
CC ProDom; PD000001; Prot_kinase; 1.
CC SMART; SM00220; S_TKC; 1.
```


QY 539 KDKPLSS-----IKADIVHAPL-----SIPSLSHSVISOTSPRAEYKATGGPAVFQKP 586
DB 578 SDTSITQGLKAFRQOLRTTKTKGFLGKLNKIKGLARQVQCAPARA-----SRGLSPHPAP 634
QY 587 VKFQVDIITYTGGBAQKNGIYSYVFTLLSGPSRRFRKRVETIQALLSTHDPAPAA 642
DB 635 AQ-----SPGLHGAAGSREG-----WSLL-----BEVLE--QORLIQLQHPAA 672

RESULT 7
ID SNIL RAT STANDARD; PRT: 776 AA.
AC Q9RIU5; Q9R081;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Probable serine/threonine protein kinase SNF1LK (EC 2.7.1.1-) (Salt-inducible protein kinase) (protein kinase KID2).
GN SNF1LK OR SIK OR KID2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Adrenal gland;
RX MEDLINE=9330184; PubMed=1040390;
RA Wang Z., Takemori H., Halder S.K., Nonaka Y., Okamoto M.;
RT "Cloning of a novel kinase (SIK) of the SNF1/AMPK family from high salt diet-treated rat adrenal."
RL FEBS Lett. 453:135-139(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Feldman J.D., Vician L., Crispino M., Hoe W., Baudry M.,
RA Herschman H.R.;
RT "The KID2 gene encodes a protein kinase induced by depolarization in brain."
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC -!- SNF1 SUBFAMILY.
CC -!- SIMILARITY: Contains 1 UBA domain.

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EMBL; AB020480; BAAB2673.1; --
DR EMBL; AF106937; AAF14191.1; --
DR HSRP; P24941; IAQ1.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser thr_kinase.
DR InterPro; IPR000449; UBA_domain.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00030; UBA; 1.
DR Transferrase; Serine/threonine-protein kinase; ATP-binding.
KW DOMAIN 27 278
FT DOMAIN 303 343
FT NP_BIND 33 41
FT BINDING 56 56
FT ACT_SITE 149 149
FT CONFLICT 473 473
SQ SEQUENCE 776 AA; 84908 MW; 7BF745AF28F17E6E CRC64;

Query Match 21.4%; Score 749; DB 1; Length 776;
Best Local Similarity 31.5%; Pred. No. 7e-31;
Matches 214; Conservative 87; Mismatches 223; Indels 156; Gaps 20;
QY 4 TGKGGGAQAQYVGPVRLKTKGQGLVGLGVHCVTCOKVAIKIVNRKLSVLMKV 63
DB 12 TGTGGGQQLRVLGVDFVRLKTKGQGLVGLGVHCVTCOKVAIKIVNRKLSVLMKV 63
QY 64 ERETAIIKLEHPLVHLKHDVYENKYLVLVLEHVSGLGDFDVLVKKGLRTPKREKFR 123
DB 72 YREVQLMKLNHPNIIKLYQVMEYKQVMTKMLYIVTEFAKNGEMFDYLTSGHLSSEARKEFW 131
QY 124 QIISALDFCHSHSICHRLDKPENILLDEKNIRIADFGMASLQVGDLSILTSCSGSPHYAC 183
DB 132 QILSAVEYCHNHIVHRLDKTENLLDGNNDIKLADFGNFKYKPGEPSTWCGSPYAA 191
QY 184 PEVIRGSKYGRKADVWSCGVILFALLVGLALPDNDLRLLEKVKRGVFMHPIPPDC 243
DB 192 PEVFEKGEYEGPQIDVLSGLVLYLVCGSLPFDGPNLPTLRQVLEGRFRIPPFMSQDC 251
QY 244 QSLRGMEVDAAARLTLEHIOKHIIWYIGGKNPEP---EQIPRKVQIRSLPSLEIDP 300
DB 252 ETLLRMLVVDPAKRITIAIQIRHWM-----QADPTLLQDDPAFMSQGYTSNLGDYNE 306
QY 301 DVLDSMHSILGCFDRNKLQDLSEENQEKMIYFLLDR-----KERYPSQEDDLPPR- 355
DB 307 QVLGIMQALGI--DRQTVESLQNSSYNHFAIYLLERLREHRSQPSRATPAPARQ 364
QY 356 -----NEI---DPPRKRVDSM-----LNHRGKRRP----- 378
DB 365 POLRNSDLSLEVPEQELPCDFRPSLLCPQALAQSLQAEIDCDLHSLQLPFLPLD 424
QY 379 -----ERKSMELVSVTDGSPVPARRAEMAHQGRSRSISGASSGLST-----S 423
DB 425 TNCSGVFRHRSISFSSLLDTAISERAKQPSLEEEQVPELPSTGSTRRTTLAEVSTHFS 484
QY 424 PLASPRVTPHSPRGSPLPKPGT-----VHPKESPA-----TPNPTPSSSPSVGG 472
DB 485 PLNPPCIIVSSAAVSP---SEGTSSDCLPFSASEGAGLGGGLATPGLLTGTSPP--- 537
QY 473 VPMARLNSIKNSFLGSPFRHRRKLQVTPPEMSN-----LTPESSE----- 515
DB 538 -----VRLAS-----QSATPVLOSAGLGATVLPVPSFQECRRASDTSLT 582
QY 516 -----LAKSWFGNFTSLKEEQIFVVIKDKPLSSIKADIVHAFSLPSLSHVSIS 566
DB 583 QGLKAFQQRKQKARTKGFGLNKK-----IKGLARQV-C 615
QY 567 QTSFRAEYKATGGPAVFQKP 586
DB 616 QSSIRG---SRGGMSITHTP 632

RESULT 8
MRK3 HUMAN STANDARD; PRT: 776 AA.
ID MRK3 HUMAN STANDARD; PRT: 776 AA.
AC P27438; O60219; Q8TE41; Q8WK93; Q96RG1; Q9UMY9; Q9UN34;
DT 01-AUG-1992 (Rel. 23, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE MAP/microtubule affinity-regulating kinase 3 (EC 2.7.1.27) (Cdc25C-associated protein kinase 1) (CTAK1) (C-TAK1) (Serine/threonine protein kinase p78) (Ser/Thr protein kinase PAR-1) (Protein kinase SKL10).
DE SKL10.
GN MARK3 OR CTAK1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RX MEDLINE=98202387; PubMed=9543386;
RA Peng C.Y., Graves P.R., Ogg S., Thoma R.S., Byrnes M.J. III, Wu Z.,

SEQ	SEQUENCE	776 AA; 86944 MW; A245496849070098 CRC64;
Query Match	21.2%; Score 742; DB 1; Length 776;	
Best Local Similarity	29.0%; Pred. No. 1.6e-30;	
Matches	218; Conservative 114; Mismatches 269; Indels 150; Gaps 20	
QY	10 AQHAQVVGPRLEKTLGKGTGLVKLGVCVTCQKVAIKIWNREKLSVLMKVRREIAI 69	
DB	47 ADEQPHIGNYLLTKTIGKGNFAVKLRAHILTGREVAIKIIDKTQLNPTSLQKLFREVI 106	
QY	70 LKLIBHPVHLKLDVYENKYLVLVLEHVSGGELFDVLYVKKGLTPEAKRPFQ----- 124	
DB	107 MKLMLNHPNIVKLFVETIEKTLYLIMEYASGEVFDYLVAGRWKKEKARSFRQCQAG 166	
QY	125 -----IISALDFCHSHGICHRLDKPENLLLDKKNIRIADFGMASLQ 166	
DB	167 QTIKVQVSFDLLSLMFTFIVSAVYCHQKRIVHRDLKAENLLLDADWNKIKADFGSNEF 226	
QY	167 VCDLSLETSCSPHYACPEVIRGKYDGRKADWSCGVIILFALLVGLPDDDNLRQLLE 226	
DB	227 TVGGKLDLTCGSPPPYAAPLPEFGKYDGPEDVMSLGVILYTVSGSLPFDGQNLKELRE 286	
QY	227 KVKRGVEMHPHFIPDCOSLLRGLMIEVDAARRLTLEHIQKHIWYIGGKNEPEPEQIPRK 286	
DB	287 RVLRGKYRIPFMSTDCNLLKRELVLNPIKRGFLEQIMKDRWINAGHBEDELKPFVE--- 344	
QY	287 VQIRSLPSLEIDIPDVLDSMHSLSGCFDRNKLQDLSSEENQEKMIYFLLDLDRKYPVS 346	
DB	345 -----PELDISDQKRIDIMVGMYSQEE---IQESLSKMKYDEITATYILLGRKS---S 392	
QY	347 QED-BDLPPRNEIDPPRKRVDSPLMNLHGKRRPERKSMEVLSYTD-----GGSPVPA 397	
DB	393 ELDAADSSSSNNLSLAKVRPSSDLNNGTG-QSPHHKVKQSVSVSSQKQRYSDHAGPAIPS 451	
QY	398 REAI-----EMAHQQRSEISGASGLSISPLSSPRVTPHPSPRGSPLTPKG 446	
DB	452 VVAYPKRSQSTADSDLKEDGISRRKSSGSAVGKGIAAPASMLGNASNPNKADIPERKK 511	
QY	447 TPVHTPKESPA-----GTNPNTPPS-----SPSVG 471	
DB	512 SST-VPSSNTASGGTRNTVCSERTADRHSVIQNGKENSTIPQRTFVASTHISISA 570	
QY	472 GVPWPARL---NSIKNSFLGSPRFRHKLQVPTPEMSNLTPESSPELAKS-----WFG 523	
DB	571 ATPDIRPRFGTASRSTPHGQPR-ERRTATVNGPPASPSLSHEATPLSQTRSRGSGTNLFS 629	
QY	524 NFIS-LEKEEQIFVVIKDKPLSSIKADIVHAFISLPSLSHVSISQTS-----F 570	
DB	630 KUTSKLITRNMSFRFIKRLPTEYERNG-----RYEGSSRNVSAEQKDEKPAKPSRLRF 683	
QY	571 RAEYKATGG--PAVFQKPKVQVD-----ITYTEGGAQKEN----- 605	
DB	684 TWSMTTSSMPDGDMMREIRKVLNANCDYEQREERFLFCVHGDDGAENLVQWMEVCKL 743	
QY	606 ---GIYSVTFTLLGSPRRFRXRVVETIQAQL 633	
DB	744 PRLSLNGVRFKRISGTSIAFNKSIANKIANEL 774	
RESULT 9		
SNIL MOUSE		
ID	SNIL MOUSE	PRT; 779 AA.
AC	Q60670;	
DT	01-NOV-1997 (Rel. 35, Created)	
DT	16-OCT-2001 (Rel. 40, last sequence update)	
DT	15-SEP-2003 (Rel. 42, last annotation update)	
DE	Probable serine/threonine protein kinase SNFILK (EC 2.7.1.-) (HRT-20)	
DE	(Myocardial SNF1-like kinase).	
GN	SNFILK OR MSK.	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.	
OX	NCBI TaxID=10090;	

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RN RP SEQUENCE FROM N.A., AND REVISIONS TO 8; 16-18; 44-45; 316 AND 435.
RC TISSUE=Embryo;
RA Ruiz J.C.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RC SEQUENCE OF 1-435 FROM N.A., AND TISSUE SPECIFICITY.
RP TISSUE=Embryo;
RX MEDLINE=95200798; PubMed=7893599;
RA Ruiz J.C., Conlon P.L., Robertson E.J.;
RT "Identification of novel protein kinases expressed in the myocardium
of the developing mouse heart.";
RL Mech. Dev. 48:153-164(1994).
CC -1- TISSUE SPECIFICITY: EXPRESSED IN LUNG, SKIN, OVARY, HEART AND
STOMACH. NO EXPRESSION IN BRAIN, LIVER OR SKELETAL MUSCLE.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC SNF1 SUBFAMILY.
CC -1- SIMILARITY: Contains 1 UBA domain.
-----
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or send an email to license@isb-sib.ch).
-----
DR EMBL; U11494; AAA67926.2; --
DR HSP; P24941; IAQL.
DR MGD; MGII104754; Snflk.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser thr pkinase.
DR InterPro; IPR000449; UBA_domain.
DR Pfam; PF00069; pkinase_1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50030; UBA; 1.
DR Transferase; Serine/threonine-protein kinase; ATP-binding.
KW DOMAIN 27 278 PROTEIN KINASE.
FT DOMAIN 303 343 UBA.
FT NP BIND 33 41 ATP (BY SIMILARITY).
FT BINDING 56 56 ATP (BY SIMILARITY).
FT ACT SITE 149 149 BY SIMILARITY.
SQ SEQUENCE 779 AA; 85027 MW; 7B0813BC46D9C4E CRC64;

Query Match 21.1%; Score 738; DB 1; Length 779;
Best Local Similarity 33.9%; Pred.No. 2.5e-30;
Matches 189; Conservative 83; Mismatches 193; Indels 92; Gaps 14;

Qy 4 TGKGGAGHAQYVGPRLKTLGKGOTGLVKLGVCVTCKVAIKIWNREKLSEVLMKV 63
Db :|::||::||::||::||::||::||::||::||::||::||::||::||::||:
12 SGTGCGQQPRLRVGYDFVERTLKGNFVAVKLAHRHVRTKTQVAIKIDTRLDSSNLEKI 71
Qy 64 ERRIATLKIEHPHLKHDDVVENKKYLIVLVHSGGELFDYLVKKGLRTPKEARKFFR 123
Db YRSVQLMKNLHNPIIKLYQVMETKMILYIVTFAKNGEMFDYLTNSGHLSENEARQKF 131
Qy 124 QITISALDFCHSHSICHRLDKPENLLDKNIRIADFGMSALQVGDSLLETSCGSPHYAC 183
Db :|::||::||::||::||::||::||::||::||::||::||::||::||::||:
132 QLISAVEYCNHHIVHRDLKTENLLDSNMWDIKLADFGGNFYFKPEPLSTCVGSPPYAA 191
Qy 184 PEVIRGEKYDGRKADVSCGVILFALLVGAIPDDDNLRQLLBKVXRGVFHMPHFIPDC 243
Db :|::||::||::||::||::||::||::||::||::||::||::||::||::||:
192 PEVFEQKEYEGPQLDVSLGWLVYLCVGSPLPDGPNLPTLRQVLREGFRIFPFMSQDC 251
Qy 244 QSLLRGMEVDAAERLTLEHQHIWYGKNEPEP---EQTPRKVQTRSLPSLEDIDP 300
Db ETIRRMVVDPAKRITIAIQIROHRW----QAEDPTLLQQDDPAFDMOGYTNSLGDYNE 306
Qy 301 DVLDSMHSIGCFDRNRKLODLISEENOEKMTYFLLLDRKERY----PSOEDELPPR- 355

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Db 307 QVLGIMQALGI--DRQRTIESLQNSYNHFAIYYLLERLKEHRSQFSSRRTPAPTRQ 364
QY 356 -----NET---DPERKRVDSPM-----LNRRGKRPP----- 378
Db 365 PQLRSSLSLEVPQELPCDPRFPLSLCQPQALQSVLQVAIDCOLHSLQPLFLPLD 424
QY 379 -----ERKSMEVLSVTDGGSVPARRAJEMAHQGRSRSISGASSGLST-----S 423
Db 425 TNCSGVFRHRSISPSLLDTAISSEARQGSFLEEEQVQEPPLGSGTGRRTLAEVSTHFS 484
QY 424 PLASPRVTPHPSRGSLPTPKGTP-----VHPKESPAQ-----TPNPTPSSSVSG 472
Db 485 PLNPPCCIIVSSATASP-----SEGTSSDCLPFSASEGPAGLGSLATPGLLGTSPP----- 537
QY 473 VPMRRLNLSIKNSPLGS 489
Db 538 -----VRLAS---PPLGS 547

RESULT 10
CDR2 SCHPO STANDARD; PRT; 775 AA.
AC P87050;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Mitosis inducer protein kinase cdr2 (EC 2.7.1.-).
GN CDR2 OR SPAC57A10.02.
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A., AND FUNCTION.
RC STRAIN=972;
RA Breeding C.S., Hudson J., Balasubramanian M.K., Hemmingen S.M.,
RA Young P.G., Gould K.L.;
RT "The cdr2(+) gene encodes a regulator of G2/M progression and
RT cytokinesis in Schizosaccharomycetes pombe.";
RL Mol. Biol. Cell 9:3399-3415(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RA MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin N., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitch E.,
RA Rutherford K., Rutter S., Saunders R., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares D., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volkart G., Aert B., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Leirach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomycetes pombe.";
RL Nature 415:871-880(2002).

FN FUNCTION, AND AUTOPHOSPHORYLATION.
RX MEDLINE=99060131; PubMed=9843572;
RA Kanoh J., Russell P.;
RT "The protein kinase Cdr2, related to Nim1/Cdr1 mitotic inducer,
RT regulates the onset of mitosis in fission yeast.";
RL Mol. Biol. Cell 9:3331-3334(1998).
CC -!- FUNCTION: Acts as a mitotic inducer. In G2 it negatively regulates
CC weel, a mitotic inhibitor. Also has a role in cytokinesis where it
CC is required for proper septum formation.
CC -!- PTM: Autophosphorylated.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC NIMI SUBFAMILY.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z94864; CAB08165.1; -;
DR EMBL; AF092508; AAC72832.1; -;
DR PIR; T38929; T38929.
DR HSSP; Q63450; 1A06.
DR GeneDB; SPombe; SPAC57A10.02; -;
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser Thr kinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot kinase; 1.
DR SMART; SM00220; S_TK; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; FALSE_NEG.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Mitosis; Phosphorylation.
FT DOMAIN 10 262 PROTEIN KINASE (BY SIMILARITY).
FT NP_BIND 16 24 ATP (BY SIMILARITY).
FT ACT_SITE 133 133 BY SIMILARITY.
FT BINDING 39 39 ATP (BY SIMILARITY).
FT SEQUENCE 775 AA; 85971 MW; 2ER2EECABC8A4PAC CRC64;
Query Match 21.0%; Score 734; DB 1; Length 775;
Best Local Similarity 29.6%; Pred. No. 4e-30;
Matches 228; Conservative 105; Mismatches 234; Indels 204; Gaps 27;
QY 16 VGPYRLEKTLGKGTGLVGLGVHCVTCQVAK-IVNREKLSVLMKVRETAIKLIE 74
DB 7 VGPWEGLSLGSGGPNSSRLAKHRETGQLAVKPIVGNSELSSQQAIEGELVLRLE 66
QY 75 HPVLVLDVYENKLYLVLEHVS GGELFDYLVKKGRLTPKEARFPRIITISALDFCHS 134
DB 67 HPNVQLIDVISAQEQLFVVVEYMPGGELFDCMLRKGSTEQDTAKFLWQLGLGEYCHK 126
QY 135 HSICHRLDPENLLDEKNRIADPGMASLQVDSLLTSCGSPHYACPEVIRGEKYDG 194
DB 127 LHICHRLDPENLYLDAGHSIGKEFGMASIQQPGKLLQTCGSPHYASPEIIMGRSYDG 186
QY 195 RKADVMSGVILLFALLVGLPDPDDNLRLLKLVKGVFMHPHFIIPDCQSLLRGMIEVD 254
DB 187 CASDIWSCGLIIFALTGTGLPDDNNIRSLLLKVCQGFEMFNSIPQAHLLYRMLDVD 246
QY 255 AARLTLEHIQKHIWYIGGKNBP-----EPBQPIPRKVOIRSLPSLEIDPDVLSMHS 308
DB 247 SSTRTMEQIREH-----PFLSCFVHPNISIP-----IISAP-IQPIDLVQHLSL 292
QY 309 L-GCFDRNKLLODLSEENQEKMYIFLLDRKERYPSQEDLPPEINEDPRKRVDS 367
DB 293 VFRCSDDPPLYEKLASQSPLEKTYLTLL--SRHLHP-----PSSAAVDNRRAVDD 343
QY 368 PM--LNRRHGKRRPERKSMELSVLTDGSGVPARRAJEMAHQGRSRS-----ISGA-- 416

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Db 344 LLGTAASNGQMDIEIECAINPT-LAPYPISVAESVPRPATASAPFLTPVTTSGETN 402
QY 417 SSGLSSTPLSPRVTPHSPRGSLP-TPKG-TP-VHTPKESPAGTNPPTPSS----- 467
Db 403 YSFNATNPQS---ILQRPATTSVAVPQLPKVTPGLAYPHDSMLSSNRPSPALSPPNF 459
QY 468 -----PSV-----GGVPRARLANSIKNSF 486
Db 460 NVSINDEPVLRRATSLDMSNDFRMNENDSVGNLAASFPFGMPKPKVTRMSEH 519
QY 487 LQ-----SPRHR-----RKLVPTPE-- 503
Db 520 TGNRVVSPPRGSAFNPRTVRENVGNEQFSNNIDNNNNYQPYANATMNSRRLRTPSGERS 579
QY 504 -----ENSLNPES-----SPELAKSW----- 521
Db 580 MRADLSQSPASYSNLNPKHRRRSLFSPSSKKLGSPPQPKRSLRRLRFSSEPSCKC 639
QY 522 -FGNFISLEKEEQIFVWIKDKPLSSIK-ADIVHAFPLSPSLSHSVISQTSFRAEYKATGG 579
Db 640 VVASIVASELEHEILLEVLRRVQLLGIGIADIYDSVS-ASISARIKQNSLNL----- 691
QY 580 PAVQKPKVQVDITYTGGGAQKENGYSYVTFLLSGPSRRFRKRVVETIQ 630
Db 692 -----KPVRFRIISVLAEFFGS-----QAVFVLESGSSTTFDHLATEFQ 729

RESULT 11
AAK2 RAT
ID AAK2 RAT STANDARD; PRT; 552 AA.
AC Q09137;
AT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 5'-AMP-activated protein kinase, catalytic alpha-2 chain (EC 2.7.1.-)
  (AMPK alpha-2 chain).
GN PRKAA2 OR AMPK2 OR AMPK.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=94209324; PubMed=7908907;
RA Carling D., Aguan K., Woods A., Verhoeven A.J.M., Beri R.K.,
RA Brennan C.H., Sidebottom C., Davison M.D., Scott J.;
RT "Mammalian AMP-activated protein kinase is homologous to yeast and
RT plant protein kinases involved in the regulation of carbon
RT metabolism.";
RL J. Biol. Chem. 269:11442-11448 (1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Liver;
RX MEDLINE=95234757; PubMed=7718624;
RA Gao G., Widmer J., Stapleton D., Teh T., Cox T., Kemp B.E.,
RA Witters L.A.;
RT "Catalytic subunits of the porcine and rat 5'-AMP-activated protein
RT kinase are members of the SNF1 protein kinase family.";
RL Biochim. Biophys. Acta 1266:73-82 (1995).
CC -!- FUNCTION: RESPONSIBLE FOR THE REGULATION OF FATTY ACID SYNTHESIS
CC BY PHOSPHORYLATION OF ACETYL-COA CARBOXYLASE. IT ALSO REGULATES
CC CHOLESTEROL SYNTHESIS VIA PHOSPHORYLATION AND INACTIVATION OF
CC HORMONE-SENSITIVE LIPASE AND HYDROXYMETHYLGLUTARYL-COA REDUCTASE.
CC APPEARS TO ACT AS A METABOLIC STRESS-SENSING PROTEIN KINASE
CC SWITCHING OFF BIOSYNTHETIC PATHWAYS WHEN CELLULAR ATP LEVELS ARE
CC DEPLETED AND WHEN 5'-AMP RISES IN RESPONSE TO FUEL LIMITATION
CC AND/OR HYPOXIA. THIS IS A CATALYTIC SUBUNIT.
CC -!- SUBUNIT: HETEROTRIMER OF A CATALYTIC SUBUNIT, A BETA AND A GAMMA
CC NON-CATALYTIC SUBUNITS.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Long;

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CC IsoId-Q09137-1; Sequence=Displayed;
CC Name=Short;
CC IsoId-Q09137-2; Sequence=VSP_004949, VSP_004950;
CC Note=Lacks the sequence parts essential for kinase activity and
CC is therefore inactive;
CC -!- TISSUE SPECIFICITY: SKELETAL MUSCLE, LOWER LEVELS IN LIVER, HEART,
CC AND KIDNEY.
CC -!- INDUCTION: BY AMP.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. SNF1
CC SUBFAMILY.
CC -----
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CC -----
CC EMBL; Z29486; CAA82620.1; -;
CC EMBL; U12149; AAA85033.1; -;
CC PIR; A53621; A53621.
CC HSP; Q63450; IAO6.
CC InterPro; IPR000719; Prot kinase.
CC InterPro; IPR002290; Ser Thr kinase.
CC InterPro; IPR001245; Tyr_kinase.
CC Pfam; PF00069; pkinase; 1.
CC PRINTS; PR00109; TYRKINASE.
CC ProDom; PD000001; Prot kinase; 1.
CC SMART; SM00220; S_TKc; 1.
CC PROSITE; PS00107; PROTEIN KINASE ATP; 1.
CC PROSITE; PS00108; PROTEIN KINASE ST; 1.
CC PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
CC Transferrase; Serine/threonine-protein kinase; Fatty acid biosynthesis;
CC Phosphorylation; ATP-binding; Multigene family; Alternative splicing.
CC DOMAIN 16 268 PROTEIN KINASE.
CC NP_BIND 22 30 ATP (BY SIMILARITY).
CC BINDING 45 45 ATP (BY SIMILARITY).
CC ACT_SITE 139 139 BY SIMILARITY.
CC MOD_RES 172 172 PHOSPHORYLATION (AUTO-) (POTENTIAL).
CC VARSPPLIC 32 388 Missing (in isoform Short).
CC FT VARSPPLIC 392 552 /FTid=VSP_004949.
CC FT VARSPPLIC 392 552 Missing (in isoform Short).
CC FT CONFLICT 355 355 /FTid=VSP_004950.
CC FT CONFLICT 462 462 M -> S (IN REF. 2).
CC SQ SEQUENCE 552 AA; 62257 MW; 2829E07F674D89B1 CRC64;

Query Match 20.9%; Score 729.5; DB 1; Length 552;
Best Local Similarity 29.8%; Pred. No. 4.5e-30;
Matches 197; Conservative 103; Mismatches 217; Indels 143; Gaps 22;

QY 16 VGPYRLKTLGKGTGLVGLGVHCVTQKVAIKVNRKL-SBSVLMKVEREIALKLE 74
Db 13 IGHVLTGDTLGVGTGKVGKIGEHQLTGHKVAVKILNRQKIRSLDVVGKIKREIQNLKLF 72
QY 75 HPHVVLKLDVYENKLYLVLEHVSQGLFDYLVKVGRLTPKEARFPFQIISALDCHS 134
Db 73 HPHIILKYQVISTPTDFFMVMEYVSGELFDYICKGHGVEVEARRLFOQLSADVYCHR 132
QY 135 HSICHRDLKLENLLDEKNIRIADFGMASLQVSDSLSETSCGSPHYACPEVIRGEKVDG 194
Db 133 HMVVRDLKPEENVLLDAQMWAKIADFGLSNMMSGDFLRTSCGSPNYAAEIVISGRLYAG 192
QY 195 RKADVMSGVLVALLVGLPFDNDNLRLQLLEKVGKGVFHMHPFIPDCQSLRGMIEVD 254
Db 193 PVDIWSGVLVALLCGTLPFDEHVTPLFKKIRGSGVFIPYLNRSIATLLMHLQVD 252
QY 255 AARLTLEHQTQKHIWYIGGKNEPEPEQIPRKVQIRSLSPLEIDDPVLDLDS-----MHS 308
Db 253 PLKRATIKDIRHEWF-----KQDLPSYL-----FPEDPSYDANVIDDEAVKEVCEK 299
QY 309 LGCFRDRNKLQLDLS-EEENQEKMIYFLLLDKRYPSQDE-----DLFPRNEIDPPRK 363

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Db 300 FEC--TESEVWNLGSDPOQLAVAYHLIDNR-RIMNOASEFYFLASSPPTG----- 349
QY 364 RVDSPMLNRHGKRPKRPERKSEVLSTVDGGSPVPARRAIEAQAQGRSRSISGASSGLSTS 423
Db 350 -----SFM-----DMAM----- 358
QY 424 PLSPRPVTHPSRGSL--PTPKGTPVHTPKESPACTNPPTPPSPSVGGVPPRARLNS 481
Db 359 --TPPGLKHPH-RMPPLIADSPRA-----RCPLDALNTTKPKSLAVKAKWHLIGRS 408
QY 482 IKNSFLGSPRFRKRLQVPTPEMSNL-----TPESPPELAKSWFGNFISSLEKEEQIFVV 537
Db 409 QSRPYDIAEAVYRAMKQDLDFEMKVNVAYHLRVRKQPV-----GNVYQWSL--QLYLV 460
QY 538 IKKPLSSIKADIVHAFSLSPISLSHVSISQTSFRAEYKATGGPAPVQKPVKFOVDITYTE 597
Db 461 -----DNRSYLLDFKSIDDEVQSRGSSSTPQRSCSAAGLHRP-RSSVDSSTAE 508
QY 598 GGEAQKENGISYVTFLLSGPSRRFRKRVVETIQALLSTHDPAPAAQHLSPTTN-CHEMMT 656
Db 509 NHS-----LSG-----SLTGLTGLSTLSSASPRLGSHMTDFFEMCASLIT 548

RESULT 12
KCC4 YEAST
ID_KCC4 YEAST STANDARD; PRT; 915 AA.
AC P25389; F87005;
DT 01-MAY-1992 (Rel. 22, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Probable serine/threonine-protein kinase YCL24W (EC 2.7.1.-).
GN YCL024W OR YCL24W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_Taxid=4932;
RN [1]
RP SEQUENCE OF 1-569 FROM N.A.
RA Duesterhoeft A., Erdmann D., Hegemann J., Philippesen P.,
RA Schweitzer B., Spiegelberg R.;
RL Submitted (MAR-1992) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 567-915 FROM N.A.
RA Oliver S.G., Anwar R., Brown A., Gent M.E., Indge K.J., James C.M.,
RA Stateva L.I.;
RL Submitted (MAR-1992) to the EMBL/GenBank/DBJ databases.
RN [3]
RP REVISIONS.
RA Gromadka R.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC NIM1 SUBFAMILY.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X59720; CAA42361.1; -
CC PIR; S74283; S74283.
CC HSSP; Q63450; 1A06.
CC SGB; S0000529; YCL024W.
CC GO; GO:0005935; C:bud neck; IDA.
CC GO; GO:0003700; F:transcription factor activity; IDA.
CC GO; GO:0007117; P:bud growth; IGI.
CC GO; GO:0000994; P:septin assembly and septum formation; IGI.
CC GO; GO:0000135; P:septin checkpoint; IGI.
CC InterPro; IPR000719; Prot kinase.
CC InterPro; IPR002290; Ser_thr_kinase.
```

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DR InterPro: IPR001245; Tyr_kinase.
DR Pfam: PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TK; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW Hypothetical protein; Transferase; Serine/threonine-protein kinase;
KW ATP-binding.
FT DOMAIN 21 285 PROTEIN KINASE.
FT NP_BIND 27 35 ATP (BY SIMILARITY).
FT BINDING 50 50 ATP (BY SIMILARITY).
FT ACT_SITE 152 152 BY SIMILARITY.
FT ACT_SITE 152 152 BY SIMILARITY.
SQ SEQUENCE 915 AA; 102688 MW; BFB01C8CA43AC181 CRC64;

Query Match 20.9%; Score 729.5; DB 1; Length 915;
Best Local Similarity 33.5%; Pred. No. 8.1e-30;
Matches 197; Conservative 90; Mismatches 202; Indels 99; Gaps 15;

QY 1 MTSTGKDGGAQAQVGPYRLEKTLGKGTGLVGLGVHCVTCQKVAIKIVREKLS---- 56
Db 3 VANTHTSAKPSSTIGPWKLGTELFGSTGKVLQAQHERTGRTAVKVISKISNNNN 62
QY 57 ----ESVL-MKVERETAILKLEHPVLKLDHVENKKYLVLEHVSOGGELDFVLVKKG 111
Db 63 HNSDVSVPYNIEREIVIMKLSHPNLSLDVWETNNNNLYLLEVAEKGFNLLVDHG 122
QY 112 RUTPKARKEFQIISALDFCHSHSICHRLDKPENLLLDKKNIRIADFGMASLQVDSL 171
Db 123 PLPEREAINCFRQIIGISYCHALGIVHRDLKPENLLLDSPYNIKIADFGMAALQTDAL 182
QY 172 LETSCGSHVACPEVIRGEKYGKADVWSCGVILFALLVGLALPPDDD--NLRLLEKVK 229
Db 183 LETSCGSHVAAPEIVSGLPYEGFASDVWSCGVILFALLTGLPFDENGVNRLLLKQV 242
QY 230 RGVFHMHP--FIPPCQSLRGMIEVDAAARLTLEHIQKH1WIYIGGKNEPEPEQIPRKV 287
Db 243 KGQFEMPNDTEISRDAQDLIGLILVDPQRKIRKIDILSH-----PLKKY 288
QY 288 Q-IRSLPSLED-----IDPDVLSMSHSLGCFRDRNKLQLDLLE 325
Db 289 QTIKDSKSKDLPRENTYLYPLADSNHNTSASIDDSILQNLVYLHGRHADDIVSKLEN 348
QY 326 EENQEKWIFLLLDKERYPSQDEDLPRNETDPPKRVDSPLNRHGRKRRPERKSMEV 385
Db 349 GTNKEKILALLY--RFKLDVSGSKNKNRKLKTKCKNRKSTLSSSSLLNNRSIQ- 405
QY 386 LSVTDGGSFVPARFAIEMAQHGQSRSSISGASSGLSTPLSPRPVTPHPSP-RGSPLP 444
Db 406 -----STPRRTSK-----RHSREFS--SKRGRSFLSSNPTDSSPILRSSKRITH 451
QY 445 KGTVPVTPKESPACTNPPTPPSPSVGGVPPRARLNSIKNSFLGSPRFRKRLQVTPPE 504
Db 452 INVASANTQATSGVNP-----HKNRSKGRSSKR 481
QY 505 MSNLTPESSPELAKSWFGNFISSLEKEEQIFVVIKD-KPLSSSIKADIV 551
Db 482 LSYMPNTRKSSLLTSKS-LSNFTNLIDDDWYEIEKDAKETSNNFATLI 528

RESULT 13
GIN4 YEAST
ID_GIN4 YEAST STANDARD; PRT; 1142 AA.
AC Q12263;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Serine/threonine-protein kinase GIN4 (EC 2.7.1.-).
GN GIN4 OR YDR507C OR D9719.13.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
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FT DOMAIN 17 29 POLY-HIS.
FT NP_BIND 52 303 PROTEIN KINASE.
FT BINDING 58 66 ATP (BY SIMILARITY).
FT ACT SITE 81 81 ATP (BY SIMILARITY).
FT MOD RES 174 174 BY SIMILARITY.
SQ SEQUENCE 207 207 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
SQ SEQUENCE 619 AA; 70323 MW; 0FCF1FC3DCE706D7 CRC64;

Query Match 20.8%; Score 726; DB 1; Length 619;
Best Local Similarity 33.1%; Pred. No. 7.8e-30;
Matches 173; Conservative 105; Mismatches 168; Indels 76; Gaps 15;

Qy 7 DGAQAQYVGPYRLEKTLGKQGLVGLVHVCVTCQKVAIKIVNRKLSVLM-KVER 65
Db 40 DPNVNPANRIGRYQIIKTLGEGSGFKVLAHQHGTGQKVALKIINRKTAKSDMQGRVER 99
Qy 66 EIALKLIHPHVLKHDVYENKKYLYLVLEHVSGBELFDYLVKKGRLTPKEARKFRQI 125
Db 100 EISVRLRLPHIILKLDYVKSDEIIMVIE-FAGKELFDYIVQKGWPEDEARRPFOI 158
Qy 126 ISALDFCHSHSICHRLDKPENLLDDEKNRIADFGWASLQVGDLSLETSCGSPHYACPE 185
Db 159 IAAVEYCHRHKIVHRDLKPENLLDDQNLKVIADFGLSNMTDGNFLKTS CGSPNYAAPE 218
Qy 186 VIRGEKDGKADYVWCGVILFALLVGLALPDDDNLRQLLEKVKRGVHFHMFPIPPDCQS 245
Db 219 VISCKLVAGPEVDWSSGVILVYMLGRLPDDDFIPALFKINSYVYTLNLYLSPGAKH 278
Qy 246 LLRMVIEVDAARRJLTLEHIOHVIWIGKNEPPEQIP---RKQVTRSLPSLEDIDPDV 302
Db 279 LLTRMLVNPVNLRTIHEIMEDEWF---KQDMPDYLLPDLKSIKTSKI----DIDEDV 330
Qy 303 LDSMHSIGCFPRDKRLQLDLSSEENQEKMIYFLLDRKERYPSQEDLPPRNEIDPPR 362
Db 331 ISAL-SVTMGYDREIIS--VIEKANREAA----- 358
Qy 363 KRVDSPMLNRHGKRRPERKSMVLSTVDGGSPVPARRAIEAQAQGRSRSISGASSGLST 422
Db 359 -----GGATPTNQSKSTNEVLDAVLLMKENHTLVKDLKKSSENI---ESFLSL 404
Qy 423 SPLSSPRVTHPSRGSPLTPKGTVPHTPKESFAGTPTNTPPPSPSVGGVFWEARLNSI 482
Db 405 SP---PPSSSPNP-GSTSSAP-GVQOSLTYQTTLVPLDSTLSTLNSTAILP--TSLPSI 457
Qy 483 KNSFLGSPFRHRRKLQVTPPEMSNLTPESSPELAKKSW-FG 523
Db 458 HRAYMTEKVNDDPQQQIPAPQPTKKL-----KTRWHFG 490

RESULT 15
AAK2 HUMAN
AC P54646; Q9H188; O9UD43.
DT 01-OCT-1996 (Rel. 34, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 5'-AMP-activated protein kinase, catalytic alpha-2 chain (EC 2.7.1.-)
DE (AMPK alpha-2 chain).
GN PRKAA2 OR AMPK2 OR AMPK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=95047501; PubMed=7959015;
RA Aguan K., Scott J., See C.G., Sarkar N.H.;
RT "Characterization and chromosomal localization of the human homologue
RT of a rat AMP-activated protein kinase-encoding gene: a major
RT regulator of lipid metabolism in mammals.";
RL Gene 149:345-350 (1994).
RN [2]
```

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RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=95080410; PubMed=7988703;
RA Beri R.K., Marley A.E., See C.G., Sopwith W.F., Aguan K., Carling D.,
RA Scott J., Carey F.;
RT "Molecular cloning, expression and chromosomal localisation of human
RT AMP-activated protein kinase.";
RL FEBS Lett. 356:117-121 (1994).
RN [3]
RP SEQUENCE OF 33-552 FROM N.A.
RA Cobley V.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: RESPONSIBLE FOR THE REGULATION OF FATTY ACID SYNTHESIS
CC BY PHOSPHORYLATION OF ACETYL-COA CARBOXYLASE. IT ALSO REGULATES
CC CHOLESTEROL SYNTHESIS VIA PHOSPHORYLATION AND INACTIVATION OF
CC HORMONE-SENSITIVE LIPASE AND HYDROXYMETHYLGUTARYL-COA REDUCTASE.
CC APPEARS TO ACT AS A METABOLIC STRESS-SENSING PROTEIN KINASE
CC SWITCHING OFF BIOSYNTHETIC PATHWAYS WHEN CELLULAR ATP LEVELS ARE
CC DEPLETED AND WHEN 5'-AMP RISES IN RESPONSE TO FUEL LIMITATION
CC AND/OR HYPOXIA. THIS IS A CATALYTIC SUBUNIT.
CC -1- SUBUNIT. HETEROTRIMER OF A CATALYTIC SUBUNIT, A BETA AND A GAMMA
CC NON-CATALYTIC SUBUNITS.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC SNF1 SUBFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch)
CC -----
CC EMBL; U06454; AAA64745.1; --
CC ENBL; AL035705; CAC17574.1; --
CC PIR; S51025; S51025.
CC HSP; Q63450; 1A06.
CC Genew; HGNC:9377; PRKAA2.
CC MIM; 600497; --
CC GO; GO:0006468; P:protein amino acid phosphorylation; TAS.
CC GO; GO:0007165; P:signal transduction; TAS.
CC InterPro; IPR000719; Prot_kinase.
CC InterPro; IPR002290; Ser_thr_kinase.
CC Pfam; PF00069; pkinase; 1.
CC ProDom; PD000001; Prot_kinase; 1.
CC SMART; SM00220; S_TKc.1.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
CC PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
CC Transferase; Serine/threonine-protein kinase; Fatty acid biosynthesis;
CC Phosphorylation; ATP-binding; Multigene family.
FT DOMAIN 16 268 PROTEIN KINASE.
FT NP_BIND 22 30 ATP (BY SIMILARITY).
FT BINDING 45 45 ATP (BY SIMILARITY).
FT ACT SITE 139 139 BY SIMILARITY.
FT MOD RES 172 172 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT CONFLICT 180 180 A -> T (IN REF. 1).
FT CONFLICT 271 271 D -> G (IN REF. 1).
FT CONFLICT 403 404 HL -> RQ (IN REF. 1).
SQ SEQUENCE 552 AA; 62319 MW; C46AAFCID5104975 CRC64;

Query Match 20.7%; Score 725.5; DB 1; Length 552;
Best Local Similarity 29.4%; Pred. No. 7.2e-30;
Matches 194; Conservative 102; Mismatches 221; Indels 143; Gaps 21;

Qy 16 VGPYRLEKTLGKQGLVGLVHVCVTCQKVAIKIVNRKLSVLMKVEREAILKLE 74
Db 13 IGHVLDGTLTGVTGFGKVGIGEHQLTGHKVAIKLRQKIRSLDVVGKIKRQNLKLF 72
Qy 75 HPHVLKLDHYENKKYLYLVLEHVSGBELFDYLVKKGRLTPKEARKFRFOIISALDFCHS 134
Db 73 HPHIILKLVISTPTDFFWMEVVSGBELFDYICKGRVEEARLFFQILSANDYCHR 132
```


GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 26, 2003, 11:57:16 ; Search time 18.3229 Seconds
(without alignments)
3506.035 Million cell updates/sec

Title: US-10-054-579-2

Perfect score: 3497

Sequence: 1 MTSTGKDGGAQAQVGVYPR.....TNCMEMTGRSLKGIIPKS 668

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_76:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1743	49.8	887	2 T20941	hypothetical prote
2	795.5	22.7	745	2 G01025	serine/threonine-s
3	790	22.6	401	2 B90120	SNF1-related prote
4	790	22.6	1518	2 S37928	probable purine nu
5	785.5	22.5	512	1 J01446	serine/threonine-s
6	772.5	22.1	504	2 T10449	probable serine/th
7	771	22.0	512	2 T52633	serine/threonine-s
8	769.5	22.0	774	2 I48609	probable serine/th
9	764	21.8	576	2 T41587	probable carbon ca
10	763.5	21.8	511	1 A56009	serine/threonine-s
11	763	21.8	562	2 T29858	hypothetical prote
12	759.5	21.7	713	2 S27966	probable serine/th
13	749	21.4	798	2 J07500	qik protein - chic
14	748	21.4	504	2 T07415	probable serine/th
15	736	21.0	1192	2 T18611	probable serine/th
16	735	21.0	1246	2 G89287	protein H39823.1
17	734.5	21.0	512	2 T07788	probable serine/th
18	734	21.0	473	1 S59941	serine/threonine-s
19	734	21.0	775	2 T38929	changed division r
20	729.5	20.9	552	1 A53621	[hydroxymethylglut
21	729.5	20.9	915	2 S74283	probable protein k
22	729	20.8	1142	2 S59359	GIN4 protein - yea
23	725.5	20.7	552	1 S51025	[hydroxymethylglut
24	722.5	20.7	472	2 B90100	SNF-related kinase
25	720.5	20.6	633	1 A26030	serine/threonine-s
26	718	20.5	602	2 S72513	FOG2 protein - yea
27	704.5	20.1	481	2 I49072	protein kinase - m
28	704.5	20.1	513	1 S60303	serine/threonine-s
29	697	19.9	1398	2 T13741	hypothetical prote

30	688	19.7	502	1 A41361	serine/threonine-s
31	686.5	19.6	513	1 S60304	serine/threonine-s
32	680	19.4	510	2 T04145	serine/threonine p
33	660	18.9	1558	2 T29253	hypothetical prote
34	647	18.5	891	2 T40503	protein kinase kin
35	646.5	18.5	651	2 S52244	p69Eg3 protein - A
36	642.5	18.4	480	2 A86427	probable serine/th
37	637	18.2	891	2 A38903	protein kinase 1 -
38	634	18.1	622	1 S44859	serine/threonine-s
39	630	18.0	726	2 T33998	hypothetical prote
40	624.5	17.9	441	2 C84667	probable protein k
41	622	17.8	440	2 T14736	probable serine/th
42	618	17.7	441	2 E85362	hypothetical prote
43	617	17.6	440	2 T14735	probable serine/th
44	609	17.4	421	2 T48202	protein kinase AK2
45	606	17.3	1064	2 S52687	serine/threonine-s

ALIGNMENTS

RESULT 1

T20941

hypothetical protein F15A2.6 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000

C;Accession: T20941

R;Gregory, J.

submitted to the EMBL Data Library, March 1996

A;Reference number: Z19349

A;Accession: T20941

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-887 <WIL>

A;Cross-references: EMBL:Z70207; PIDN:CAA94127.1; GSPDB:GN00028; CESP:F15A2.6

A;Experimental source: clone F15A2

C;Genetics:

A;Gene: CESP:F15A2.6

A;Map position: X

A;Introns: 32/1; 63/3; 92/2; 139/2; 189/3; 328/2; 448/2; 516/3; 604/2; 684/3; 735/2; 777/

Query Match 49.8%; Score 1743; DB 2; Length 887;

Best Local Similarity 51.1%; Pred. No. 9.6e-61;

Matches 380; Conservative 75; Mismatches 138; Indels 150; Gaps 17;

Qy	13	AQVGPYRLEKTKGOTGLVKGVCVTCOKVAIKIVNKEKLSVLMKVREIAI LKL	72
Db	14	AQYCGPYKLEKTKGOTGLVKTGTHCITGRKVAIKIVNKEKLSVLMKVREIAI LKL	73
Qy	73	IEHPHVLKLDVYENKYLVLVLEHVSGGELFDYLVKGRLLTPKEARKFFRQIISALDFC	132
Db	74	IEHPHVLHLVDVYENKYLVLVLEHVSGGELFDYLVKGRLLTPKEARKFFRQIISALDFC	133
Qy	133	HSHSIHRDLKPNLLDKNIRIADFGMASIQVDSLSLETSCGSPHYACPEVIRGEKY	192
Db	134	HAHNIHRDLKPNLLDKNIRIADFGMASIQVDSLSLETSCGSPHYACPEVIRGEKY	193
Qy	193	DGRKADVMSGCVILFALLVGLPDDNLRQLLEKVKRGVFMHPRTPPCOSILRMIE	252
Db	194	DGRKADVMSGCVILFALLVGLPDDNLRQLLEKVKRGVFMHPRTPPCOSILRMIE	253
Qy	253	VDAAARLTLEHIOKHIIWYIG-KGNEPEPEOPIPRKVIQIRSLSDIDDPVLDSMHSLGC	311
Db	254	VDGKRYSLADVPKHPVMSGTTKADPELELPMSQVQVTHVIPGEDSDIDPVLHNMCLGC	313
Qy	312	FRDRNKLQDLLSEENQEKIYFLLLDRKVRPSGEDEDLPPRNEI-----DPPR	362
Db	314	FKDKQKLINELLSPKHNTEKNWYFLLLDRKRRRPAQEDD-----TEIVLRGAQAQNDPPK	368
Qy	363	KRVDSPLNLR-----HGKER-----PERKSNEVLSDVD	390
Db	369	KRTDSSRTSRYPMGSIADGSPINPRKTYGRNQKSGRHSILGSGFTSPSRSTRDLFGSSS	428

391 GGS-----PVPARRALEMAQH----- 406
429 SGSSAARAGEDDRGRASASTNSHYHTQDPDTLAEARHVRDQAQRRERDSGRGS 488
407 ---QQRSSISGASGLSTPLSSPRVTPHPSRGSPPLTPKGTPTVHTPKES---PAGTP 460
489 SRKESKORSKDSKSSSSCKNDASSTSSVPH-----KSPSPVMSSESVVSSSTM 537
461 NPTPPSS-----PSVGV--PWRARLINSIKNSFLGSPRFRHRRKLQVTPTEMSNLT 509
538 NSTNSSTNSLIAGNSQTSIGTSGTSPWRSKLNINIKNSFLGTFRFRHK-----MSNGT 589
510 PESSPE-----LAKSMFNGF--ISLEKEQIFVVIKDKPLSSIKADIVHAFLSI 557
590 AESDESQMDITDLYKKSFWGLASMSVERDTHCVPGVGTLSIKALIRAFLOI 649
558 PLSHSHSVISQTSFRAEYK--ATGPAVQKPVKQVDITYTE-----GGEAQKENGYSYV 610
650 HELSHSVVGQNCFRVEYKRGPTVGVSVFSGIKMNVDIIPSQQWVIAGETP-----TYVV 705
611 TPTLLSGSPRRPKRVVETIQAO 633
706 QFVLLAGEVRRFKRLVEHLSAIL 728

RESULT 2

G01025
serine/threonine protein kinase - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 16-Dec-1998
A;Accession: G01025
R;Navarro, E.
submitted to the EMBL Data Library, April 1996
A;Reference number: H00564
A;Accession: G01025
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-745 <NAV>
A;Cross-references: EMBL:X97630; NID:g1310674
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
F;18-271/Domain: protein kinase homology <KIN>

Query Match 22.7%; Score 795.5; DB 2; Length 745;
Best Local Similarity 29.1%; Pred. No. 3.4e-24;
Matches 224; Conservative 120; Mismatches 243; Indels 183; Gaps 21;
QY 10 AQHAQYGPYLEKTLGKGTGLVKGVCVTCQKVAIKIVNREKLSVLMKVEREIAI 69
DB 11 ADEQPHIGNYRLTKTIGKGNFAKVLARHILTKGEVAVKIIDKTLNSSLQKLFREVRI 70
QY 70 LKLIHPPHVLKLDVYENKYLIVLHVSGGELFDYLVKKGRLTPKEARFFQIISAL 129
DB 71 MKVLNHPNIVKLFVETIEKTLVLYMEYASGEVFDYLVHGRMKKEARAKFRQIVSAV 130
QY 130 DFCHSHSICHRDLKPENLLDEKNIRIADFGMASLQVSDLSLETSCGSPHYACPEVIRG 189
DB 131 QYCHQKFIHRDLKAENLLDADNWKIADFGSNEFTGKNDLTFGSPYAAPELPQ 190
QY 190 EKYDRKADVMSGCVILFALLVGLPDDNLRQLLEKVKGVFMHPHFIIPDCQSLIRG 249
DB 191 KKYDGPEDVMSGLVILTVLSGSLFPDQNLKELRERVLGRKVRIPYMTDCENLLKK 250
QY 250 MIEVDAARLTLEHIOKHIWYIGGKNEPEPEQIPRKVQIRSLSPLEDDIPDVLDSMHS 309
DB 251 FLILNPSKRGTLQEWKDRWNVGHEDDE-----LKYVPELPDYK--DPRTELWMSM 302
QY 310 GCFRDRNKLQDLLSEENQERKMYFLLLDRKERYPSQDEDEDLPPRNEID----- 359
DB 303 GYTREE---IQDSLGVQRYNEWATYLLGYKSSLEGGDTITLPRPSADLTNSSAQPPS 359
QY 360 -----PPRKVDS-----PMLNRHGK-----RRPE-----RKM----- 383
DB 360 HKVQRSANPKQRRFSDQAGPAIFTSYSKKTQSNNAENAKNREDRESGRKASSTAKV 419

QY 384 -----EVLVTDG---GSPVPARRAIEWA---OHQORSRSISG--A 416
DB 420 PASPLPGLERKKTTPPTSTNSVLSTSTNRSRNSPLERASLQASIQNGKDLTWPGSRA 479
QY 417 SSGLSTPLSSSRVTPH-----PSRGSPPLTPKGTPTVHTPKESPA-- 457
DB 480 STASASAGVSAARPRQHOKSMGSHVHPKASGLPPTESNCEVPRPSTAPQRPVVASPSAH 539
QY 458 -----GTNPPT-----PPSPSVGGVFWRARLNS 481
DB 540 NISSSGCAPDRTPFRGVSSRSTFHAGQURQVRDQNLFPYGVTPASPSGSHSGRRGASGS 599
QY 482 IKNSFLGSPRFRHRRKLOVP--TPEMSNLTTP-----ESSPELAKKSW-FG 523
DB 600 IFSKP--TSKFRVRLNNEPESKDRVETLPHVVVGGNDKEKEEFREAKPRSLRFTWSMK 657
QY 524 NFISSKEQIFVVIKDKPLSSIKADIVHAFLSIPSLSHSVISQTSFRAEYKATGGPAVF 583
DB 658 TTSSMEPNEMREIRKVLDAKNSQSELHEKYMLL--CMHGTPGHEDP----- 702
QY 584 QRPVKQVDITYTEGGEAQKENGISVTFLLSGSPRRPKRVVETIQAO 633
DB 703 ---VOMEVEVC-----KLPRLSLNGVRFRKRSIGTSMAPFNIAASKIANEL 743

RESULT 3

B90120
SNF1-related protein kinase [imported] - Guillardia theta nucleomorph
C;Species: nucleomorph Guillardia theta
A;Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
A;Accession: B90120
R;Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Reit
Nature 410, 1091-1096, 2001
A;Title: The highly reduced genome of an enslaved algal nucleus.
A;Reference number: A99082; PMID:11323671; PMID:11323671
A;Accession: B90120
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-401 <DOU>
A;Cross-references: GB:AF083031; NID:g13794278; PIDN:AAK39655.1; GSPDB:GN00152
C;Genetics:
A;Gene: kin(snf2)
A;Map position: 3
A;Genome: nucleomorph
C;Keywords: nucleomorph

Query Match 22.6%; Score 790; DB 2; Length 401;
Best Local Similarity 42.7%; Pred. No. 3.1e-24;
Matches 159; Conservative 87; Mismatches 102; Indels 24; Gaps 7;

QY 14 QYGVPRLEKTLGKGTGLVKGVCVTCQKVAIKIVNREKLS--SVLMKVERETAILK 71
DB 10 RFVGYLDTLGVGATGKVKLAHGRTEKKEKGVKIKKDLFYDKPSLRKIQREISVMK 69
QY 72 LIEHPHVLKLDVYENKYLIVLHVSGGELFDYLVKKGRLTPKEARFFROIISALDF 131
DB 70 LMFHPHVIKLYDVLESKYLFLIIEVASKGELENYLVKREKLENREALKFFHIIISLEY 129
QY 132 CHGSHICHRDLKPENLLDEKNIRIADFGMASLQVSDLSLETSCGSPHYACPEVIRGEK 191
DB 130 CHKHICHRDLKLENLLDMKQLKIADFGMASLSIPNIMLKTFCGSPHYASPEVWSNEP 189
QY 192 YDRKADVMSGCVILFALLVGLPDD--DNLRLLEKVKGVFMHPHFIIPDCQSLIRG 249
DB 190 YNGIKADINSGCIIYALVVGKLPYDEENDNMKLFNKFIRFPPRIPIIHPDCRDLIRA 249
QY 250 MIEVDAARLTLEHIOKHIWYIGGKNEPEPEQIPRKVQIRSLP-----SLEDIPDVL 303
DB 250 LLTINPKRITIDIKIKHPY---KSPPLPES---CRISQNLSPASVQNPINPDEII 303
QY 304 DSMHSLGCFDRNKLQDLLSEENQERKMYFLLLDRKERYPSQDEDEDLPPRNEIDPPRK 363

```
Db 304 SFLLPLQLVQDKTKTLCGILSTKPSFLVLYRQLEWRKQKMDSVRSNLI---NEANFKRK 360
Qy 364 RVDSPMLNRHGK 375
Db 361 K-----LFGQK 367

RESULT 4
S37928
probable purine nucleotide-binding protein YKL101w - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein YKL433
C:Species: Saccharomyces cerevisiae
C>Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 24-Sep-1999
C:Accession: S37928; S39084
R:Cheret, G.; Fukuhara, H.; Bolotin-Fukuhara, M.; Daignan-Fornier, B.; Pallier, C.; Puzo
submitted to the Protein Sequence Database, March 1994
A:Reference number: S37920
A:Accession: S37928
A:Molecule type: DNA
A:Residues: 1-1518 <CHR>
A:Cross-references: EMBL:Z28101; NID:G486168; PIDN:CAA81941.1; PID:G486169; MIPS:YKL101w
A:Experimental source: strain S288C
R:Pallier, C.; Valens, M.; Puzos, V.; Fukuhara, H.; Cheret, G.; Sor, F.; Bolotin-Fukuhara
Yeast 9, 1149-1155, 1993
A:Title: DNA sequence analysis of a 17 kb fragment of yeast chromosome XI physically loc
protein kinases.
A:Reference number: S39084; MUID:94078677; PMID:8256524
A:Accession: S39084
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-1518 <PAL>
A:Cross-references: EMBL:X71133; NID:G431205; PIDN:CAA50456.1; PID:G431215
A:Experimental source: strain S288C
C:Genetics:
A:Gene: SGD:HS11
A:Cross-references: SGD:S0001584; MIPS:YKL101w
A:Map position: 11L
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog
C:Keywords: ATP; P-loop; purine nucleotide binding; serine/threonine-specific protein ki
F:79-369/Domain: protein kinase homolog <KIN>
F:79-86/Region: nucleotide-binding motif A (P-loop)
F:87-95/Region: protein kinase ATP-binding motif
F:85/Binding site: ATP/GTP (lys) #status predicted

Query Match 22.6%; Score 790; DB 2; Length 1518;
Best Local Similarity 30.1%; Pred. No. 1.1e-23;
Matches 239; Conservative 107; Mismatches 265; Indels 182; Gaps 21;

Qy 16 VGPYRLKTLGKGTGLVGLGVHCVTCQKVAIKIYNREKL----- 55
Db 78 VGPWKLKTLGKSGSRVRLAKNMTGQLAAIKIVPKKAFVHCSSNGTVPNSYSSMVT 137
Qy 56 ----SESVLMK-----VERETAILKLEHPVHLKHDVYENKKYLYLVLEHVS 99
Db 138 SNVSPSTASREHNSHTNPFGIERIVIMKLSHTNMALFEWENKSELYLVLEYVD 197
Qy 100 GGEFLDYLVKGRLLTPKEARKFFROIISALDPCHSHSICHRDLKPENLLDLKKN-NIRIA 158
Db 198 GGEFLDYLVKGRLLTPKEARKFFROIISALDPCHSHSICHRDLKPENLLDLKKN-NIRIA 257
Qy 159 DFGMASLQVDSLLSTSCSPHYACPEVIRGEKDYGRKADVMSCGVILFALLVGLPFPDD 218
Db 258 DFGMAALEPNKLLKTSKSPHYASPEIVMGPRPYHGGPSDVWSCGIVLFALLTGHLPND 317
Qy 219 DNLROLLEKVRGVFMHPHFPDPCQSLRGMIEVDAARRLTLEHIQHIWYGGKNEPE 278
Db 318 DNIKKLLKVGSKGYQMPFNSLSSEARDLISLVIDPEKRITTOELKH--PLIKKYDDL 375
Qy 279 PEQPIPRKVO-----IRSLPLEDIDPDVLDMSHSLGCFDRDN 316
Db 376 PVNVLRLKRNKDNMARGNSDLHLNNVSPSIVTLHSGKEIDESILRSLOILMHGVSRE 435
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Qy 317 KLLQDLILSEBENQEKMIYFLLLDRKERY-----PSOEDDLPPRNEIDPPRKVDSPMLN 371
Db 436 LITAKLLQKPMSEKLFYSLLQYKQHSISLSSSENKKSATSESSVNERIEVASKTAN 495
Qy 372 RHGKRAPER--KSNEVLVS-TDGGSPVPARRAIE-----MAHQGRSRS----- 412
Db 496 NTGLRSENNDVKTLHSLLEIHSDETSTVQNQNAITGVNTINAPVLAQKQSFINTLSQPE 555
Qy 413 -----ISGASSG-----LSTSPLSPRVTPHPSPR 437
Db 556 SDKAERAVTLPAIPFNASSRIFRNSVTSSRRRRLRLSNLSLSTSRSTVH 615
Qy 438 GSPLTPKGTPTVHTPKESPAGTPTNTPSPSPSYGGVPMRRLNSIKNSFLGSPRFHRKL 497
Db 616 DNEMPLPQ-LPKSPSRVSLSRRAIHASPSKSIH-----KSLSRKNIAATVAARRTL 666
Qy 498 QVTPPEMSNLTPESPPELAKKWFNGFISLEKEEQIFVVIKPKPLSSIADIVHAFLSI 557
Db 667 Q-----NSASKRSYLSQSIKRS-----LNLND-----LLVFDPLPSKPKPASENVNKE 712
Qy 558 PSLSHSVISOTSRA-----EYKATGGPAVFOKPVKFOVDITVTE 597
Db 713 P-----HSLSDSDFEILCDQLFGNALDRILEEEDNEKERDQORQNDTKSSADTTIS 769
Qy 598 GGBAQRKEN-----GIYSVTFTLLSGPSRRFRKV-----VETIQALLSTHDPAA 642
Db 770 GVSTNKENEGPEYPTKIEKNQFNMYKPSNMGLSFPPIFEKENTLSSSYLEEQKPKRA 829
Qy 643 QHLSDDTTCNMEMM 655
Db 830 A-LSDDITNSFNKM 841

RESULT 5
JC1446
serine/threonine-specific protein kinase (EC 2.7.1.-) AK21 - Arabidopsis thaliana
N:Alternate names: protein kinase SNF1 homolog
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 11-Jun-1999
C:Accession: JC1446; S5266; S66334
R:LeGuen, L.; Thomas, M.; Bianchi, M.; Halford, N.G.; Kreis, M.
Gene 120, 249-254, 1992
A:Title: Structure and expression of a gene from Arabidopsis thaliana encoding a protein
A:Reference number: JC1446; MUID:93013041; PMID:1339373
A:Accession: JC1446
A:Molecule type: DNA
A:Residues: 1-512 <LEG>
A:Cross-references: GB:M93023; NID:G166599; PIDN:AAA32736.1; PID:G166600
R:Thuemmler, F.; Kirchner, M.; Teuber, R.; Ditttrich, P.
submitted to the EMBL Data Library, May 1995
A:Description: Differential accumulation of the transcripts of 22 novel protein kinase ge
A:Reference number: S58256
A:Accession: S58266
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 144-198 <THU>
R:Thuemmler, F.; Kirchner, M.; Teuber, R.; Ditttrich, P.
Plant Mol. Biol. 29, 551-565, 1995
A:Title: Differential accumulation of the transcripts of 22 novel protein kinase genes ir
A:Reference number: S66314; MUID:96123233; PMID:8534852
A:Accession: S66334
A:Molecule type: DNA
A:Residues: 144-198 <TH2>
A:Cross-references: EMBL:X86966; NID:G928909; PIDN:CAA60529.1; PID:G928910
C:Comment: This enzyme plays an important role in a signal transduction cascade regulati
C:Genetics:
A:Gene: AK1n10; AK21
A:Introns: 64/1; 125/3; 186/3; 230/3; 292/3; 322/3; 350/3; 396/3; 475/3
C:Function:
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine
C:Superfamily: AMP-activated protein kinase; protein kinase homolog
C:Keywords: ATP; magnesium; phosphotransferase; serine/threonine-specific protein kinase
```

[illegible]

db 359 -RTPEA-----GASPVGHWIPAHVDHYGLGARS 385

1 28 CUBRI KRENTI I DEVAINTPIA DECMASI OV/CDNI I ETSCCSPHYA CBEVITRGEKYDCRKA 1 9

[illegible]

33

A_Map position: X .
 n | r

RESULT 12

Query M

Query Match 21.7%; Score 759.5; DB 2; Length 713;

Best Local Similarity 29.6%, Pred. No. 8e-23;
Matches 213; Conservative 110; Mismatches 246; Indels 151; Gaps 18;

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QY      10 AQAQYVGPYRLEKTLGKGTGLVKKLGVCVTCOKVAIKIWNREKLGSEVLVKYVERETAI 69
      DB      47 ADSQPHIGNYRLKTLKTKGKGNFAKVKLARHILTGREVAIKIDKTLQNPSTSLQKLFREVI 106
QY      70 LKLEIHPHVAKLHDVYENKKYLYLVLEHVSGGELFDYLVKKGRUTPTPEARKFPQIISAL 129
      DB      107 MKTLNHPNIYVKLFEVETQKTLYLIMEYASGGKVFYDLVAHGRMKKEARSKFRQIVSAV 166
QY      130 DFCHSHSICHRDLKPENLLDDEKNRIRIADFGMASLQVGDLSLLETSCGSHVACPEVIRG 189
      DB      167 QYCHQKRIVARDLKAENLLDADWNIIKIADFGFNEFTVVGKGLDTFCGSPPYAPELLFQG 226
QY      190 EKYDGRKADYVSCGVILFALLVAGALPDDDNLRLQLLEKVKRGVFMHPHFIIPDQCQSLLRG 249
      DB      227 KKYDGPVDVMSLGVILVTVSGSLPPDQGNLKELRERVLRGKYRIIPPYMTDCENLLKR 286
QY      250 MIEVDAARRLTLEHIOQHIIWYIGKNPEPEPQPIPRKVOIRSLPSLEDIDDPDVLDSMHSL 309
      DB      287 FLVLNPIKRGTLQEIQMDKRWINAGHEEDLKPFEV-----PELDISDOKRIDIMVGM 338
QY      310 GCFDRNRKLLQDLLSEENOSKMIYFLLLDKERYPSQEDDLPPRNEIDPPRKVDSPM 369
      DB      339 GYSGQE---IQESLSKWKYDEITATYLLGRKS-----SEVRP-----SSD 376
QY      370 LNRHGKRPRKSKMEVLVSVD-----GGSPVPARRAI-----EMAQHGQRS 410
      DB      377 LNNSTGQSPHHKVRQSVSSSQKQRRYSDHAGPGIPSVVAYPKRSQTSSTADSLKEDGISS 436
QY      411 RSTSGASSGLSTPLSPSPRVTPHPSPRGSPPLTPKPGTPVHTPKESPA-----457
      DB      437 RKSTGSVAGGKGIAPASPMLGASNPKNKADIPERKKSST-VFSSNTASGCGMTRRNTYVCS 495
QY      458 -----CTPNPTPPS-----SPSVGGVPWEARL---NSIKNSFLGSPRF 492
      DB      496 ERTTDDRHSHVIQNGKENSITPDQRTPVASTHISAAATPDRIRPRGTASRSTFHGQPR- 554
QY      493 HRRKLQVPTPEEMSNLTPSSPELAKXS-----WFGNFI-SLEKEQIFVVIKD-----K 541
      DB      555 ERRTATYNGPPASPSPSLGHEATPLQSTRSGSTTLFSLKTSKLTSRNVSAKQKDNKEAK 614
QY      542 PLSSIKADIHAFILSIPLSHSVISQTSFRAEYKATGG--PAVFQPKPVKFOVD-----592
      DB      615 PRS-----LRFWTSMKTTSSMDPGDMWRERIKVYLDANNCDYE 651
QY      593 -----ITYTGEGAQKEN-----GIYSVTFITLLSGPSRRFRKRWETIQAOQL 633
      DB      652 QRERFLFCVHGDDHAENLVQWMEVCKLPRLSLNGVRFKISGTISIAFKNIASKIANEL 711
```

RESULT 13
JC7500
qik protein - chicken
N;Alternate names: Qin-induced kinase
C;Species: Gallus gallus (chicken)
C;Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 17-Nov-2000
C;Accession: JC7500
R;Xia, Y.; Zhang, Z.; Kruse, U.; Vogt, P.K.; Li, J.
Biochem. Biophys. Res. Commun. 276, 564-570, 2000
A;Title: The new serine:threonine kinase, Qik, is a target of the qin oncogene
A;Reference number: JC7500
A;Contents: Embryo fibroblasts
A;Accession: JC7500
A;Molecule type: mRNA
A;Residues: 1-798 <XIA>
A;Cross-references: GB:AF219232
C;Comment: This protein, a member of the AMPK/SNF1 family of serine/threonine X
C;Genetics:
A;Gene: qik
C;Keywords: protein kinase

```

RESULT 14
T07415
probable serine/threonine-specific protein kinase (EC 2.7.1.1.-) PKIN1 - potato
N;Alternate names: SNF1-related protein kinase
C;Species: Solanum tuberosum (potato)
C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 20-Jun-2000
C;Accession: T07415
R;Halford, N.G.
submitted to the EMBL Data Library, March 1996
A;Reference number: Z15022
A;Accession: T07415
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-504 <HAL>
A;Cross-references: EMBL:X95997; NID:g1216279; PIDN:CAA65244.1
C;Genetics:

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Search completed: November 26, 2003, 12:02:38
Job time : 21.3229 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 26, 2003, 11:49:36 ; Search time 36.6897 Seconds
(without alignments)
2630.326 Million cell updates/sec

Title: US-10-054-579-4

Perfect score: 3188

Sequence: 1 MKVEREAILKIEHPHLK.....TNCMEMTGRLSKGIIPKS 608

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq 19Jun03.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3188	100.0	608	23	Human kinase NHP #
2	3188	100.0	664	23	Human PKIN-18 prot
3	3188	100.0	668	23	Human kinase NHP #
4	3188	100.0	668	24	Human serine prote
5	3065	96.1	674	23	Human protein kina
6	3028	95.0	585	24	Human serine prote
7	2545.5	79.8	703	24	Human kinase #3.
8	2545.5	79.8	778	24	Human kinase #1.
9	2545.5	79.8	794	22	Human protein kina

10	2545.5	79.8	794	23	AAE16271	Human kinase PKIN-
11	2514.5	78.9	754	24	AAO16504	Human cell cycle-r
12	2386.5	74.9	762	24	ABE98744	Human kinase #2.
13	1754	55.0	851	22	ABE62061	Drosophila melanog
14	1036.5	32.5	301	22	ABE11052	Human HRPK-1 hom
15	766.5	24.0	1349	22	AAE70854	C albicans apoptos
16	695	21.8	514	21	AAE03420	Soybean putative c
17	695	21.8	514	21	ABR40714	Glycine max oil tr
18	693.5	21.8	761	24	ABP96068	Human protein kina
19	689	21.6	768	24	AAW78349	Human protein SEQ
20	688.5	21.6	745	24	AAE33550	Human microtubule
21	688.5	21.6	796	24	ABU11830	Human WDDT polypep
22	686.5	21.5	691	23	AAE19050	Human PAR-1B alpha
23	686.5	21.5	724	23	AAE19051	Human PAR-1B beta
24	686	21.5	504	24	ABR40815	Cucumis sativus oi
25	685.5	21.5	724	24	ABU08527	Human serine/threo
26	685.5	21.5	775	24	AAO16606	Cell cycle-regulat
27	684	21.5	769	23	ABP62966	Human polypeptide
28	682.5	21.4	722	17	AAE98227	Rat neuronal prote
29	681.5	21.4	452	21	AAE36159	Arabidopsis thalia
30	681.5	21.4	454	21	AAE36158	Arabidopsis thalia
31	681.5	21.4	512	21	AAE36157	Arabidopsis thalia
32	681.5	21.4	512	23	AAO17663	A thaliana AKIN11.
33	680	21.3	505	24	ABR40810	Oryza sativa oil t
34	679	21.3	514	24	ABR40816	Glycine max oil tr
35	679	21.3	515	21	AAE03422	Soybean putative c
36	679	21.3	515	24	ABR40716	Glycine max oil tr
37	677	21.2	579	21	AAE03417	Corn putative carb
38	677	21.2	579	24	ABR40709	Zea mays oil trait
39	676.5	21.2	512	23	AAO17664	A thaliana AKIN11
40	675.5	21.2	752	22	AAE11782	Human kinase (PKIN
41	675.5	21.2	752	22	AAE93956	Human polypeptide.
42	675.5	21.2	752	23	ABE04433	Human neuronal ser
43	675.5	21.2	752	24	ABE73794	Human MARK protein
44	672.5	21.1	923	22	AAE11773	Human kinase (PKIN
45	672.5	21.1	926	22	AAE65631	Novel protein kina

ALIGNMENTS

RESULT 1

ABB09558
ID ABB09558 standard; Protein; 608 AA.

XX ABB09558;

XX 21-OCT-2002 (first entry)

XX Human kinase NHP #2, SEQ ID NO:4.

XX Human; kinase; NHP; chromosome 11; signal transduction; cytoplasmic;
XX nuclear; brain; pituitary; hypothalamus; adipose; cerebellum;
XX adrenal gland; foetal lung; foetal brain; cancer; drug screening;
XX mental disorder; diagnostic reagent; clinical trial monitoring; cosmetic;
XX nutraceutical; mutation detection; gene expression analysis;
XX chromosome mapping; transgenic animal; cytostatic; gene therapy;
XX enzyme.

XX Homo sapiens.

XX WO200259287-A2.

XX 01-AUG-2002.

XX 22-JAN-2002; 2002WO-US01818.

XX 23-JAN-2001; 2001US-263378P.

XX (LEXI-) LEXICON GENETICS INC.

XX Turner CA, Mathur B;

XX

DR WPI: 2002-599780/64.
 DR N-PSDB; ABQ77626.
 XX Novel polynucleotide encoding human proteins sharing sequence
 PT similarity with animal kinases, useful for drug screening, diagnosis,
 PT in gene therapy of disorders and diseases e.g. cancer -
 XX
 PS Claim 4; Page 39-40; 40pp; English.
 XX
 CC The invention relates to novel human kinases (AB095557, AAB09558),
 CC referred to as NHPs, and to nucleic acids encoding them (ABQ77625,
 CC ABQ77626). The NHPs have structural similarity with animal kinases
 CC including serine-threonine kinases, carbon catabolite repressing kinases,
 CC calcium/calmodulin-dependent protein kinases, and cAMP-dependent protein
 CC kinases. The NHPs do not contain consensus signal sequences, indicating
 CC that they may be cytoplasmic or nuclear proteins, and are thought to be
 CC involved in signal transduction. Polynucleotides encoding NHPs were
 CC obtained using human brain, pituitary, hypothalamus, adipose, cerebellum,
 CC adrenal gland, foetal lung, and foetal brain cDNAs and primers derived
 CC from human genomic DNA. The gene encoding the NHPs is located on
 CC chromosome 11. NHP nucleotides and proteins are useful for treating
 CC mental, biological or medical disorders including cancer, and for
 CC screening compounds useful in the treatment of such conditions. They can
 CC also be used as diagnostic reagents, in clinical trial monitoring and in
 CC cosmetic and nutraceutical applications. NHP nucleotides can additionally
 CC be used in the detection of disease-associated mutations, in the analysis
 CC of gene expression, for mapping chromosome 11, for the recombinant
 CC expression of NHPs, to generate transgenic animals, in gene therapy,
 CC and as part of ribozyme and/or triple helix sequences useful in the
 CC modulation of NHP gene expression. The present sequence represents a
 CC 608 amino acid NHP (#2).
 XX
 SQ Sequence 608 AA;
 Query Match 100.0%; Score 3188; DB 23; Length 608;
 Best Local Similarity 100.0%; Pred. No. 2.2e-228;
 Matches 608; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 MKVERETAILKLEHSHVHLKLDVYENKYLVLVLEHVSGLGELFDYLVKGRLLTPKEARK 60
 1 MKVERETAILKLEHSHVHLKLDVYENKYLVLVLEHVSGLGELFDYLVKGRLLTPKEARK 60
 61 FFRQIISALDFCHSHSICHRDLKLENLLDEKNNIRIADFGWASLQVGSLSLETSCGSPH 120
 61 FFRQIISALDFCHSHSICHRDLKLENLLDEKNNIRIADFGWASLQVGSLSLETSCGSPH 120
 121 YACPEVIRGEKYDGRKADVWCGVILFALLVGLALPFDNDNLRLQLEKVKRGVFMHPFIP 180
 121 YACPEVIRGEKYDGRKADVWCGVILFALLVGLALPFDNDNLRLQLEKVKRGVFMHPFIP 180
 181 PDCOSLLRGMTEVDAARLTLEHIOKHITWYIGGKNEPEPEQIPRKVQIRSLPSLEIDP 240
 181 PDCOSLLRGMTEVDAARLTLEHIOKHITWYIGGKNEPEPEQIPRKVQIRSLPSLEIDP 240
 241 DVLDSMSLGCFRDRNKLQDLLSEENQERKMIFLLDRKERYPSQDEDELPNREIDP 300
 241 DVLDSMSLGCFRDRNKLQDLLSEENQERKMIFLLDRKERYPSQDEDELPNREIDP 300
 301 PRKRVDSPLNRHGRKRRPERKSMVELSVTDGGSVPAPARRAEMAQHQRSSISGASGL 360
 301 PRKRVDSPLNRHGRKRRPERKSMVELSVTDGGSVPAPARRAEMAQHQRSSISGASGL 360
 361 STPLSSPRVTPHPSPRGSPPLTPKGTVPHTPKSPAGTNPPTPSSPSVGVVPMARLN 420
 361 STPLSSPRVTPHPSPRGSPPLTPKGTVPHTPKSPAGTNPPTPSSPSVGVVPMARLN 420
 421 SIKNSFLGSPFRHRRKLQVPTPEEMSNLTPESSPELAKKSWFGNFISLEKEEQIFVWIKD 480
 421 SIKNSFLGSPFRHRRKLQVPTPEEMSNLTPESSPELAKKSWFGNFISLEKEEQIFVWIKD 480
 481 KPLSSIKADIVHAFISLPSLSHVSISQTSFRAEYKATGPGVAFQKPVKFDVITYTEGGE 540
 481 KPLSSIKADIVHAFISLPSLSHVSISQTSFRAEYKATGPGVAFQKPVKFDVITYTEGGE 540

QY 541 AOKENGIYVETLLSGSPRRKRVVETIOAQLISTHDPAAQHLSDDTTCMMMTGRLS 600
 DB 541 AOKENGIYVETLLSGSPRRKRVVETIOAQLISTHDPAAQHLSDDTTCMMMTGRLS 600
 QY 601 KCGIIPKS 608
 DB 601 KCGIIPKS 608
 RESULT 2
 ID AAE21723
 XX AAE21723 standard; Protein; 664 AA.
 AC AAE21723;
 DT 16-JUL-2002 (first entry)
 XX Human PKIN-18 protein.
 KW Human; kinase; enzyme; PKIN-18 protein; immune system disorder; anaemia;
 KW acquired immune deficiency syndrome; thymic hypoplasia; Crohn's disease;
 KW asthma; neurological disorder; epilepsy; Charcot-Marie-Tooth disease;
 KW AIDS; seizures; cell proliferative disorder; cancer; adenocarcinoma;
 KW leukaemia; lymphoma; melanoma; myeloma; sarcoma; developmental disorder;
 KW Down's syndrome; gene therapy; protein therapy; cytostatic.
 XX Homo sapiens.
 OS
 FH Key
 FT Domain 15..266
 FT /note= "Eukaryotic protein kinase domain"
 FT Domain 16..257
 FT /note= "Protein kinase domain"
 FT Domain 17..257
 FT /note= "Protein kinase domain"
 FT Domain 36..256
 FT /note= "Protein kinase domain"
 FT WO200218557-A2.
 XX 07-MAR-2002.
 XX 31-AUG-2001; 2001WO-US27219.
 XX 31-AUG-2000; 2000US-229873P.
 PR 08-SEP-2000; 2000US-231357P.
 PR 14-SEP-2000; 2000US-232654P.
 PR 22-SEP-2000; 2000US-234902P.
 PR 29-SEP-2000; 2000US-236499P.
 PR 06-OCT-2000; 2000US-238389P.
 PR 13-OCT-2000; 2000US-240542P.
 XX (INCY-) INCYTE GENOMICS INC.
 XX Bandman O, Nguyen DB, Wallia NK, Hafalia AJA, Yao MG, Gandhi AR;
 XX Gururajan R, Ding L, Patterson C, Yue H, Baughn MR, Tribouley CM;
 XX Thornton M, Elliott VS, Lu Y, Ison CH, Au-Young J, Tang YT;
 XX Azimzai Y, Burrill JB, Marcus GA, Zingler KA, Lu DM, Lal PG;
 XX Ramkumar J, Warren BA, Kearney L, Pollicky JL, Thangavelu K;
 XX Burford N;
 XX WPI: 2002-329769/36.
 DR N-PSDB; AAD34315.
 DR
 XX New human kinases, useful for diagnosing, treating or preventing immune
 PT system disorders (e.g. Crohn's disease), neurological disorders (e.g.
 PT epilepsy), or cell proliferative disorders (e.g. cancers such as
 PT leukemia or lymphoma) -
 XX
 PS Claim 73; Page 181-183; 218pp; English.
 XX The present invention relates to human kinases (PKIN) and polynucleotides
 CC

CC encoding such proteins. PKIN sequences of the invention are useful for
CC diagnosing, treating or preventing disorders associated with aberrant
CC expression of PKIN, particularly immune system disorders (e.g. acquired
CC immune deficiency syndrome (AIDS), thymic hypoplasia, Crohn's disease,
CC anaemia, asthma), neurological disorders (e.g. epilepsy, Charcot-Marie-
CC Tooth disease or seizures), cell proliferative disorders (e.g. cancers
CC such as adenocarcinoma, leukaemia, lymphoma, melanoma, myeloma, sarcoma),
CC and developmental disorders (e.g. Down's syndrome). They are also used
CC in gene therapy and protein therapy. The present sequence is human
CC PKIN-18 protein.
XX
SQ Sequence 664 AA;

Query Match 100.0%; Score 3188; DB 23; Length 664;
Best Local Similarity 100.0%; Pred. No. 2.4e-228;
Matches 608; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MKVEREIAILKLIIEHPHVLKLDVYENKYLVLVLEHVSQGLFDYLVKGRLLTPKEARK 60
Db 57 MKVEREIAILKLIIEHPHVLKLDVYENKYLVLVLEHVSQGLFDYLVKGRLLTPKEARK 116
Qy 61 FFRQIISALDFCHSHSICHRLDKPENLLDEKNNIRIADFGWASIQVDSLETSCGSPH 120
Db 117 FFRQIISALDFCHSHSICHRLDKPENLLDEKNNIRIADFGWASIQVDSLETSCGSPH 176
Qy 121 YACPEVIRGEKYGDKADVWSCGVILFALLVGLPFDNRLQLLEKVKRGVFMHPFIP 180
Db 177 YACPEVIRGEKYGDKADVWSCGVILFALLVGLPFDNRLQLLEKVKRGVFMHPFIP 236
Qy 181 PDCQSLLRGMIEVDAAARLLTLEHIQKHIWYIGKQNEPEPEQIPRKVQIRSLPSLEDIDP 240
Db 237 PDCQSLLRGMIEVDAAARLLTLEHIQKHIWYIGKQNEPEPEQIPRKVQIRSLPSLEDIDP 296
Qy 241 DVLDSMHSIGCFDRNKLQDLSEENQEKMIYFLLLDKERYPSQDEDLPPRNEIDP 300
Db 297 DVLDSMHSIGCFDRNKLQDLSEENQEKMIYFLLLDKERYPSQDEDLPPRNEIDP 356
Qy 301 PRKRVDSPLMLNHRGRRPERKSMESVLSVTDGSPVPARRAIEAQMAGORSISGASSGL 360
Db 357 PRKRVDSPLMLNHRGRRPERKSMESVLSVTDGSPVPARRAIEAQMAGORSISGASSGL 416
Qy 361 STSPSSSRVTPHPSPRSGPLTPKGTVPHTPKESPAGTPNPPTPSSPSVGVVWRAELN 420
Db 417 STSPSSSRVTPHPSPRSGPLTPKGTVPHTPKESPAGTPNPPTPSSPSVGVVWRAELN 476
Qy 421 STKNSFLGSPRHRKLVQPTPEMSNLTPSSPELAKKSWFGNFISLEKEQIFVWIKD 480
Db 477 STKNSFLGSPRHRKLVQPTPEMSNLTPSSPELAKKSWFGNFISLEKEQIFVWIKD 536
Qy 481 KPLSSIKADIVHAFSLISPLSHSVISQTSFRAEYKATGPAVFPKPVQFVDITYEGGE 540
Db 537 KPLSSIKADIVHAFSLISPLSHSVISQTSFRAEYKATGPAVFPKPVQFVDITYEGGE 596
Qy 541 AQKENGIVSVTTLTSGSRRRPRVETIQALLSTHDPAAQHLSDTTNCWEMMTGRLS 600
Db 597 AQKENGIVSVTTLTSGSRRRPRVETIQALLSTHDPAAQHLSDTTNCWEMMTGRLS 656
Qy 601 KCGIIPKS 608
Db 657 KCGIIPKS 664

RESULT 3
ABB09557
ID ABB09557 standard; Protein; 668 AA.
XX
AC ABB09557;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human kinase NHP #1, SEQ ID NO:2.
XX
KW Human; kinase; NHP; chromosome 11; signal transduction; cytoplasmic;

KW nuclear; brain; pituitary; hypothalamus; adipose; cerebellum;
KW adrenal gland; foetal lung; foetal brain; cancer; drug screening;
KW mental disorder; diagnostic reagent; clinical trial monitoring; cosmetic;
KW nutraceutical; mutation detection; gene expression analysis;
KW chromosome mapping; transgenic animal; cycostatic; gene therapy;
XX
OS Homo sapiens.
XX
PN W0200259287-A2.
XX
PD 01-AUG-2002.
XX
PF 22-JAN-2002; 2002WO-US01818.
XX
PR 23-JAN-2001; 2001US-263378P.
XX
FA (LEXI-) LEXICON GENETICS INC.
XX
PI Turner CA, Mathur B;
XX
DR MPI: 2002-599780/64.
DR N-PSDB; ABQ77625.
XX
PT Novel polynucleotide encoding human proteins sharing sequence
PT similarity with animal kinases, useful for drug screening, diagnosis,
PT in gene therapy of disorders and diseases e.g. cancer -
XX
PS Claim 2; Page 37-38; 40pp; English.
XX
CC The invention relates to novel human kinases (ABB09557, AAB09558),
CC referred to as NHPs, and to nucleic acids encoding them (ABQ77625,
CC ABQ77626). The NHPs have structural similarity with animal kinases
CC including serine-threonine kinases, carbon catabolite repressing kinases,
CC calcium/calmodulin-dependent protein kinases, and cAMP-dependent protein
CC kinases. The NHPs do not contain consensus signal sequences, indicating
CC that they may be cytoplasmic or nuclear proteins, and are thought to be
CC involved in signal transduction. Polynucleotides encoding NHPs were
CC obtained using human brain, pituitary, hypothalamus, adipose, cerebellum,
CC adrenal gland, foetal lung, and foetal brain cDNAs and primers derived
CC from human genomic DNA. The gene encoding the NHPs is located on
CC chromosome 11. NHP nucleotides and proteins are useful for treating
CC mental, biological or medical disorders including cancer, and for
CC screening compounds useful in the treatment of such conditions. They can
CC also be used as diagnostic reagents, in clinical trial monitoring and in
CC cosmetic and nutraceutical applications. NHP nucleotides can additionally
CC be used in the detection of disease-associated mutations, in the analysis
CC of gene expression, for mapping chromosome 11, for the recombinant
CC expression of NHPs, to generate transgenic animals, in gene therapy,
CC and as part of ribozyme and/or triple helix sequences useful in the
CC modulation of NHP gene expression. The present sequence represents a
CC 668 amino acid NHP (#1).
XX
SQ Sequence 668 AA;

Query Match 100.0%; Score 3188; DB 23; Length 668;
Best Local Similarity 100.0%; Pred. No. 2.5e-228;
Matches 608; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MKVEREIAILKLIIEHPHVLKLDVYENKYLVLVLEHVSQGLFDYLVKGRLLTPKEARK 60
Db 61 MKVEREIAILKLIIEHPHVLKLDVYENKYLVLVLEHVSQGLFDYLVKGRLLTPKEARK 120
Qy 61 FFRQIISALDFCHSHSICHRLDKPENLLDEKNNIRIADFGWASIQVDSLETSCGSPH 120
Db 121 FFRQIISALDFCHSHSICHRLDKPENLLDEKNNIRIADFGWASIQVDSLETSCGSPH 180
Qy 121 YACPEVIRGEKYGDKADVWSCGVILFALLVGLPFDNRLQLLEKVKRGVFMHPFIP 180
Db 181 YACPEVIRGEKYGDKADVWSCGVILFALLVGLPFDNRLQLLEKVKRGVFMHPFIP 240
Qy 181 PDCQSLLRGMIEVDAAARLLTLEHIQKHIWYIGKQNEPEPEQIPRKVQIRSLPSLEDIDP 240
KW Human; kinase; NHP; chromosome 11; signal transduction; cytoplasmic;

Db 241 PDCQSLRGMIETVDAARRLTLEHIQKHIWYIGKNEPEPEQIPRKVQIRSLPSLEDIDP 300
 Qy 241 DVLDMSHSLGCFRDRNKLQDLISEENQKMIYFLLDRKERYPSQEDDLPRNEIDP 300
 Db 301 DVLDMSHSLGCFRDRNKLQDLISEENQKMIYFLLDRKERYPSQEDDLPRNEIDP 360
 Qy 301 PRKRVDSPLNHRHGKRRPERKSMVLSVTDGSPVPARRAIEMAHQGQRSISGASSGL 360
 Db 361 PRKRVDSPLNHRHGKRRPERKSMVLSVTDGSPVPARRAIEMAHQGQRSISGASSGL 420
 Qy 361 STSPLSSPRVTPHPSGRGSPPLTPKGTVPVHTPKESPACTNPPTPPSPSVGGVFWARLN 420
 Db 421 STSPLSSPRVTPHPSGRGSPPLTPKGTVPVHTPKESPACTNPPTPPSPSVGGVFWARLN 480
 Qy 421 SIKNSFLGSPFRHRRKLQVPTPEMSNLTPESSPELAKKSWFGNFISLEKEBOIFVVIKD 480
 Db 481 SIKNSFLGSPFRHRRKLQVPTPEMSNLTPESSPELAKKSWFGNFISLEKEBOIFVVIKD 540
 Qy 481 KPLSSIKADIVHAFSLPSLSHVSISQTSFRAEYKATGGPAVFQKPVKQVDITYTEGGE 540
 Db 541 KPLSSIKADIVHAFSLPSLSHVSISQTSFRAEYKATGGPAVFQKPVKQVDITYTEGGE 600
 Qy 541 AQKNGIYSVTFTLLSGSPRRFRKRVVETIQAOQLLSTHDPAAOHLSDTTNCMEMWTGRLS 600
 Db 601 AQKNGIYSVTFTLLSGSPRRFRKRVVETIQAOQLLSTHDPAAOHLSDTTNCMEMWTGRLS 660
 Qy 601 KCGIIPKS 608
 Db 661 KCGIIPKS 668

RESULT 4

ABG72382
 ID ABG72382 standard; Protein; 668 AA.
 XX ABG72382;
 AC
 DT 10-FEB-2003 (first entry)
 XX Human serine protein kinase KSE336-1.
 DE
 XX Human; enzyme; chromosome 11p15.5-pter; astrocytoma; meningioma;
 KW pancreatic adenocarcinoma; insulin-dependent diabetes mellitus 2;
 KW helicoid peripapillary chorioretinal degeneration; brain; pancreas;
 KW Beckwith-Wiedemann syndrome; congenital hyperinsulinism; KSE336.
 XX
 OS Homo sapiens.
 XX
 FN US6455292-B1.
 XX
 PD 24-SEP-2002.
 XX
 PF 16-AUG-2001; 2001US-0930181.
 XX
 PR 16-AUG-2001; 2001US-0930181.
 XX
 PA (ORIG-) ORIGENE TECHNOLOGIES INC.
 XX
 PI Shu Y, Fan W, Kovacs KF, Zidanic M, Jay G;
 XX
 DR WPI; 2003-066233/06.
 XX
 DR N-PSDB; ABX13583.
 XX
 PT New isolated polynucleotide coding without interruption for a human
 PT KSE336 polypeptide useful for preventing or treating
 PT diseases/conditions relating to brain and pancreas, e.g. meningioma,
 PT insulin-dependent diabetes mellitus 2
 XX
 PS Claim 1; Fig 2; 34pp; English.
 XX
 CC The invention relates to an isolated polynucleotide (its complement
 CC or a sequence 99% similar to it) coding without interruption for a human
 CC KSE336 polypeptide, a serine protein kinase, comprising the KSE336-1 and

CC KSE336-2 splice variants appearing as ABG72382 and ABG72383. Also
 CC included is a method of identifying an agent that modulates the
 CC expression of KSE336 in brain, pancreas, brain progenitor or pancreas
 CC progenitor cells comprising: (a) contacting a cell population comprising
 CC the cells with a test agent under conditions effective for the test agent
 CC to modulate the expression of KSE336; and (b) determining if the test
 CC agent modulates the expression of KSE336. The polynucleotides are useful
 CC as molecular targets or drug targets, and for detecting, diagnosing,
 CC staging, monitoring, prognosticating, preventing or treating diseases or
 CC conditions relating to brain and pancreas, such as astrocytoma,
 CC meningioma, pancreatic adenocarcinoma, insulin-dependent diabetes
 CC mellitus 2, helicoid peripapillary chorioretinal degeneration, Beckwith-
 CC Wiedemann syndrome or congenital hyperinsulinism. The method and
 CC polynucleotides are useful in research, diagnosis, drug discovery,
 CC therapy, clinical medicine, forensic science and pathology.
 CC The gene for KSE336 is located on chromosome 11p15.5-pter.
 CC The present sequence represents the KSE336 variant KSE366-1.
 XX

SQ Sequence 668 AA;
 Query Match 100.0%; Score 3188; DB 24; Length 668;
 Best Local Similarity 100.0%; Pred. No. 2.5e-228;
 Matches 608; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MKVEREIALKLEIHPHVLKLDHVVYENKYLVLVLEHVSGGELFDYLVKKGRLTPKEARK 60
 Db 61 MKVEREIALKLEIHPHVLKLDHVVYENKYLVLVLEHVSGGELFDYLVKKGRLTPKEARK 120
 Qy 61 FFRQIISALDFCHSHSICHRLDKPENLLDEKNNIRIADFGWASLOVGSLLTSCGSPH 120
 Db 121 FFRQIISALDFCHSHSICHRLDKPENLLDEKNNIRIADFGWASLOVGSLLTSCGSPH 180
 Qy 121 YACPEVIRGEKVDGRKADVWSCGVILFALLVGVLPDNDNLQLEKVKRGVFMHFFIP 180
 Db 181 YACPEVIRGEKVDGRKADVWSCGVILFALLVGVLPDNDNLQLEKVKRGVFMHFFIP 240
 Qy 181 PDCQSLRGMIETVDAARRLTLEHIQKHIWYIGKNEPEPEQIPRKVQIRSLPSLEDIDP 240
 Db 241 PDCQSLRGMIETVDAARRLTLEHIQKHIWYIGKNEPEPEQIPRKVQIRSLPSLEDIDP 300
 Qy 241 DVLDMSHSLGCFRDRNKLQDLISEENQKMIYFLLDRKERYPSQEDDLPRNEIDP 300
 Db 301 DVLDMSHSLGCFRDRNKLQDLISEENQKMIYFLLDRKERYPSQEDDLPRNEIDP 360
 Qy 301 PRKRVDSPLNHRHGKRRPERKSMVLSVTDGSPVPARRAIEMAHQGQRSISGASSGL 360
 Db 361 PRKRVDSPLNHRHGKRRPERKSMVLSVTDGSPVPARRAIEMAHQGQRSISGASSGL 420
 Qy 361 STSPLSSPRVTPHPSGRGSPPLTPKGTVPVHTPKESPACTNPPTPPSPSVGGVFWARLN 420
 Db 421 STSPLSSPRVTPHPSGRGSPPLTPKGTVPVHTPKESPACTNPPTPPSPSVGGVFWARLN 480
 Qy 421 SIKNSFLGSPFRHRRKLQVPTPEMSNLTPESSPELAKKSWFGNFISLEKEBOIFVVIKD 480
 Db 481 SIKNSFLGSPFRHRRKLQVPTPEMSNLTPESSPELAKKSWFGNFISLEKEBOIFVVIKD 540
 Qy 481 KPLSSIKADIVHAFSLPSLSHVSISQTSFRAEYKATGGPAVFQKPVKQVDITYTEGGE 540
 Db 541 KPLSSIKADIVHAFSLPSLSHVSISQTSFRAEYKATGGPAVFQKPVKQVDITYTEGGE 600
 Qy 541 AQKNGIYSVTFTLLSGSPRRFRKRVVETIQAOQLLSTHDPAAOHLSDTTNCMEMWTGRLS 600
 Db 601 AQKNGIYSVTFTLLSGSPRRFRKRVVETIQAOQLLSTHDPAAOHLSDTTNCMEMWTGRLS 660
 Qy 601 KCGIIPKS 608
 Db 661 KCGIIPKS 668

RESULT 5

AAM47830
 ID AAM47830 standard; Protein; 674 AA.
 XX

AA047830;
19-FEB-2002 (first entry)
Human protein kinase 2246 SEQ ID NO 2.
Human; protein kinase 2246; cytostatic; immunomodulator; carcinoma;
anti-inflammatory; analgesic; cardiovascular; cancer; sarcoma;
cellular proliferation disorder; cellular differentiation disorder;
metastatic; haematopoietic disorder; leukaemia; immune disorder;
inflammatory disorder; arthritis; autoimmune disease; diabetes mellitus;
psoriasis; Crohn's disease; cardiovascular disease; virus; pain;
gene therapy.
Homo sapiens.
W0200181588-A2.
01-NOV-2001.
25-APR-2001; 2001WO-US13784.
25-APR-2000; 2000US-199391P.
(MILL-) MILLENNIUM PHARM INC.
Meyers R;
WPI; 2002-045281/06.
N-PSDB; ABA02994, ABA02995.
New protein kinase nucleic acid and polypeptide molecules, designated
2246, useful for diagnosing, preventing or treating cancer or a
cellular proliferation/differentiation disorders, e.g. carcinoma,
sarcoma or leukaemias -
Claim 4; Fig 1; 11pp; English.
The invention relates to the human protein kinase 2246 gene and the
isolated encoded polypeptide with cytostatic, immunomodulator,
anti-inflammatory, analgesic and cardiovascular activity. The 2246
nucleic acid and polypeptide are useful for diagnosing, preventing or
treating a subject having cancer or a cellular proliferation and/or
differentiation disorder or at risk of developing cancer or a cellular
proliferation and/or differentiation disorder. In particular, the
disorder includes carcinoma, sarcoma, metastatic or haematopoietic
disorders (e.g. leukaemias) or cancers of the lung, breast, thyroid, head
neck, prostate or genito-urinary tract. The 2246 nucleic acid and
polypeptide are also useful for treating immune disorders, e.g.
inflammatory (e.g. respiratory inflammation or arthritis), autoimmune
disease (e.g. diabetes mellitus, psoriasis, Wegener's granulomatosis,
Crohn's disease or Grave's disease), for treating cardiovascular
diseases, endothelial cell disorder, viral diseases or pain. The nucleic
acid and polypeptide are also useful for evaluating the efficacy of a
treatment of cancer or a cellular proliferation and/or differentiation
disorder. The nucleic acid is useful for gene therapy. The present
sequence is that of the 2246 protein kinase.
Sequence 674 AA;
Query Match 96.1%; Score 3065; DB 23; Length 674;
Best Local Similarity 99.7%; Pred. No. 3.5e-219;
Matches 585; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MKVEREAILKLEPHVYKLDVYENKYLVLVLEHVSQGLFDYLVKGRLLTPKARK 60
Db 61 MKVEREAILKLEPHVYKLDVYENKYLVLVLEHVSQGLFDYLVKGRLLTPKARK 120
Qy 61 FFRQIISALDFCHSHSICHRDLKPNLLDKNNIRIADFGWASIQVDSILETSCGSPH 120
Db 121 FFRQIISALDFCHSHSICHRDLKPNLLDKNNIRIADFGWASIQVDSILETSCGSPH 180
Qy 121 YACPEVIRGEKYDGRKADVWSCGVILFALLVGPFDNDNLRQLLEKVKRGVFMHFP 180

Db 181 YACPEVIRGEKYDGRKADVWSCGVILFALLVGPFDNDNLRQLLEKVKRGVFMHFP 240
Qy 181 PDCQSLRGMIENVDAARLLTLEHIQKHIVYIGGKNEPEPEPIPRKQVIRSLPSLEDIDP 240
Db 241 PDCQSLRGMIENVDAARLLTLEHIQKHIVYIGGKNEPEPEPIPRKQVIRSLPSLEDIDP 300
Qy 241 DVLDMSHSLGCFDRNKLQDLSEENQEKMIYFLLDKERYPSQEDDLPPRNEIDP 300
Db 301 DVLDMSHSLGCFDRNKLQDLSEENQEKMIYFLLDKERYPSQEDDLPPRNEIDP 360
Qy 301 PRKRVDSPLNLRHGRKPRPKSMVLSVTGGSPVPARRAIEAQAQGRSRSISGASSGL 360
Db 361 PRKRVDSPLNLRHGRKPRPKSMVLSVTGGSPVPARRAIEAQAQGRSRSISGASSGL 420
Qy 361 STSPLSSPRVTPHPSPRGSPPLTPKGTVPVHTPKESPACTNPPTPPSPSVGGVPMARLN 420
Db 421 STSPLSSPRVTPHPSPRGSPPLTPKGTVPVHTPKESPACTNPPTPPSPSVGGVPMARLN 480
Qy 421 SIKNSFLGSPRRHRRKLOVPTPEMSNLTPESSPELAKKSWFCNFIISLEKEEIQFVVIKD 480
Db 481 SIKNSFLGSPRRHRRKLOVPTPEMSNLTPESSPELAKKSWFCNFIISLEKEEIQFVVIKD 540
Qy 481 KPLSSIKADIVHAFSLPSLSHSHSVISQTSFRAEYKATGGPAVFKQPKVQFDITYTEGGE 540
Db 541 KPLSSIKADIVHAFSLPSLSHSHSVISQTSFRAEYKATGGPAVFKQPKVQFDITYTEGGE 600
Qy 541 AQKENGISYVTFLLSGPSRRKRVVETIQAQLLSTHDPAAQHLSD 587
Db 601 AQKENGISYVTFLLSGPSRRKRVVETIQAQLLSTHDPAAQHLSE 647
RESULT 6
ABG72383
ID ABG72383 standard; Protein; 585 AA.
XX AC ABG72383;
XX XX
DT 10-FEB-2003 (first entry)
XX DE Human serine protein kinase KSE336-2.
XX KW Human; enzyme; chromosome 11p15.5-pter; astrocytoma; meningioma;
pancreatic adenocarcinoma; insulin-dependent diabetes mellitus 2;
helicoid peripapillary chorioretinal degeneration; brain; pancreas;
Beckwith-Wiedemann syndrome; congenital hyperinsulinism; KSE336.
XX KW Homo sapiens.
XX OS US6455292-B1.
XX PN 24-SEP-2002.
XX PD 16-AUG-2001; 2001US-0930181.
XX PF 16-AUG-2001; 2001US-0930181.
XX PR (ORIG-) ORIGENE TECHNOLOGIES INC.
XX PA
XX PI Shu Y, Fan W, Kovacs KF, Zidanic M, Jay G;
XX WPI; 2003-066233/06.
XX DR N-PSDB; ABX13584.
XX XX
PT New isolated polynucleotide coding without interruption for a human
KSE336 polypeptide useful for preventing or treating
diseases/conditions relating to brain and pancreas, e.g. meningioma,
insulin-dependent diabetes mellitus 2 -
XX PS Claim 1; Fig 2; 34pp; English.
XX CC The invention relates to an isolated polynucleotide (its complement
or a sequence 99% similar to it) coding without interruption for a human

CC KSE336 polypeptide, a serine protein kinase, comprising the KSE336-1 and
CC KSE336-2 splice variants appearing as ABG72382 and ABG72383. Also
CC included is a method of identifying an agent that modulates the
CC expression of KSE336 in brain, pancreas, brain progenitor or pancreas
CC progenitor cells comprising: (a) contacting a cell population comprising
CC the cells with a test agent under conditions effective for the test agent
CC to modulate the expression of KSE336; and (b) determining if the test
CC agent modulates the expression of KSE336. The polynucleotides are useful
CC as molecular targets or drug targets, and for detecting, diagnosing,
CC staging, monitoring, prognosticating, preventing or treating diseases or
CC conditions relating to brain and pancreas, such as astrocytoma,
CC meningioma, pancreatic adenocarcinoma, insulin-dependent diabetes
CC mellitus 2, helicoid papillary choroidretinal degeneration, Beckwith-
CC Wiedemann syndrome or congenital hyperinsulinism. The method and
CC polynucleotides are useful in research, diagnosis, drug discovery,
CC therapy, clinical medicine, forensic science and pathology.
CC The gene for KSE336 is located on chromosome 11p15.5-pter.
CC The present sequence represents the KSE366 variant KSE366-2.
XX
XX
XX Sequence 585 AA;

Query Match 95.0%; Score 3028; DB 24; Length 585;
Best Local Similarity 100.0%; Pred. No. 1.6e-216;
Matches 577; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 YLVLEHVSGLGELFDYLVKGRITPKARKEFFROIISALDFCHSHSICHRDLKPENLLDE 91
DB 9 YLVLEHVSGLGELFDYLVKGRITPKARKEFFROIISALDFCHSHSICHRDLKPENLLDE 68
QY 92 KNNIRIADFGMASLQVDSLLETSCGSPHYACPEVIRGEKYDGRKADWVSCGVILFALLV 151
DB 69 KNNIRIADFGMASLQVDSLLETSCGSPHYACPEVIRGEKYDGRKADWVSCGVILFALLV 128
QY 152 GALPFDNDNLRLLEKVKRGVFMHPHPIPDCCOSLLRGMIIEVDAAARLTLEHIQKHIWI 211
DB 129 GALPFDNDNLRLLEKVKRGVFMHPHPIPDCCOSLLRGMIIEVDAAARLTLEHIQKHIWI 188
QY 212 GGNKEPEPEQIPRKVQIRSLPSLEDDPDVLDMSHSLGCFDRDNKLLQDLLSEENQEK 271
DB 189 GGNKEPEPEQIPRKVQIRSLPSLEDDPDVLDMSHSLGCFDRDNKLLQDLLSEENQEK 248
QY 272 MIYFLLDRKERYPSQDEDLPPRNEIDPPRKRVDSPLMRHGRKRRPERKSMVLSVTDG 331
DB 249 MIYFLLDRKERYPSQDEDLPPRNEIDPPRKRVDSPLMRHGRKRRPERKSMVLSVTDG 308
QY 332 GSPVPARRAIEAQAQGRSISGASSGLSTSPSSPRVTPHSPRGSPLTPKGTVPHT 391
DB 309 GSPVPARRAIEAQAQGRSISGASSGLSTSPSSPRVTPHSPRGSPLTPKGTVPHT 368
QY 392 PKESPAGTNPPTPPSPSVGGVPMRRLNSIKNSFLGSPRFRHKLQVPTPEMSNLTP 451
DB 369 PKESPAGTNPPTPPSPSVGGVPMRRLNSIKNSFLGSPRFRHKLQVPTPEMSNLTP 428
QY 452 SSPELAKSWFGNFIISLEKEEQIFVWIKDPLSIKADIVAHFISPSLSHSVTSQTSFR 511
DB 429 SSPELAKSWFGNFIISLEKEEQIFVWIKDPLSIKADIVAHFISPSLSHSVTSQTSFR 488
QY 512 ABEYKATGGPAVQKPVKQFVDITVTEGEAQKNGIYSVFTLLSGPSRRKRVVETIOA 571
DB 489 ABEYKATGGPAVQKPVKQFVDITVTEGEAQKNGIYSVFTLLSGPSRRKRVVETIOA 548
QY 572 QLLSTHPPAAQHLSDTTNCMMMTGRLSKCGIIPKS 608
DB 549 QLLSTHPPAAQHLSDTTNCMMMTGRLSKCGIIPKS 585

RESULT 7
ABB98745
ID ABB98745 standard; Protein; 703 AA.
XX
XX
AC ABB98745;
XX
DT 20-JAN-2003 (first entry)

XX Human kinase #3.
DE
XX Human; kinase; chromosome 19.
XX
XX Homo sapiens.
OS
XX WO200281670-A1.
PN
XX 17-OCT-2002.
PD
XX 04-APR-2002; 2002WO-US10786.
PF
XX 06-APR-2001; 2001US-282036P.
PR
XX (LEXI-) LEXICON GENETICS INC.
PA
XX Turner CA, Mathur B, Friddle CJ;
PI
XX WPI: 2003-058538/05.
XX N-PSDB; ABV74559.
DR
XX New human kinase proteins useful for diagnosis, drug screening, and
PT clinical trial monitoring, treatment of disorders and diseases, and
PT cosmetic and nutritional applications
XX
XX Claim 5; Page 44-46; 47pp; English.
XX
XX The present sequence is a novel human kinase. The genomic locus encoding
CC the kinase is thought to be on human chromosome 19. The kinase and its
CC coding sequence are useful for diagnosis, drug screening, clinical trial
CC monitoring, treatment of disorders and diseases, and cosmetic and
CC nutritional applications.
XX
XX Sequence 703 AA;
SQ
Query Match 79.8%; Score 2545.5; DB 24; Length 703;
Best Local Similarity 75.6%; Pred. No. 1.5e-180;
Matches 495; Conservative 51; Mismatches 44; Indels 65; Gaps 7;
QY 1 MKVEREIALTKLIEHPHVLKHDVYENKYLVLVLEHVSGLGELFDYLVKGRITPKAR 60
DB 1 MKVEREIALTKLIEHPHVLKHDVYENKYLVLVLEHVSGLGELFDYLVKGRITPKAR 60
QY 61 FFRQIISALDFCHSHSICHRDLKPENLLDEKNNIRIADFGMASLQVDSLLETSCGSPH 120
DB 61 FFRQIISALDFCHSHSICHRDLKPENLLDEKNNIRIADFGMASLQVDSLLETSCGSPH 120
QY 121 YACPEVIRGEKYDGRKADWVSCGVILFALLVGLALPPDDNLRLLEKVKRGVFMHPHFI 180
DB 121 YACPEVIRGEKYDGRKADWVSCGVILFALLVGLALPPDDNLRLLEKVKRGVFMHPHFI 180
QY 181 PDCOSLLRGMIIEVDAAARLTLEHIQKHIWVIGKNEPEP-EQIP-RKQVIRSLPSLEDI 238
DB 181 PDCOSLLRGMIIEVDAAARLTLEHIQKHIWVIGKNEPEP-EQIP-RKQVIRSLPSLEDI 238
QY 239 DPVLDMSHSLGCFDRDNKLLQDLLSEENQEKMIYFLLDRKERYPSQDEDLPPRNEI 298
DB 241 DPVLDMSHSLGCFDRDNKLLQDLLSEENQEKMIYFLLDRKERYPSQDEDLPPRNDV 300
QY 299 DPPRKRVDSPLMRHGRKRRPERKSMVLSVTDG---CGSPVPARRAIEAQAQGRSISG 355
DB 301 DPPRKRVDSPLMRHGRKRRPERKSMVLSITDAGGGGSPVPTRRALLEMAQAQHSQRSVSG 360
QY 356 ASSGLSTSPSSPR-----VTPHP 374
DB 361 ASSGLSTSPSSPRSPVFSFSPFGAGDEARGGSGTSKQTQLPSRGRGCGGAGEQPPPP 420
QY 375 SPRGSELPKPG-----TPVHTPKESPAGTNPPTPPSSP--SVGVPVWRRLNS 421
DB 421 SARSTPLPGPGSPSSGGTFLHSLPHTPRASPTGTPTTPPSPGGVGGAARSLNS 480
QY 422 IKNSFLGSPRFRHKLQVPTPEMSNLTPSSPELAKSWFGNFIISLEKEEQIFVWIKD 481

```
Db 481 IRNSFLGSPRRHRRKMQVPTAEEMSSLTPESSPELAKRSWFGNFISLDKESQIFLVLDK 540
Qy 482 PLSSIKADIVHAFSLPSLSHSHSVISQTSFRAEYKATGPAVFQKPVKQVDITYTGEA 541
Db 541 PLSSIKADIVHAFSLPSLSHSHSVISQTSFRAEYKASGGPSVFQKPVQVDISSEGEPEP 600
Qy 542 QKE-----NGIYSTFTLLSGPSRRFRKRVVETIQALLSTHDPAAQHLSDTTN 590
Db 601 SPRDGGGGGIYSTFTLLSGPSRRFRKRVVETIQALLSTHDPQSVQALADEKN 655

RESULT 8
ID ABB98743 standard; Protein; 778 AA.
AC ABB98743;
XX
DT 20-JAN-2003 (first entry)
DE Human kinase #1.
KW Human; kinase; chromosome 19.
OS Homo sapiens.
XX
PN WO200281670-A1.
PD 17-OCT-2002.
PF 04-APR-2002; 2002WO-US10786.
PR 06-APR-2001; 2001US-282036P.
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Turner CA, Mathur B, Friddle CJ;
XX
DR WPI; 2003-058538/05.
DR N-PSDB; ABV74557.
XX
New human kinase proteins useful for diagnosis, drug screening, and
PT clinical trial monitoring, treatment of disorders and diseases, and
PT cosmetic and nutritional applications -
XX
PS Claim 5; Page 40-41; 47pp; English.
XX
CC The present sequence is a novel human kinase. The genomic locus encoding
CC the kinase is thought to be on human chromosome 19. The kinase and its
CC coding sequence are useful for diagnosis, drug screening, clinical trial
CC monitoring, treatment of disorders and diseases, and cosmetic and
CC nutritional applications.
XX
SQ Sequence 778 AA;

Query Match 79.8%; Score 2545.5; DB 24; Length 778;
Best Local Similarity 75.6%; Pred. No. 1.7e-180;
Matches 495; Conservative 51; Mismatches 44; Indels 65; Gaps 7;

Qy 1 MKVEREIALKLTIEHPHVLKLDHVDYENKKYLVLEHVS GGELFDYLVKKGLTPKEARK 60
Db 76 MKVEREIALKLTIEHPHVLKLDHVDYENKKYLVLEHVS GGELFDYLVKKGLTPKEARK 135
Qy 61 FFRQISALDFCHSHSICHRDLKPENLLDEKNIRIADFGMASIQVGDLSLETSCGSPH 120
Db 136 FFRQIVSALDFCHSYISICHRDLKPENLLDEKNIRIADFGMASIQVGDLSLETSCGSPH 195
Qy 121 YACPEVIREKYGDKADVWSCGVILFALLVGLPFDDNLRQLLEKVKRGVFNHPHIP 180
Db 196 YACPEVIRKGYDKGRADWMSGVILFALLVGLPFDDNLRQLLEKVKRGVFNHPHIP 255
Qy 181 PQCSLLRGMIEVDARRLTLEHIOKHIWYIGKNEPEP-EQIP-RKVQIRSLPSLEDI 238
Db 238 PQCSLLRGMIEVDPEKRLSLEQIKHPWYLGKHEDPDCLEPAPGRVRVAMRSLPSNGEL 315
Qy 239 DPVDLSMHSLGCFRDRNKLQDLLSEENQEKMIYFLLLDKERYPSQEDDLPPENEI 298
Db 316 DPVDLESMAISLGCFRDRERLHRELRSSEENQEKMIYFLLLDKERYPSCEDQDLPPENDV 375
Qy 299 DPPKRVDSPLNHRHGKRRKPERKSMELSVTD---GGSPVARRAIEMAHQGQRSISG 355
Db 376 DPPKRVDSPLNHRHGKRRKPERKSMELSVTDAGGGSPVPTRRALEMAHQSRSRSVSG 435
Qy 356 ASSGLSTPLSSPR-----VTPHP 374
Db 436 ASTGLSSPLSSPRSPVPSPEPGAGDEARGGSPSTKTQTLPSRPGRGGAGEQPPPP 495
Qy 375 SPRGSPLTPKG-----TPVHTPKESAGTNPPTPPSSP--SVGQVPMRRLNS 421
Db 496 SARSTPLPGPPGSPRSSGGTPLHSLHTPRASPTGTPTTPTTTPSPGGGCGGAARSLNS 555
Qy 422 IKNSFLGSPRHRKLOVPTPEMSNLTPSSPELAKRSWFGNFISLDKESQIFLVLDK 481
Db 556 IRNSFLGSPRHRKMQVPTAEEMSSLTPESSPELAKRSWFGNFISLDKESQIFLVLDK 615
Qy 482 PLSSIKADIVHAFSLPSLSHSHSVISQTSFRAEYKATGPAVFQKPVKQVDITYTGEA 541
Db 616 PLSSIKADIVHAFSLPSLSHSHSVISQTSFRAEYKASGGPSVFQKPVQVDISSEGEPEP 675
Qy 542 QKE-----NGIYSTFTLLSGPSRRFRKRVVETIQALLSTHDPAAQHLSDTTN 590
Db 676 SPRDGGGGGIYSTFTLLSGPSRRFRKRVVETIQALLSTHDPQSVQALADEKN 730

RESULT 9
AAU03517
ID AAU03517 standard; Protein; 794 AA.
XX
AC AAU03517;
XX
DT 12-SEP-2001 (first entry)
DE Human protein kinase #17.
XX
KW Human; protein kinase; PTK; STK; cancer; cardiovascular disease;
KW metabolic disorder; immune related disease; neurological disorder;
KW neurodegenerative disorder; inflammatory disorder; infectious disease;
KW reproductive disorder.
XX
OS Homo sapiens.
XX
XX WO200138503-A2.
XX
XX 31-MAY-2001.
XX
XX 22-NOV-2000; 2000WO-US32085.
XX
XX 24-NOV-1999; 99US-0167482.
XX
XX (SUGE-) SUGEN INC.
XX
PI Plowman GD, Whyte D, Manning G, Sudarsanam S, Martinez R;
PI Flanagan P, Clary D;
XX
XX WPI; 2001-343950/36.
XX
XX N-PSDB; AAS06717.
XX
Nucleic acids encoding human kinase polypeptides, useful for preventing
PT diagnosing and/or treating e.g. cancer, immune, cardiovascular and
PT neuronal-associated diseases, and microbial infections -
XX
PS Claim 7; Figure 2; 433pp; English.
XX
AAU03501-AAU03557 represent novel human protein kinases #1-57. The
CC novel protein kinases have been identified as members of the tyrosine
CC or serine/threonine kinase (PTK and STK) families. The polynucleotides
```

encoding protein kinases and the polypeptides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate kinase expression. For example, they may be used to treat cancers (especially cancers of haematopoietic origin), cardiovascular disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes), immune related diseases (e.g. rheumatoid arthritis), neurological disorders (e.g. schizophrenia), neurodegenerative disorders (e.g. Parkinson's disease), inflammatory disorders (e.g. asthma), infectious disease (e.g. HIV) and reproductive disorders (e.g. infertility). Additionally, polynucleotides encoding protein kinases may be used for gene therapy and as DNA probes in diagnostic assays. The protein kinase polypeptides may be used as antigens in the production of antibodies against the protein kinases and in assays to identify modulators of protein kinase expression and activity.

SQ	Sequence	794 AA;
	Query Match	79.8%; Score 2545.5; DB 22; Length 794;
	Best Local Similarity	75.6%; Pred. No. 1.8e-180;
	Matches 495; Conservative	51; Mismatches 44; Indels 65; Gaps

QY	1	MKVREIEAIIKL	IBHPVILKLDHYENKYL	YLVL	EHVSGGELFDYL	VKKGRBLTPKEARK	60	
DB	92	MKVREIEAIIKL	IBHPVILKLDHYENKYL	YLVL	EHVSGGELFDYL	VKKGRBLTPKEARK	151	
QY	61	FFRQIISALDF	CHSHSICHRDL	KPENLLDEKNNIR	IADFGMASLQV	SGDLSLETSCGSPH	120	
DB	152	FFRQIVSALDF	CHSVSICHRDL	KPENLLDEKNNIR	IADFGMASLQV	SGDLSLETSCGSPH	211	
QY	121	YACPEVIRGEKY	DGRKADVWGCVIL	FALLV	GAALPFDDDN	LROLLEKVRGVFHHMFTIP	180	
DB	212	YACPEVIRGEKY	DGRADWMSGVIL	FALLV	GAALPFDDDN	LROLLEKVRGVFHHMFTIP	271	
QY	181	PDQCILLRGMTEV	DAARLTLEH	QIKHVI	GGKNEPEP-EQIP	-RKVQIRSLPSLEDI	238	
DB	272	PDQCILLRGMTEV	EPKEKLSLEQ	QKHPWIL	GGKHEDPCLE	FAPGRVRVAMSLNSGEL	331	
QY	239	DPDVLDSMHS	LGCFDRNKLQD	LLSEENQEKMI	YLLLDLRKERYPS	QEDDLPPRNEI	298	
DB	332	DPDVLDSMAS	LGCFDRERLHRE	LRSSEENQEKMI	YLLLDLRKERYPS	CEDQDLPPRNDV	391	
QY	299	DPPRKRVDS	PMLNRHCKRPR	PKSMVL	SVTD---GGSPV	APARATEMAQHGRSSISG	355	
DB	392	DPPRKRVDS	PMLSRHGRKPR	PKSMVL	SI	TDAGGGSPVTRRALEMAQHGRSSVSG	451	
QY	356	ASSGLSTPLSSPR	-----	-----	-----	-----VTPHP	374	
DB	452	ASTGLSSPLSSPR	SVFSFSP	EPGAGDEARGGSP	TSKTQLPSR	CGGGAGEQPPPP	511	
QY	375	SPRSGPLTPKG	-----	-----	-----	TPVHTPKESPAGTNP	TPPSPP--SVGGVWRARLNS	421
DB	512	SARSTPLPGP	PPGSPRSSGGT	PLHSLPH	TPRASPTGTPT	TPPPSPGGVGGAAMRSLNS	571	
QY	422	IKNSFLGSPR	FRHRKLQVPT	PEMSNLTP	ESSPELAKKSWFGNFI	SLSEKEEQIFVVIKDK	481	
DB	572	IRNSFLGSPR	FRHRKQVPTAE	MSLSLTPESS	PELAKRSMFGNFI	SILDKEEQIFLVIKDK	631	
QY	482	PLSSIKADIV	HAFLSIP	SLSHSVISQTS	FRAYEKATGGPAV	FQKPVKQVDITYTTEGGA	541	
DB	632	PLSSIKADIV	HAFLSIP	SLSHSVISQTS	FRAYEKASGGPS	VFQKPVRFQVDISSSGGPEP	691	
QY	542	QKE-----	NGIYSVTFTLL	IGSPSRFRKRVVET	IQALLSTHDP	APAAHLSDITN	590	
DB	692	SPRDRGGGGGI	YSVTFTLLIS	GPSPRFRKRVVET	IQALLSTHDP	QSVQALADEKN	746	
RESULT 10								
AAE16271								
ID	AAE16271 standard; Protein; 794 AA.							
XX	AAE16271;							
XX	26-MAR-2002 (first entry)							
DT								

RESULT 10
AAE16271
ID AAE1
XX
AC AAE1
XX
DT 26-M

XX		Human kinase PKIN-17 protein.
DE		
XX		
KW		Human; kinase; PKIN-17; cancer; leukaemia; adenocarcinoma; osteoporosis;
KW		immune disorder; atherosclerosis; Crohn's disease; Hodgkin's disease;
KW		Acquired Immune Deficiency Syndrome; AIDS; Addison's disease; anaemia;
KW		allergy; asthma; adult respiratory distress syndrome; multiple sclerosis;
KW		autoimmune thyroiditis; bronchitis; diabetes mellitus; osteoarthritis;
KW		Good pasture's syndrome; Graves' disease; pancreatitis; psoriasis;
KW		rheumatoid arthritis; ulcerative colitis; cirrhosis; Cushing's syndrome;
KW		hepatitis; hypothyroidism; cerebral palsy; cataract; angina pectoris;
KW		cardiovascular disease; hypertension; vasculitis; myocarditis; obesity;
KW		congestive heart failure; ischaemic heart disease; lung tumour; gout;
KW		fatty liver; Niemann-Pick's disease; gene therapy.
XX		
OS	Homo sapiens.	
FH	Key	Location/Qualifiers
FT	Domain	50..301
FT	/note=	"Eukaryotic protein kinase domain"
FT	Domain	51..292
FT	/label=	Protein_kinase_domain
FT	Domain	52..292
FT	/label=	Protein_kinase_domain
FT	Domain	71..292
FT	/label=	Protein_kinase_domain
XX		
PX	WO200196547-A2.	
PN		
PD	20-DEC-2001.	
XX		
PF	14-JUN-2001; 2001WO-US19444.	
PR	15-JUN-2000; 2000US-212073P.	
PR	23-JUN-2000; 2000US-213467P.	
PR	30-JUN-2000; 2000US-215651P.	
PR	07-JUL-2000; 2000US-218605P.	
PR	13-JUL-2000; 2000US-218372P.	
PR	25-AUG-2000; 2000US-228056P.	
XX	(INCY-) INCYTE GENOMICS INC.	
PA		
PI	Yue H, Ial P, Bandman O, Borowsky ML, Au-Young J, Lu Y;	
PI	Gandhi AR, Tribouley CW, Walla NK, Yao MG, Lu DAM, Greenwald SR;	
PI	Ramkumar J, Griffin JA, Kearney L, Burford N, Nguyen DB, Tang YT;	
PI	Baughn MR, He A, Thornton M, Hafalia A, Patterson C, Gururajan R;	
PI	Lo TP, Khan F, Recipon SA, Azimzai Y, Policky JL, Ding Li;	
PI	Grether M, Elliott VS, Thangavelu K, Batra S, Ison CH;	
DR	WPI; 2002-090207/12.	
XX	N-PSDB; AAD26464.	
PT	New polypeptides, useful for diagnosing, treating or preventing	
PT	disorders of growth and development, cardiovascular and lipid, and	
PT	diseases such as cancer, comprise human kinase polypeptides -	
XX		
XS	Claim 1; Page 159-161; 197pp; English.	
XX		
CC	The invention relates to human kinase PKIN proteins and their	
CC	corresponding cDNAs. A composition containing PKIN agonist is useful for	
CC	treating a disease or condition associated with decreased expression of	
CC	PKIN and a composition comprising PKIN antagonist is useful for treating	
CC	a disease or condition associated with overexpression of PKIN. The	
CC	disorders include cancer (leukaemia, adenocarcinoma, lymphoma, melanoma,	
CC	myeloma, sarcoma, teratocarcinoma, Hodgkin's disease); immune disorder	
CC	(Acquired Immune Deficiency Syndrome (AIDS), asthma, Addison's disease,	
CC	atherosclerosis, anaemia, allergies, adult respiratory distress syndrome,	
CC	autoimmune thyroiditis, gout, bronchitis, Crohn's disease, diabetes	
CC	mellitus, multiple sclerosis, Good pasture's syndrome, Graves' disease,	
CC	osteoarthritis, osteoporosis, pancreatitis, psoriasis, Reiter's syndrome,	
CC	rheumatoid arthritis, Sjogren's syndrome, uveitis, ulcerative colitis,	
CC	bacterial, parasitic, fungal, viral, protozoal and helminthic infections)	
CC	growth and development disorders (arteriosclerosis, cirrhosis, hepatitis,	

CC	Cushing's syndrome, hypothyroidism, cerebral palsy, cataracts); cardio
CC	vascular disease (arteriovenous fistula, hypertension, myocarditis,
CC	aneurysms, congestive heart failure, angina pectoris, myocardiitis,
CC	ischemic heart disease, chronic bronchitis, lung tumours); lipid
CC	disorder (fatty liver, Fabry's disease, Niemann-Pick's disease,
CC	hypercholesterolaemia, obesity); PKIN DNA is useful for assessing
CC	toxicity of a test compound and in gene therapy. The present sequence
XX	is human PKIN-17 protein.
SQ	Sequence 794 AA;
	Query Match 79.8%; Score 2545.5; DB 23; Length 794;
	Best Local Similarity 75.6%; Pred. No. 1.8e-180;
	Matches 495; Conservative 51; Mismatches 44; Indels 65; Gaps 7;
QY	1 MKVERETAILKLI EHPHVLKLDHYVENKKYLVLVLEHVSGGELFDYLVKGRLTPKEARK 60
DB	92 MKVERETAILKLI EHPHVLKLDHYENKKYLVLVLEHVSGGELFDYLVKGRLTPKEARK 151
QY	61 FFRQIISALDFCHSHSICHRDLKPENLLDKNNIRIADFWMASLQVGDLSLETSCGSFH 120
DB	152 FFRQIVSALDFCHSVSYICHRDLKPENLLDKNNIRIADFWMASLQVGDLSLETSCGSFH 211
QY	121 YACPEVTIGEKYDGRKADWCGVILFALLVGALPFDDNLRQLLEKVKGCVFMHFIP 180
DB	212 YACPEVIKGEKYDGRRADWCGVILFALLVGALPFDDNLRQLLEKVKGCVFMHFIP 271
QY	181 PDCOSLARGMTEVDAAERLTLEHQIKHWIYGKNREPEP-EQPIE-RKVQIRSLPSLEDI 238
DB	272 PDCOSLARGMLEVEPEKRKLSEUQKHWPYLGGHKEPLDPCLPEAPGARVRVMSLPNGEL 331
QY	239 DPVDLDSMHSLGCFRDRNKLIQDLLSEENQEKMIYELLIDRKERYPSOEDELPPENEI 298
DB	332 DPVDLESWSLGCFFDRERLHLRELSEENQEKMIYILLIDRKERYPSCEDQLPPNDV 391
QY	299 DPPRKRVDSPLMLNRHGKRRPERKSMEVLSTVD---GGSPVPARAIEMAHQGQRSRISG 355
DB	392 DPPRKRVDSPLMSRHGKRRPERKSMEVLSTIDAGGGSPVPTRRALEMAQHRSQRSVSG 451
QY	356 ASSGLSTSPSSPR-----VTPHP 374
DB	452 ASGLSSSPUSSSPVSFSPEFGADEARGGSPSTKTOTLPSRPGRGAGEQP PPP 511
QY	375 SPRGSPPLTPKG-----TPVHTPKESPAGTNPPTPPSP--SVGGVPWRRLNS 421
DB	512 SARSTPLPGPGSPRSSGGTFLHSPLHTPRASPTGTCTTPPPSPGGVGAAWRSRLNS 571
QY	422 IKNSFLGSPRPHRKLQVPTPEEMSNLTPESSPELAKSMFGNFISLEKEEQIFVWKDK 481
DB	572 IRNSFLGSPRPHRRKMVPVTAEBESSLTPESSPELAKRSWFGNFISLDEKEQIFLVKDK 631
QY	482 PLSSIKADIHAFLSIPLSHSVLSQTSFRAEYKATGPAVFQPKVFQVIDITTEGEA 541
DB	632 PLSSIKADIHAFLSIPLSHSVLSQTSFRAEYKASGPSVFQKPVRFQVIDISSEGEP 691
QY	542 QKE-----NGIYSVTFTLLSGPERRKRVVETIQALLSTHDPPAAQHLSDTTN 590
DB	692 SPRDGGGGGIYSVTFTLLSGPERRKRVVETIQALLSTHDQPSVOALADEKN 746
RESULT 11	
AAO16604	
ID	AAO16604 standard; protein; 754 AA.
XX	
AC	AAO16604;
XX	
XX	08-MAY-2003 (first entry)
XX	
XX	Human cell cycle-regulatory factor Cdr2.
DE	
XX	Human; cell cycle-regulatory factor; Cdr2; kinase; proliferative disease;
KW	anticancer agent; wound-healing drug.
XX	

Qy 506 SOTSFRAYKATGPAVQKPVQVDITYTEGGAQKE-----NGIYSVTFTLLSGPS 559
Db 616 SOTSFRAYKATGPAVQKPVQVDITYTEGGAQKE-----NGIYSVTFTLLSGPS 675
Qy 560 RRFKRVVETIQALLSTHDPAAQHLSDTTN 590
Db 676 RRFKRVVETIQALLSTHDPAAQHLSDTTN 706
RESULT 12
ABB98744
ID ABB98744 standard; Protein; 762 AA.
XX AC ABB98744;
XX DT 20-JAN-2003 (first entry)
XX DE Human kinase #2.
XX KW Human; kinase; chromosome 19.
XX OS Homo sapiens.
XX WO20020281670-A1.
XX PD 17-OCT-2002.
XX PF 04-APR-2002; 2002WO-US10786.
XX PR 06-APR-2001; 2001US-282036P.
XX PA (LEXI-) LEXICON GENETICS INC.
XX PI Turner CA, Mathur B, Friddle CJ;
XX WPI; 2003-058538/05.
DR N-PSDB; ABV74558.
XX New human kinase proteins useful for diagnosis, drug screening, and
PT clinical trial monitoring, treatment of disorders and diseases, and
PT cosmetic and nutritional applications
XX Claim 5; Page 42-43; 47pp; English.
XX The present sequence is a novel human kinase. The genomic locus encoding
CC the kinase is thought to be on human chromosome 19. The kinase and its
CC coding sequence are useful for diagnosis, drug screening, clinical trial
CC monitoring, treatment of disorders and diseases, and cosmetic and
CC nutritional applications.
SQ Sequence 762 AA;
Query Match 74.9%; Score 2386.5; DB 24; Length 762;
Best Local Similarity 74.1%; Pred. No. 1.1e-168;
Matches 464; Conservative 52; Mismatches 45; Indels 65; Gaps 7;
Qy 30 YLYLVHVSQGELEFDLVKXGRITPKARFFRQIISALDFCHSHSICHRLDKPENLL 89
Db 89 FRYLVHVSQGELEFDLVKXGRITPKARFFRQIISALDFCHSHSICHRLDKPENLL 148
Qy 90 DEKNIRIADFQMASLQVDSLLTSCGSPHYACPEVIRGEKYDGRKADVWSCGVILPAL 149
Db 149 DEKNIRIADFQMASLQVDSLLTSCGSPHYACPEVIRGEKYDGRKADVWSCGVILPAL 208
Qy 150 LVGALPFDDNLRQLLEKVRGVFHMHPFIPDCOSLLRGMTEVDAAARLTLEHIQHIW 209
Db 209 LVGALPFDDNLRQLLEKVRGVFHMHPFIPDCOSLLRGMTEVDAAARLTLEHIQHIW 268
Qy 210 YTGKNEPEP-EQPIP-RKVQIRSLPSLEIDIPDVLDSNMHSLGCFRDRNKLQDLSEEE 267
Db 269 YLGKHEPDPCLPEAPAGRVAMRSLPSNGELDPDVLDSNMHSLGCFRDRNKLQDLSEEE 328
Qy 268 NOEKMIYFLLDRKERYPSQEDLPPRNEIDPPRKRVDSPMLNRHGKRRPERKSMVLS 327

Db 329 NQEKMIYFLLDRKERYPSQEDLPPRNDVDPKRKRVDSPLSRHGKRRPERKSMVLS 388
Qy 328 VTD---GGSPVARRAIEMAHQGRSRTISGASSGLSTPLSSPR----- 369
Db 389 ITDAGGGSPVPTRRALEMAHQHSQRSSVSGASTGLSSPLSSPRSPVSPSPSPGACDE 448
Qy 370 -----VTPHPSRGSPLFTPKG-----TPVHTP 392
Db 449 ARGGSPTSKTQTLPSRGRPGGAGBQPPPPARSTPLPGPPGSPRSSGGTPLHSLHTP 508
Qy 393 KESPACTNPPTPSSP--SVGVFWARLNSIKNSFLGSPRFRHRKLVPTPEMSNLTP 450
Db 509 RASPTCTGCTTTPPPSGGVGGAARSLNSIRNSFLGSPRFRHRKLVPTPEMSNLTP 568
Qy 451 ESSPELAKKSWFGNFTSLERQIFVWIKDKPLSSIKADIVHAFLSIPLSHSVISQTSF 510
Db 569 ESSPELAKKSWFGNFTSLERQIFVWIKDKPLSSIKADIVHAFLSIPLSHSVISQTSF 628
Qy 511 RAEYKATGPAVQKPVQVDITYTEGGAQKE-----NGIYSVTFTLLSGPSRRFKR 564
Db 629 RAEYKATGPAVQKPVQVDITYTEGGAQKE-----NGIYSVTFTLLSGPSRRFKR 688
Qy 565 VVETIQALLSTHDPAAQHLSDTTN 590
Db 689 VVETIQALLSTHDPAAQHLSDTTN 714
RESULT 13
ABB62061
ID ABB62061 standard; Protein; 851 AA.
XX AC ABB62061;
XX DT 26-MAR-2002 (first entry)
XX DE Drosophila melanogaster polypeptide SEQ ID NO 12975.
XX KW Drosophila; developmental biology; cell signalling; insecticide;
XX KW pharmaceutical.
XX OS Drosophila melanogaster.
XX WO200171042-A2.
XX PD 27-SEP-2001.
XX PF 23-MAR-2001; 2001WO-US09231.
XX PR 23-MAR-2000; 2000US-191637P.
XX PR 11-JUL-2000; 2000US-0614150.
XX (PEKE) PE CORP NY.
XX Venter JC, Adams M, Li PWD, Myers EW;
XX WPI; 2001-656860/75.
DR N-PSDB; ABL06164.
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX Disclosure; SEQ ID NO 12975; 21pp + Sequence Listing; English.
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (ABB57737-ABB72072).

CC screening techniques. The present sequence represents a novel human
CC polypeptide of the invention.

XX
SQ Sequence 301 AA;
Query Match 32.5%; Score 1036.5; DB 22; Length 301;
Best Local Similarity 79.4%; Pred. No. 7.2e-69;
Matches 197; Conservative 10; Mismatches 6; Indels 35; Gaps 1;
Qy 1 MKVERETAILKLIHHPVILKLDVYENKYL----- 31
Db 50 MKVERETAILKLIHHPVILKLDVYENKYLPPPPDELTSGLPMLAQVSPHGKLSARRSWDL 109
Qy 32 -----YLVLHVSGGELFDLVKKGRLTPKEARKFRQIISALDFCHSHSICHRLDKPE 85
Db 110 LSGPPRIVLVHVSGLFDLVKKGRLTPKEARKFRQIVSALDFCHSYICHRLDKPE 169
Qy 86 NLLDEKNIRIADFGMASLQVDSLETSCGSPHYACPEVIRGEKYDGRKADVWMSGVI 145
Db 170 NLLDEKNIRIADFGMASLQVDSLETSCGSPHYACPEVIRGEKYDGRADWMSGVI 229
Qy 146 LFAVLGALPDDNRLQLLEKVRGVFHPHFIPDDCQSLRGMIWDAAARLTLEHIQ 205
Db 230 LFAVLGALPDDNRLQLLEKVRGVFHPHFIPDDCQSLRGMIWDAAARLTLEHIQ 289
Qy 206 KHIWYIGG 213
Db 290 KHPWYIGG 297

RESULT 15

AAG70854
ID AAG70854 standard; Protein; 1349 AA.

AC AAG70854;

DT 27-JUL-2001 (first entry)

DE C albicans apoptosis associated protein #34.

KW Yeast; fungus; apoptosis; infection; proliferative disease;
KW vaccine; autoimmune disease; ischaemia; neurodegeneration.

XX Candida albicans.

XX WO200102550-A2.

XX 11-JAN-2001.

XX 03-JUL-2000; 2000WO-BE00077.

XX 01-JUL-1999; 99EP-0870141.

XX (JANC) JANSSEN PHARM NV.

XX Contreras RH, De Backer MD, Luyten WHML, Malcorps IKL;

XX Nelissen BJM, Reekmans RJ;

XX WPI; 2001-367042/38.

XX N-PSDB; AAH29890.

PT Yeast and fungal nucleic acids encoding proteins involved in a pathway
PT leading to programmed cell death, useful for treating proliferative
PT disorders, yeast and fungal infections, or for preventing apoptosis in
PT certain diseases -

XX Claim 24; Fig 2; 218pp; English.

XX The present invention provides the protein and coding sequences of a
CC number of apoptosis associated proteins from the yeast *Saccharomyces*
CC *cerevisiae* and the fungus *Candida albicans*. These can be used to identify
CC treatments for fungal and yeast infections, for proliferative diseases
CC and for apoptosis related diseases such as autoimmune diseases, ischaemia

CC and neurodegeneration. The present sequence is one of the *C. albicans*
CC proteins of the invention.

XX SQ Sequence 1349 AA;

Query Match 24.0%; Score 766.5; DB 22; Length 1349;
Best Local Similarity 33.5%; Pred. No. 6e-48;
Matches 211; Conservative 97; Mismatches 216; Indels 105; Gaps 20;
Qy 3 VRETAAILKLIHHPVILKLDVYENKYLVLHVSGGELFDLVKKGRLTPKEARKPE 62
Db 80 IREIIMKLIHHPVILKLDVYENKYLVLHVSGGELFDLVKKGRLTPKEARKPE 139
Qy 63 ROIISALDFCHSHSICHRLDKPENLILDEKNIRIADFGMASLQVDSLETSCGSPHYA 122
Db 140 ROIISALDFCHSHSICHRLDKPENLILDEKNIRIADFGMASLQVDSLETSCGSPHYA 199
Qy 123 CEPVIRGEKYDGRKADVWMSGVIILFALLVGAALPDDNRLQLLEKVRGVFHPHFIP 181
Db 200 APEIVSGLKYHGAASDVWMSGVIILFALLVGAALPDDNRLQLLEKVRGVFHPF 259
Qy 182 DCQSLLRGMIWDAAARLTLEHIQKH---IWYIGKNEPEPEQPIPR-KVQIRSLPSLED 237
Db 260 EARDLIARLMEVDPMRRISTEKILRHPLTKTPMSNEDLISEKSLPHPTGTGKSLGVRN 319
Qy 238 IDPDVLDMSHSLGCFRDRNKLQDLLESEENOEKMIYFLLDKRYPSQEDDLPPRNE 297
Db 320 IDKQILSNLTILWDRPEBEIVDCLLKDGSPKFTYALLM---RYKHQDDN---TNN 372
Qy 298 IDPPKRKVDSPMLNRHGRK-----RPERKSMVLSVTDGSGSPVPARRAIEMAHQGRSRS 352
Db 373 NSPKKSTSFNNKVVRSKYSGLNGTTPRRKRASHISVS-----RPTSFOYKSNP 420
Qy 353 ISGASSGLSTSPSSPRVTPHPSGRGSLPTPKGTVPVHTPKESPAG--TPNPTPPSSPSV 410
Db 421 GAGATANRNSVARHSVASSANNSPRKSPYKSPYRSPYKSPYKSPYKSPYKSPYKSPYK 477
Qy 411 GGVPWRARLNSIKNSFLGSP-RFHRRLKLVPTPEMSNLT-PESSPELAKKSWFGNFISL 468
Db 478 ---PYGRSNS-QRFENEPLKAKPRNIYNEIVDAQSNFSLPPLPP-----SL 522
Qy 469 EKEEQIFVVKDKPLSSIKADIVHAFSLSPSLSHSVISQTSFRAEYKATGGPAVFOKPVK 528
Db 523 PSKDSRYMI--DEP-----NOPLOQPALSQ-----VPENPIVDESP-- 557
Qy 529 FOVDITVTGGEAKENGIV-----SVTFTLLSGPSRRFRKRVRVETIOA 571
Db 558 ---DLMQSAKISSGKNSIIGKNNNSNKNRMSKRSIRASMTTGLKR-----NSITM 608
Qy 572 QLLSTHDPAAQHLSDTTNMEMMTGRLS 600
Db 609 KLLSTY---AKLSGDDDDWEYMDKQTKRTS 634

Search completed: November 26, 2003, 11:59:56
Job time : 38.6897 secs

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OM protein - protein search, using sw model

Run on: November 26, 2003, 11:58:31 ; Search time 14.2947 Seconds
(without alignments)
1799.622 Million cell updates/sec

Title: US-10-054-579-4
Perfect score: 3188
Sequence: 1 MKVERETAILKLEHPPHVLK.....TNCMEMVTGRLSKGIIIPKS 608

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PTCUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3188	100.0	668	US-09-930-181-2	Sequence 2, Appli
2	3028	95.0	585	US-09-930-181-4	Sequence 4, Appli
3	3015	94.6	603	US-09-930-181-17	Sequence 17, Appl
4	688.5	21.6	745	US-09-523-849-36	Sequence 36, Appl
5	685.5	21.5	724	US-09-984-890-2	Sequence 2, Appli
6	684.5	21.5	722	US-09-984-890-4	Sequence 4, Appli
7	682.5	21.4	722	US-08-817-832B-32	Sequence 32, Appl
8	680	21.3	149	US-09-930-181-18	Sequence 18, Appl
9	663.5	20.8	729	US-08-677-298-2	Sequence 2, Appli
10	657.5	20.6	793	US-09-523-849-33	Sequence 33, Appl
11	657.5	20.6	793	US-09-523-849-32	Sequence 32, Appl
12	642	20.1	779	US-08-817-832B-31	Sequence 31, Appl
13	638	20.0	776	US-09-523-849-34	Sequence 34, Appl
14	636	19.9	552	US-08-557-006C-40	Sequence 40, Appl
15	621.5	19.5	345	US-09-101-146-1	Sequence 1, Appli
16	616	19.3	633	US-08-557-006C-43	Sequence 43, Appl
17	606	19.0	257	US-09-101-146-6	Sequence 6, Appli
18	581.5	18.2	257	US-07-857-224B-25	Sequence 25, Appl
19	579	18.2	604	US-09-523-849-35	Sequence 35, Appl
20	553.5	17.4	631	US-09-579-664B-11	Sequence 11, Appl
21	461.5	14.5	252	US-07-857-224B-26	Sequence 26, Appl
22	458.5	14.4	353	US-08-688-988-31	Sequence 31, Appl
23	458.5	14.4	363	US-08-688-988-30	Sequence 30, Appl
24	451	14.1	260	US-07-857-224B-27	Sequence 27, Appl
25	449.5	14.1	354	US-08-688-988-29	Sequence 29, Appl
26	445.5	14.0	351	US-08-688-988-28	Sequence 28, Appl
27	442.5	13.9	339	US-08-688-988-33	Sequence 33, Appl

28	440	13.8	359	3	US-08-688-988-32	Sequence 32, Appl
29	439	13.8	260	2	US-07-857-224B-28	Sequence 28, Appl
30	434	13.6	355	4	US-09-579-664B-10	Sequence 10, Appl
31	433	13.6	370	2	US-08-878-989-19	Sequence 19, Appl
32	433	13.6	370	3	US-09-272-796-19	Sequence 19, Appl
33	433	13.6	370	4	US-09-457-040B-31	Sequence 31, Appl
34	432.5	13.6	1037	4	US-09-428-711A-21	Sequence 21, Appl
35	429.5	13.5	556	4	US-09-800-960-4	Sequence 4, Appli
36	427	13.4	290	4	US-09-734-673-4	Sequence 4, Appli
37	427	13.4	334	4	US-09-523-849-31	Sequence 31, Appl
38	425	13.3	339	3	US-08-688-988-2	Sequence 2, Appli
39	423	13.3	565	4	US-09-800-960-2	Sequence 2, Appli
40	420.5	13.2	436	4	US-09-734-673-2	Sequence 2, Appli
41	420.5	13.2	436	4	US-09-523-849-2	Sequence 2, Appli
42	417.5	13.1	433	2	US-08-913-050A-7	Sequence 7, Appli
43	417.5	13.1	433	2	US-08-749-902-5	Sequence 5, Appli
44	413	13.0	1050	4	US-09-428-711A-16	Sequence 16, Appl
45	409.5	12.8	456	1	US-08-464-164-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-930-181-2
; Sequence 2, Application US/09930181
; Patent No. 6455292
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies
; TITLE OF INVENTION: Full-Length Serine Protein Kinase in Brain and Pancreas
; FILE REFERENCE: 16U 101 V1
; CURRENT APPLICATION NUMBER: US/09/930.181
; CURRENT FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 668
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-930-181-2

Query Match 100.0%; Score 3188; DB 4; Length 668;
Best Local Similarity 100.0%; Pred. No. 6.8e-218;
Matches 608; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MKVERETAILKLEHPPHVLKLDHVENKYLVLVLEHVS	GELFDYLVKKGRLTPKEARK	60
Db	61	MKVERETAILKLEHPPHVLKLDHVENKYLVLVLEHVS	GELFDYLVKKGRLTPKEARK	120
Qy	61	FFROIISALDFCHSHSICHRLDPENLLDEKNIRIADFG	MASLQVDSLLTSCGSPH	120
Db	121	FFROIISALDFCHSHSICHRLDPENLLDEKNIRIADFG	MASLQVDSLLTSCGSPH	180
Qy	121	YACPEVIRGEKYDGRKADVMSCGVILFALLV	GVLPFDNNLRQLLEKVGVPFHPFIP	180
Db	181	YACPEVIRGEKYDGRKADVMSCGVILFALLV	GVLPFDNNLRQLLEKVGVPFHPFIP	240
Qy	181	PDCOSLARGMEVDAAARLTLEHIQKHWYIGGKNEPE	PEQPIPRKVQIRSLPSLEIDP	240
Db	241	PDCOSLARGMEVDAAARLTLEHIQKHWYIGGKNEPE	PEQPIPRKVQIRSLPSLEIDP	300
Qy	241	DVLDSMHSGLCFDRDNKLLQDLSEENQEKMIYFLLL	DRKERYPSQDEDLPPRNEIDP	300
Db	301	DVLDSMHSGLCFDRDNKLLQDLSEENQEKMIYFLLL	DRKERYPSQDEDLPPRNEIDP	360
Qy	301	PRKVDSPMLNRHGRKRPERSKMEVLVTDGGSVP	PARRAIEMAHQGRSISGASSGL	360
Db	361	PRKVDSPMLNRHGRKRPERSKMEVLVTDGGSVP	PARRAIEMAHQGRSISGASSGL	420
Qy	361	STPSLSSPRVTPHPSPRGSLPTPKGTPVHTPKES	PAGTNPPTPPSPSVGGVFWARLN	420
Db	421	STPSLSSPRVTPHPSPRGSLPTPKGTPVHTPKES	PAGTNPPTPPSPSVGGVFWARLN	480

Qy 421 SIKNSFLGSPRRHRRKLVQPTPEEMSNLTBPSSELPALAKSWFGNFISLEKEEQIFVVIKD 480
Db 481 SIKNSFLGSPRRHRRKLVQPTPEEMSNLTBPSSELPALAKSWFGNFISLEKEEQIFVVIKD 540
Qy 481 KPLSSIKADIVHAFSLSPSLSHSVISQTSFRAEYKATGGPAVFOKPVKQFQVDITYTTEGGE 540
Db 541 KPLSSIKADIVHAFSLSPSLSHSVISQTSFRAEYKATGGPAVFOKPVKQFQVDITYTTEGGE 600
Qy 541 AQKENGYSVFTLLSGSPRRFKVWETIQALLSTHDPDPAQHLSDTTNCMENMTGRLS 600
Db 601 AQKENGYSVFTLLSGSPRRFKVWETIQALLSTHDPDPAQHLSDTTNCMENMTGRLS 660
Qy 601 KCGIIPKS 608
Db 661 KCGIIPKS 668

RESULT 2
US-09-930-181-4
; Sequence 4, Application US/09930181
; Patent No. 6455292
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies
; TITLE OF INVENTION: Full-Length Serine Protein Kinase in Brain and Pancreas
; FILE REFERENCE: 16U 101 V1
; CURRENT APPLICATION NUMBER: US/09/930.181
; CURRENT FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 4
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-930-181-4

Query Match 95.0%; Score 3028; DB 4; Length 585;
Best Local Similarity 100.0%; Pred. No. 1.2e-206;
Matches 577; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 YLVLEHVSQGGELFDYLVKKGRLTPKEARKFQRIISALDFCHSHSICHRLDKPENLLDDE 91
Db 9 YLVLEHVSQGGELFDYLVKKGRLTPKEARKFQRIISALDFCHSHSICHRLDKPENLLDDE 68
Qy 92 KNRIADFGMASLQVGSLLSETSCGSPHYACPEVIRGEKYDGRKADVMSQGVILFALLV 151
Db 69 KNRIADFGMASLQVGSLLSETSCGSPHYACPEVIRGEKYDGRKADVMSQGVILFALLV 128
Qy 152 GALPDDDDNLRLQLEKVKRGVFMHPHFTPPDCQSLIRGMI EVDAAARLTLEHIOKHIWI 211
Db 129 GALPDDDDNLRLQLEKVKRGVFMHPHFTPPDCQSLIRGMI EVDAAARLTLEHIOKHIWI 188
Qy 212 GKGNEPEQPTPRKQVIRSLPSLEDIDPDVLDMSHSLGCFDRDKLQDILLSEENOEK 271
Db 189 GKGNEPEQPTPRKQVIRSLPSLEDIDPDVLDMSHSLGCFDRDKLQDILLSEENOEK 248
Qy 272 MIYFLLDRKERYPSQEDIDLPRNEIDPPRKRVDSPLNHRGKRPRKSMVLSVTDG 331
Db 249 MIYFLLDRKERYPSQEDIDLPRNEIDPPRKRVDSPLNHRGKRPRKSMVLSVTDG 308
Qy 332 GSPVPAARAIEMAHQGRSRISGASSGLSTSPSSPVTPHPSRGSPLTPKGTPTVHT 391
Db 309 GSPVPAARAIEMAHQGRSRISGASSGLSTSPSSPVTPHPSRGSPLTPKGTPTVHT 368
Qy 392 PKESAGTPTNPTPPSPSPVGGVPMRLNLSKNSFLGSPRRHRRKLVQPTPEEMSNLTPE 451
Db 369 PKESAGTPTNPTPPSPSPVGGVPMRLNLSKNSFLGSPRRHRRKLVQPTPEEMSNLTPE 428
Qy 452 SSPALAKSWFGNFISLEKEEQIFVVIKDKPLSSIKADIVHAFSLSPSLSHSVISQTSFR 511
Db 429 SSPALAKSWFGNFISLEKEEQIFVVIKDKPLSSIKADIVHAFSLSPSLSHSVISQTSFR 488
Qy 512 AEYKATGGPAVFOKPVKQFQVDITYTTEGGEAQKENGYSVFTLLSGSPRRFKVWETIQ 571

Db 489 AEYKATGGPAVFOKPVKQFQVDITYTTEGGEAQKENGYSVFTLLSGSPRRFKVWETIQ 548
Qy 572 QLLSTHDPDPAQHLSDTTNCMENMTGRLSKCGIIPKS 608
Db 549 QLLSTHDPDPAQHLSDTTNCMENMTGRLSKCGIIPKS 585

RESULT 3
US-09-930-181-17
; Sequence 17, Application US/09930181
; Patent No. 6455292
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies
; TITLE OF INVENTION: Full-Length Serine Protein Kinase in Brain and Pancreas
; FILE REFERENCE: 16U 101 V1
; CURRENT APPLICATION NUMBER: US/09/930.181
; CURRENT FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 17
; LENGTH: 603
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-930-181-17

Query Match 94.6%; Score 3015; DB 4; Length 603;
Best Local Similarity 99.7%; Pred. No. 1.1e-205;
Matches 574; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 12 LIHHPVLKLDVYENKYLVLVLEHVSQGGELFDYLVKKGRLTPKEARKFQRIISALDF 71
Db 1 LIHHPVLKLDVYENKYLVLVLEHVSQGGELFDYLVKKGRLTPKEARKFQRIISALDF 60
Qy 72 CHSHSICHRLDKPENLLDDEKNRIADFGMASLQVGSLLSETSCGSPHYACPEVIRGEK 131
Db 61 CHSHSICHRLDKPENLLDDEKNRIADFGMASLQVGSLLSETSCGSPHYACPEVIRGEK 120
Qy 132 YDGRKADVMSQGVILFALLVQALPDDDDNLRLQLEKVKRGVFMHPHFTPPDCQSLIRGMI 191
Db 121 YDGRKADVMSQGVILFALLVQALPDDDDNLRLQLEKVKRGVFMHPHFTPPDCQSLIRGMS 180
Qy 192 EVDAAARLTLEHIOKHIWIYIGGKNEPEPEQPIPRKQVIRSLPSLEDIDPDVLDMSHSLGC 251
Db 181 EVDAAARLTLEHIOKHIWIYIGGKNEPEPEQPIPRKQVIRSLPSLEDIDPDVLDMSHSLGC 240
Qy 252 FRDRNKLLQDILLSEENOEKMIYFLLDRKERYPSQEDIDLPRNEIDPPRKRVDSPLN 311
Db 241 FRDRNKLLQDILLSEENOEKMIYFLLDRKERYPSQEDIDLPRNEIDPPRKRVDSPLN 300
Qy 312 RHGKRPRKSMVLSVTDGSGSPVPARRAIEMAHQGRSRISGASSGLSTSPSSPVTP 371
Db 301 RHGKRPRKSMVLSVTDGSGSPVPARRAIEMAHQGRSRISGASSGLSTSPSSPVTP 360
Qy 372 PHSPRGSPLTPKGTPTVHTPKESAGTPTNPTPPSPSPVGGVPMRLNLSKNSFLGSPR 431
Db 361 PHSPRGSPLTPKGTPTVHTPKESAGTPTNPTPPSPSPVGGVPMRLNLSKNSFLGSPR 420
Qy 432 FHRKLVQPTPEEMSNLTPESSPELAKSWFGNFISLEKEEQIFVVIKDKPLSSIKADIV 491
Db 421 FHRKLVQPTPEEMSNLTPESSPELAKSWFGNFISLEKEEQIFVVIKDKPLSSIKADIV 480
Qy 492 HAFSLSPSLSHSVISQTSFRAEYKATGGPAVFOKPVKQFQVDITYTTEGGEAQKENGYSVT 551
Db 481 HAFSLSPSLSHSVISQTSFRAEYKATGGPAVFOKPVKQFQVDITYTTEGGEAQKENGYSVT 540
Qy 552 FTLLSGSPRRFKVWETIQALLSTHDPDPAQHLSD 587
Db 541 FTLLSGSPRRFKVWETIQALLSTHDPDPAQHLSD 576

RESULT 4
US-09-523-849-36
; Sequence 36, Application US/09523849

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/ Patent No. 6458561
/ GENERAL INFORMATION:
/ APPLICANT: Bandman, Olga
/ APPLICANT: Molteni, Angela
/ APPLICANT: Magnaghi, Paola
/ APPLICANT: Bosotti, Roberta
/ APPLICANT: Scacheri, Emanuela
/ APPLICANT: Isacchi, Antonella
/ APPLICANT: Hodgson, Dave
/ TITLE OF INVENTION: HUMAN NIMI KINASE
/ FILE REFERENCE: PC-0009 US
/ CURRENT APPLICATION NUMBER: US/09/523,849
/ CURRENT FILING DATE: 2000-03-13
/ NUMBER OF SEQ ID NOS: 39
/ SOFTWARE: PERL Program
/ SEQ ID NO 36
/ LENGTH: 745
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc feature
/ OTHER INFORMATION: GenBank Accession No. 6458561 g1749794
US-09-523-849-36

Query Match      21.6%; Score 688.5; DB 4; Length 745;
Best Local Similarity 28.1%; Pred. No. 7.8e-41;
Matches 202; Conservative 108; Mismatches 225; Indels 183; Gaps 21;

QY      2 KVEREIAILKLEHPRVHLKLDHYVYENKYLVLVLEHVS GGELFDYLVKKGRLTPKEARKP 61
DB      63 KLFREVRIMKVLNHPNIVKLFVETETKTLVLMVEYASGGVFDYLVAGHRMKEKEARAK 122
QY      62 FQIITISALDFCHSHSICHRLDKPENLLLDKKNIRIADFGMASLQVGSLLTSCGSPHY 121
DB      123 FQIVSAVQYCHQKFIVRHDLKAENLLLDADNMIKIADFGFNSFTFCNKLDTCGSPPY 182
QY      122 ACEVIRGEKYDGRKADVMSCGVILFALLVAGLPDNDNLRQLLEKVKRGVFMHPHFTIPP 181
DB      183 AAPELFQGGKYDGEVDVMSGLVILYTLVSGSLPFDGQNLKELRERVLRGKYRIFPYNST 242
QY      182 DCQSLLRGMIEVDAAARLTLEHIQKHIWYIGGKNEPEPEQIPRKVQIRSLPSLEIDPD 241
DB      243 DCENLLKFLILNPSKRGTLQIMKDRMNMVGHEDDE-----LKPYYEPLPDYK--DPR 294
QY      242 VLDMSHSLGCFDRNKLQDLSEENQEKMIYFLLLDKRYKYPQEDDLPPRNEIDP-- 299
DB      295 RTELVMVMGYTREB-----IQDSLVGQRYNEVMATYLLLGYSSELEGDTITLKPSPADLT 351
QY      300 -----PPRKRVDSD-----PMLNRHKG-----RREPE-----R 320
DB      352 NSSAQPSSHVKVQSVSANPKQRRFSDQAGPAITPSNSYSKKTQSNNAENKREEDRESGR 411
QY      321 KSM-----EVLVTDG-----GSPVPARRAIEMA--OHGQRS 350
DB      412 KASSTAKVPASPLPGLERKKTTPFTSTNSVLSTNRSRNSPLLRASLQASIQNGKDS 471
QY      351 RSIIG--ASSGLSTSPSPVTPH-----PSPRGSLPTPKTPVHT 391
DB      472 LTPGSRASATASAAVAASARPRQKQKMSASVHPNKASGLPPTESNCEVPSTAPORV 531
QY      392 PKESP-----GTPNPT-----PPSPSPVGGV 413
DB      532 PVASPSAHNIISSGGAPDRTNFPRGVSSRSTFHAGQLRQVRQDQNLPGVTPPASFGHSQ 591
QY      414 PWRALNLSIKNSFLGSPRHRRLQVP--TPEMSNLTP-----ESSPEL 456
DB      592 GRRGASGSIFSKF--TSKFVRNLNLEPESKDRVETLRPHVVGSGGNDKEKEBFREAKPRS 649
QY      457 AKKSW--FGNFISLEKEEQIFVVIKDKPLSSIKADIVHAFSLPSLSHVSISQTSFRAEYK 515
DB      650 LFTWSMKTTSMEPNEMMREIRKVLVDANSQCSSELEKYMLL--CMHGTGPHEDF----- 702
QY      516 ATGGPAVQKPVKQVQDITYTTEGGEAQKENGIVSVTFTLLSGFSRRFRKRVVETIQAL 573

Db      703 -----VQWMEVC-----KLPRLSLNGVRFKRISGTSMAFKNIASKANEL 743

RESULT 5
US-09-984-890-2
; Sequence 2, Application US/09984890
; Patent No. 6492156
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001306
; CURRENT APPLICATION NUMBER: US/09/984,890
; CURRENT FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 724
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-984-890-2

Query Match      21.5%; Score 685.5; DB 4; Length 724;
Best Local Similarity 28.9%; Pred. No. 1.2e-40;
Matches 194; Conservative 103; Mismatches 230; Indels 145; Gaps 19;

QY      2 KVEREIAILKLEHPRVHLKLDHYVYENKYLVLVLEHVS GGELFDYLVKKGRLTPKEARKP 61
DB      96 KLFREVRIMKVLNHPNIVKLFVETETKTLVLMVEYASGGVFDYLVAGHRMKEKEARAK 155
QY      62 FQIITISALDFCHSHSICHRLDKPENLLLDKKNIRIADFGMASLQVGSLLTSCGSPHY 121
DB      156 FQIVSAVQYCHQKFIVRHDLKAENLLLDADNMIKIADFGFNSFTFCNKLDTCGSPPY 215
QY      122 ACEVIRGEKYDGRKADVMSCGVILFALLVAGLPDNDNLRQLLEKVKRGVFMHPHFTIPP 181
DB      216 AAPELFQGGKYDGEVDVMSGLVILYTLVSGSLPFDGQNLKELRERVLRGKYRIFPYNST 275
QY      182 DCQSLLRGMIEVDAAARLTLEHIQKHIWYIGGKNEPEPEQIPRKVQIRSLPSLEIDPD 241
DB      276 DCENLLKFLILNPSKRGTLQIMKDRMNMVGHEDDE-----LKPYYEPLPDYK--DPR 327
QY      242 VLDMSHSLGCFDRNKLQDLSEENQEKMIYFLLLDKRYKYPQEDDLPPRNEIDPP 301
DB      328 RTELVMVMGYTREB-----IQDSLVGQRYNEVMATYLLLGYSSELEGDTITLKPSPADLT 384
QY      302 RKRVDSP--MLNRHKGKRPKRKSMVLSVTDGSGSPVA-----RRAIEMA 344
DB      385 NSSAPSPSHKVQSVSANPKQRRFS---DQAGPAITPSNSYSKKTQSNNAENKREEDR 440
QY      345 OHGQRSISGASGLSTSP---LSSPRVTPHPS-----PRGSP-- 381
DB      441 ESGRKASS---TAKVPASPLPGLERKKTTPFTSTNSVLSTNRSRNSPLLRASLQQA 496
QY      382 -----PTPKGTPVHTPK---ESPAGTNPV----- 403
DB      497 SIQNGKOSTAQRPVPVSPASAHNIISSGGAPDRTNFPRGVSSRSTFHAGQLRQVRDQNL 556
QY      404 -----PPSPSPVGGVFWPWRALNLSIKNSFLGSPRHRRLQVP--TPEMSNLTP----- 450
DB      557 PYGVTTPASPSGHSQRRGASGSIFSKF--TSKFVRNLNLEPESKDRVETLRPHVVGSGN 614
QY      451 -----ESSPELAKSW--FGNFISLEKEEQIFVVIKDKPLSSIKADIVHAFSLPSLS 501
DB      615 DKEKEEFREAKPRSLRFTWSMKTTSMEPNEMMREIRKVLVDANSQCSSELEKYMLL--CM 672
QY      502 HSLVISQTSFRAEYKATGGPAVQKPVKQVQDITYTTEGGEAQKENGIVSVTFTLLSGFSRR 561
DB      673 HGTGPHEDF-----VQWMEVC-----KLPRLSLNGVRFKRISGTSMA 710
QY      562 FKRVVETIQAL 573
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Db 711 FKNTASKIANEL 722

RESULT 6

US-09-984-890-4

Sequence 4, Application US/09984890

Patent No. 6492156

GENERAL INFORMATION:

APPLICANT: YAN, Chunhua et al.

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

FILE REFERENCE: CL001306

CURRENT APPLICATION NUMBER: US/09/984.890

CURRENT FILING DATE: 2001-10-31

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 4

LENGTH: 722

TYPE: PRT

ORGANISM: Rattus norvegicus

US-09-984-890-4

Query Match 21.5%; Score 684.5; DB 4; Length 722;

Best Local Similarity 29.3%; Pred. No. 1.4e-40;

Matches 195; Conservative 103; Mismatches 233; Indels 135; Gaps 18;

Qy 2 KVERETAILKLIHPHVLKLDVYENKYLVLVLEHVSGLGDFYLVKKGRLTPKEARKF 61

Db 96 KLFREVRIMKVLNHPNIVKLFVETETKTLVLYVMEYASGGEVDFYLVAGHGMKEKEARAK 155

Qy 62 FROIISALDFCHSHSICHRLDKPENLLDKNNIRIADFGMASIQVGDLSLETSCGSPHY 121

Db 156 FROIISAVQYCHKFIHVHRLKAENLLDADNMKIADFGSNEFTGKNDLTPCGSPY 215

Qy 122 ACPEVIRGEYDKGRKADVWCGVILFALLVGLPFDNDNLRLLEKVKRGVFMHPHIPP 181

Db 216 AAPELFGQKDYDGPEDVWVSLGVILYLVSGSLPFDGQNLKELRERVLGRKYRIPFTYMT 275

Qy 182 DCQSLLRGMIEVDAAARLTLEHIQKHIWYIGKNEPEPEQIPRKVQIRSLPSLEIDPD 241

Db 276 DCENLLKFLILNPSKRGTELEQIMKDRVMNVGHEDDE-----LKYVEPLPDYK--DPR 327

Qy 242 VLDMSHSLGCFDRNKLQDLSSEENQEKMIYFLLDRKERYPSQDEDLPPRNEID-- 299

Db 328 RTELMSVSGYTREE---IQDSLVGQRYNEVWATYLLGLYKSELEGDTITLKPRPSADLT 384

Qy 300 -----PPRKRVDS-----PMLNRHGK-----RRPE-----RKS 322

Db 385 NSSAPSPSHKVQSVSANPKQRSSDQAVPAIPTSNYSYKKTQSNNAENKRPETGRKA 444

Qy 323 MEVLVTDGSGVPARRAIEWAHQGRSRISGASSGLSTSP----- 365

Db 445 SSTAQVP--ASPLGLDRKKTTPTPTSTNSVLSTSTNRNSPFLDRASLQASIQNGKDS 502

Qy 366 SSPRYTPHPSPRGSLPTPKGTPVHTPKESPAGT-----PNPTTP 405

Db 503 TAPQVVPASPAHNISSSGAPDRT--NFRKGVSSRTFHAGQRLQVRDQNLDPFGVTP 560

Qy 406 SSPSVGGVPMARLANSIKNSFLGSPFRHRRKLQVP--TPEMSNLTP----- 450

Db 561 ASPSGHSGQRRGASGSIKSF--TSKFVRNRLNEPESKDRVETLPHVVGSGTDEKEE 618

Qy 451 --ESSPELAKGW--GNFSLSEKEEQIFVVIKDKPLSSIKADIVAFISLSLSHVSISQ 507

Db 619 FREAKPRSLRFTWSMKTTSSEPNEMREIRKVLDSANCSQSELHERYMLL--CVHGTGPH 676

Qy 508 TSFRAEYKATGPAPVQKPVKQVDITYTEGGEAQKENGIIYVTTLLSGSPRRPKRVVE 567

Db 677 ENF-----VQWEMEVC-----KLPRLSLNGVRPKRISGTSMAFNATAS 714

Qy 568 TIQAQL 573

Db 715 KIANEL 720

RESULT 7

US-08-817-832B-32

Sequence 32, Application US/08817832B

Patent No. 6579691

GENERAL INFORMATION:

APPLICANT: MANDELKOW, Eckhard, et al.

TITLE OF INVENTION: No. 6579691el Protein Kinase (NPK-110)

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 233 S. Wacker Drive, 6300 Sears Tower

CITY: Chicago

STATE: Illinois

COUNTRY: US

ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/817,832B

FILING DATE: 28-APR-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/EP95/04258

FILING DATE: 30-OCT-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 94 11 7122.5

FILING DATE: 28-OCT-1994

INFORMATION FOR SEQ ID NO: 32:

SEQUENCE CHARACTERISTICS:

LENGTH: 722 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-817-832B-32

Query Match 21.4%; Score 682.5; DB 4; Length 722;

Best Local Similarity 29.3%; Pred. No. 2e-40;

Matches 195; Conservative 103; Mismatches 233; Indels 135; Gaps 18;

Qy 2 KVERETAILKLIHPHVLKLDVYENKYLVLVLEHVSGLGDFYLVKKGRLTPKEARKF 61

Db 96 KLFREVRIMKVLNHPNIVKLFVETETKTLVLYVMEYASGGEVDFYLVAGHGMKEKEARAK 155

Qy 62 FROIISALDFCHSHSICHRLDKPENLLDKNNIRIADFGMASIQVGDLSLETSCGSPHY 121

Db 156 FROIISAVQYCHKFIHVHRLKAENLLDADNMKIADFGSNEFTGKNDLTPCGSPY 215

Qy 122 ACPEVIRGEYDKGRKADVWCGVILFALLVGLPFDNDNLRLLEKVKRGVFMHPHIPP 181

Db 216 AAPELFGQKDYDGPEDVWVSLGVILYLVSGSLPFDGQNLKELRERVLGRKYRIPFTYMT 275

Qy 182 DCQSLLRGMIEVDAAARLTLEHIQKHIWYIGKNEPEPEQIPRKVQIRSLPSLEIDPD 241

Db 276 DCENLLKFLILNPSKRGTELEQIMKDRVMNVGHEDDE-----LKYVEPLPDYK--DPR 327

Qy 242 VLDMSHSLGCFDRNKLQDLSSEENQEKMIYFLLDRKERYPSQDEDLPPRNEID-- 299

Db 328 RTELMSVSGYTREE---IQDSLVGQRYNEVWATYLLGLYKSELEGDTITLKPRPSADLT 384

Qy 300 -----PPRKRVDS-----PMLNRHGK-----RRPE-----RKS 322

Db 385 NSSAPSPSHKVQSVSANPKQRSSDQAVPAIPTSNYSYKKTQSNNAENKRPETGRKA 444

Qy 323 MEVLVTDGSGVPARRAIEWAHQGRSRISGASSGLSTSP----- 365

Db 445 SSTAQVP--ASPLGLDRKKTTPTPTSTNSVLSTSTNRNSPFLDRASLQASIQNGKDS 502


```

363  ROPQURNDSLASLEVPQBEILPCDFRPSLLCPOQOALASVLOAQETDCDLHSSLOQLFFP 422
319  -----ERKSMEVLSVTDGGSPVPARRAIEAQAHQGRSRISGASGLST----- 362
423  LDTCNSGVFRHRSISPSLLDTAISERARQPSLEEEQVQEPPLPGSTGRRHTLAEBVSTH 482
363  SPLSSPVTHPSPRGSPPLTPKGP-----VHTPKESPAG-----TPNTPPSSPSV 410
483  F8PLNPPCCIIVSSSAAVSP-----SGTSSDCLPPSASEGPAGUGGLATPGLLTSSP-- 537
411  GGVWRPRLNLSKNSFLGSPRFRHKLQVTPTEMSN-----LTPESSPE----- 455
538  -----VRLAS-----PFLGS-----QSATPVLQSQAGLGATVLPVPSFQGRRASDTS 580
456  -----LAKKSWFGNFISLEKEEQIFVVIKDKPLSSIRAKDIVHAFSLTSPISHSV 504
581  LTQGLKAFRQQLRKWARTKGFGLNKL-----IKGLARQV 614
505  ISQTSFRAEYKATGGPFAVQKP 526
615  -CQSSIRG---SRGGMSTFHTP 632

```

```

RESULT 14
US-08-557-006C-40
; Sequence 40, Application US/08557006C
; Patent No. 6258547
; GENERAL INFORMATION:
; APPLICANT: Beri, Rajindar K.
; APPLICANT: Carling, David
; APPLICANT: Forder, Robert A.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING AMP-ACTIVATED PROTEIN KINASE
; FILE REFERENCE: NGAP/PM37588/UST
; CURRENT APPLICATION NUMBER: US/08/557,006C
; CURRENT FILING DATE: 1996-03-06
; PRIOR APPLICATION NUMBER: PCT/GB94/01093
; PRIOR FILING DATE: 1994-05-20
; PRIOR APPLICATION NUMBER: GB 9310489.1
; PRIOR FILING DATE: 1993-05-21
; PRIOR APPLICATION NUMBER: GB 9318010.7
; PRIOR FILING DATE: 1993-08-31
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 40
; LENGTH: 552
; TYPE: PRT
; ORGANISM: Rat
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)..(1747)
; OTHER INFORMATION: Full length cDNA sequence fragment of Human AMPK -
; OTHER INFORMATION: fragment begins at nucleotide 24 and ends with
; OTHER INFORMATION: nucleotide 1765
US-08-557-006C-40

```

[illegible]

Db	240	SIATLLMHMLQVDPDKRATIKOIREHEWF-----KODLP SYUL-----FPEDPSYDAN	286
QY	242	VLDS-----MHSLGCFRDNKLLQDILLS--EENQKMYIFLLDLRKERYPQOEDE----	290
Db	267	VIDDEAVKEVCEKEFC--TESEVNMSLYSGDPQDLAVAHLIIDNR-RIMNQASEFYLA	343
QY	291	DLPPRENEIDPPRKVRDSEMLNRHGKRPKRKSEMEVLSVTDGGSFVPARRAIEWAHQGQRS	350
Db	344	SSPPTG-----SFM D-----DNAMH-----	358
QY	351	RSISGASGLSTSPSSPRVTPHPSPRGSP L--PTPKGTGVHTPKESPAGTNPPTPPSP	408
Db	359	-----IPGGLKHPPE-RMPLIADSPKA-----RCPLDALNTTKPKSL	395
QY	409	SYGVGVPMRPARLNSIKNGLSGSPFRHRKLOVPTPEMSNL-----TPESSPELAKKSWFGN	464
Db	396	AVKKAHWLGIRSQSKPYDIAEYVRAMKQLDPFEMKVVAHYHLRVRKXNPVT-----GN	449
QY	465	FISLEKEQOIFWIKDXPLSKADIYHAFLSIPSLSHSVISQTSFRAEYKATGGPAVPQ	524
Db	450	YVKMSL--QLYLV-----DNRSYLLDPFKSIDDEVVEQRSGSTPQRSCSAAGLH	496
QY	525	KVKKFQVDITVTEGEQAQKNGIYSVFTLLSGSPRRFRKRVETIOAQLLLSTHDPDPAQH	584
Db	497	RP-RSSVDSSTAENHS-----LSG-----SLTOSLTGSTLSSASPRLGSH	535
QY	585	LSDTTN-CWEMMT	596
Db	536	TWDFFEMCASLIT	548

```

RESULT 15
US-09-101-146-1
; Sequence 1, Application US/09101146
; Patent No. 6124125
; GENERAL INFORMATION:
; APPLICANT: Dartmouth College, St. Vincent's Institute of
; APPLICANT: Medical Research, Kemp et al.
; TITLE OF INVENTION: No. 6124125el AMP Activated Protein Kinase
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jane Massey Licata, Esq.
; STREET: 66 E. Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: USA
; ZIP: 08053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PC
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: WORDPERFECT 6.0 FOR WINDOWS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/101,146
; FILING DATE: October 7, 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PN7450
; FILING DATE: 8 JAN 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: DC-0050
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (856) 810-1515
; TELEFAX: (856) 810-1454
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 345
; TYPE: Amino acid
; TOPOLOGY: Linear
US-09-101-146-1

```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 26, 2003, 11:57:16 ; Search time 16.6771 Seconds
(without alignments)
3506.035 Million cell updates/sec

Title: US-10-054-579-4

Perfect score: 3188

Sequence: 1 MKVERETAILKLEHPHVLK.....TNCMEMMTGRSLKCGIIPKS 608

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Pir1.*
2: Pir2.*
3: Pir3.*
4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES:

Result No.	Score	Query Match	Length	DB ID	Description
1	1536	48.2	887	2 T20941	hypothetical prote
2	722	22.6	1518	2 S37928	probable purine nu
3	698	21.9	401	2 B90120	SNF1-related prote
4	698	21.9	512	1 J21446	serine/threonine-s
5	687.5	21.6	745	2 G01025	serine/threonine p
6	686	21.5	504	2 T10449	probable serine/th
7	685.5	21.5	775	2 T38929	changed division r
8	681.5	21.4	512	2 T52633	serine/threonine-s
9	672.5	21.1	473	1 S59941	serine/threonine-s
10	668.5	21.0	1142	2 S59359	GIN4 protein - yea
11	668	21.0	511	1 A56009	serine/threonine-s
12	662.5	20.8	576	2 T41587	probable carbon ca
13	661.5	20.7	774	2 T48609	probable serine/th
14	660.5	20.7	562	2 T29858	hypothetical prote
15	655	20.5	915	2 S74283	probable protein k
16	654.5	20.5	713	2 S27966	probable serine/th
17	650	20.4	512	2 T07788	probable serine/th
18	649	20.4	798	2 J27500	gik protein - chic
19	642.5	20.2	504	2 T07415	probable serine/th
20	636	19.9	552	1 A53621	hydroxymethylglut
21	632	19.8	552	1 S51025	[hydroxymethylglut
22	625	19.6	1192	2 T18611	probable serine/th
23	624	19.6	1246	2 G89287	protein H3E23.1 [
24	620	19.4	472	2 B90100	SNF-related kinase
25	616.5	19.3	1558	2 T29253	hypothetical prote
26	616	19.3	633	1 A26030	serine/threonine-s
27	611.5	19.2	502	1 A41361	serine/threonine-s
28	609	19.1	602	2 S72513	FOG2 protein - yea
29	606	19.0	513	1 S60303	serine/threonine-s

ALIGNMENTS

RESULT 1

T20941

hypothetical protein F15A2.6 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000

C;Accession: T20941

R;Gregory, J.

submitted to the EMBL Data Library, March 1996

A;Reference number: Z19349

A;Accession: T20941

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-887 <WIL>

A;Cross-references: EMBL:Z70207; PIDN:CAA94127.1; GSPDB:GN00028; CESP:F15A2.6

A;Experimental source: clone F15A2

C;Genetics:

A;Gene: CESP:F15A2.6

A;Map position: X

A;Introns: 32/1; 63/3; 92/2; 139/2; 189/3; 328/2; 448/2; 516/3; 604/2; 684/3; 735/2; 777/

Query Match 48.2%; Score 1536; DB 2; Length 887;

Best Local Similarity 49.0%; Pred. No. 5.6e-56;

Matches 340; Conservative 71; Mismatches 133; Indels 150; Gaps 17;

Qy 2 KVERETAILKLEHPHVLKLDVYENKLYLVLEHVSGLGELFDYLVKGRGLTPKGRKF 61

Db 63 KVERETAILKLEHPHVLKLDVYENKLYLVLEHVSGLGELFDYLVKGRGLTPKGRKF 122

Qy 62 FROIISALDFCHSHSICHRDLKPENLLLDKNNIRIADFGMASLQVGDLSLETSCGSPHY 121

Db 123 FROIISALDFCHAHNICHRLDKPENLLLDKNNIKVADFGMASLQVGDLSLETSCGSPHY 182

Qy 122 ACEPVIKGEYKGRKADVMSCGVILFALLVGLPFDNNLRQLLEKVKRGVFMHPFPP 181

Db 183 ACEPVIKGEYKGRKADVMSCGVILFALLVGLPFDNNLRQLLEKVKRGVFMHPFPP 242

Qy 182 DCQSLLRGMIEVDAARLRLTEHQHIWYIG-KGNEPEPEQPIPRKQVIRSLPSLEDIDP 240

Db 243 DVQSLLRGMIEVDPGRKYSIADVFVKHPWVGTTKADPELPLMSQVQVTHVIFGEDSIDP 302

Qy 241 DVLDMSHSLGCFDRNKLQDLISEENOEKMYFYLLDRKERYPSQEDDEDLPPRNEI-- 298

Db 303 DVLHNMNLCGCFCKQKLINELLSPKHTKMYFYLLDRKRRPAQEDD-----TEIVL 357

Qy 299 -----DPRKEVDSPMLNR-----HGKRR-----PE 319

Db 358 RGAQNNDPPKKTDSRTSRYPMGSIADGSPINPRKTYGRNOKSGRHSLSGSGSPTESPR 417

Qy 320 RKMEVLSVTDGGS-----PVPARRAIEMAQH----- 346

Db 418 SSTEDLFGSSSSSYARAGEDRDGRSASRSINSVHYTQPVDPQTALAAARVRDAQE 477

protein kinase - m

hypothetical prote

serine/threonine p

serine/threonine-s

protein kinase kin

protein kinase 1 -

probable serine/th

p698g3 protein - A

protein kinase AK2

probable protein k

hypothetical prote

serine/threonine-s

probable serine/th

hypothetical prote

probable serine/th

serine/threonine-s

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QY 347 -----GORSRSICASSGLSTPLSSPRVTHPSPRGSLPTPKGTPVHTP 392
Db 478 RRESRDSGRGSRKESKDRSDKSSSSCKNDASSSTSSVPH-----KYSPSPVM 526
QY 393 KES---PAGTPNPTPSS-----PSVGGV--PWARLNSIKNSFLGSPRFRHRKQ 438
Db 527 SESVSVSSSTMNSTNSIAGNSQTSIGTSGPWSKLNINKNSFLGTFRFHRK-- 584
QY 439 VTPPEMSNLTTPSSDE-----LAKSWGCFN---ISLEKEQIFVWIKDPLSSI 486
Db 585 -----MSGTAESDESDQMDITDLVKKSWFGSLASSMSVERDDTHCVPVQGTLSI 638
QY 487 KADIVHAFSLPSLSHVSISQTSFRAEYK--ATGGPAVFOKPVKFOVDITYTE-----GG 539
Db 639 KAEIIRAFQLIHELHSHVQCNCFRVEYKGPVGVSGVSRGKIMNDIIPSPQVVIAG 698
QY 540 EAKENGIVSVTFTLLSGPSRRRFRVVEVETIOAQL 573
Db 699 ETP---TYVVOFVLLAGPVRRFKRLVEHLSAIL 728

RESULT 2
S37928
probable purine nucleotide-binding protein YKL101w - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein YKL453
C;Species: Saccharomyces cerevisiae
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 24-Sep-1999
C;Accession: S37928; S39084
R;Cheret, G.; Fukuhara, H.; Bolotin-Fukuhara, M.; Daignan-Fornier, B.; Pallier, C.; Puzos,
submitted to the Protein Sequence Database, March 1994
A;Reference number: S37920
A;Accession: S37928
A;Molecule type: DNA
A;Residues: 1-1518 <CHR>
A;Cross-references: EMBL:Z28101; NID:9486168; PIDN:CAA81941.1; PID:9486169; MIPS:YKL101w
A;Experimental source: strain S288C
R;Pallier, C.; Valens, M.; Puzos, V.; Fukuhara, H.; Cheret, G.; Sor, F.; Bolotin-Fukuhara,
Yeast 9, 1149-1155, 1993
A;Title: DNA sequence analysis of a 17 kb fragment of yeast chromosome XI physically loc
protein kinases.
A;Reference number: S39084; MUID:94078677; PMID:8256524
A;Accession: S39084
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-1518 <PAL>
A;Cross-references: EMBL:X71133; NID:9431205; PIDN:CAA50456.1; PID:9431215
A;Experimental source: strain S288C
C;Genetics:
A;Gene: SGD:HSL1
A;Cross-references: SGD:S0001584; MIPS:YKL101w
A;Map position: 11L
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog
F;Keywords: ATP; P-loop; purine nucleotide binding; serine/threonine-specific protein ki
F;79-86/Region: protein kinase homology <KIN>
F;87-95/Region: nucleotide-binding motif A (P-loop)
F;85/Binding site: ATP/GTP (Lys) #status predicted

Query Match 22.6%; Score 722; DB 2; Length 1518;
Best Local Similarity 30.4%; Pred. No. 1.6e-22;
Matches 216; Conservative 98; Mismatches 250; Indels 146; Gaps 19;

QY 3 VERIATILKLEHPLVHLKLDVYENKYLVLVLEHVSGLGELFDYLVKKGRITPKAEAKFF 62
Db 161 IERIVIMKLSHTNVNMFALFEWENKSELVILVLEVGGELFDYLVKGLKPEREATHYF 220
QY 63 RQITISALDFCHSHICHRLDKPENLLDERKN-NIRIADFGMASIQVGDLSLETSCGSPHY 121
Db 221 KQIVGVSVYCHSFNICHRLDKPENLLDKNRIKIADFGMAELPNKLLKTSCTGSPHY 280
QY 122 ACPEVIRGEKVDGRKADYVSCGVILFALLVGCALPPDDNLRQLLEKVKRGVFMHPHP 181
Db 281 ASPEIVMGRPYHGGPSDVMSCGIVFALLTGLHLPNDNLIKLLKLLKQSGKYQMPNLS 340
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QY 182 DCQSILRCMIWDAARRLTLEHIOKHIWYIGGKNEPEPEQPIPRKVO----- 228
Db 341 EARDLISKILVIDPEKRITTOEILKH--PLIKKKYDDLPVNVLRKRNKONMARGKNSDL 398
QY 229 -----IRSLPSLEDIDPDVLDMSHSLGCFDRNKLQDLJSEENQERMIYFLLLD 279
Db 399 HLLANNVSPSIVTLHSGEIDSEILRSLOILWHGVSRELITAKLLQKPMSEKLPYSLLIQ 458
QY 280 RKERY-----PSQEDEDLPPNEIDPPRKRVDSPLNHRHGKRRP--KSMEVLSV-TDG 331
Db 459 YKQRHSISLSSSENKKSATSESSVNEPIEYASKTANNTGLRSENNDVKTLHLSIHSED 518
QY 332 GSPVPARAIE-----MAHQGRSRS-----ISCASSG 359
Db 519 TSTVQNQNAITGVNTEINAPVLAQKSQFSINTLSQPSDKAEAEAVTLPPAIPFNASS 578
QY 360 -----LSTPSLSPRVTHPSPRGSLPTPKGTPVHTPKESPAAGTP 400
Db 579 RIFRNSYTSISRSRRSLNSRLSASTSRETVDHONEMPLQ-LPKSPSRYSLSRA 637
QY 401 NTPPSSPSVGVGPWRARLNSIKNSFLGSPRHRKLVQVPTPEMSNLTPESSPLAKKS 460
Db 638 IHASPTKSIH-----KSLRKNIAATVAARTLQ-----NSASKRSLYSLSQSIKRS 685
QY 461 WFGNFIISLEKEQIFVWIKDKPLSIKADIVHAFSLPSLSHVSISQTSFRA----- 512
Db 686 -----LNLND-----LLVDFDPLPSKPSASENVKSEP--HSLSDSDDFELCDQILFG 732
QY 513 -----EYKATGGPAVQKPVQVDITVTEGGEAOKEN-----GIYSVTPT 553
Db 733 NALDRILEEEDNEKERDQORQNDTKSSADTFTISGVSTNKNEGEPEYPTKIKNOFN 792
QY 554 LLSGPSRRPKRV-----VETIOAQLSTHDPAPAAQHLSDTTNCMEMM 595
Db 793 MSYKPSNNSSGLSPFPEKENTLSSYLEEQPKRAA-LSDITNSFNKM 841

RESULT 3
B90120
SNF1-related protein kinase [imported] - Guillardia theta nucleomorph
C;Species: nucleomorph Guillardia theta
A;Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
C;Accession: B90120
R;Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Reit
Nature 410, 1091-1096, 2001
A;Title: The highly reduced genome of an enslaved algal nucleus.
A;Reference number: A99082; MUID:11323671; PMID:11323671
A;Accession: B90120
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-401 <DOU>
A;Cross-references: GB:AF083031; NID:913794278; PIDN:AAK39655.1; GSPDB:GN00152
C;Genetics:
A;Gene: kin(gmf2)
A;Map position: 3
A;Genome: nucleomorph
C;Keywords: nucleomorph

Query Match 21.9%; Score 698; DB 2; Length 401;
Best Local Similarity 42.7%; Pred. No. 4.1e-22;
Matches 138; Conservative 77; Mismatches 86; Indels 22; Gaps 6;

QY 1 MKVERIATILKLEHPLVHLKLDVYENKYLVLVLEHVSGLGELFDYLVKKGRITPKAEAK 60
Db 59 LKTOIRISVNMKLMHPHVIKIYDVLSDSKYLFILIIYASKGELFNLYVEKRLKENREALK 118
QY 61 FFRQITISALDFCHSHICHRLDKPENLLDERKNIRIADFGMASIQVGDLSLETSCGSPH 120
Db 119 FFHEIISGLGYCHKRICHRDLKLENLLDMKLOIKIADFGMASISIPNIMLTKTCGSPH 178
QY 121 YACPEVIRGEKVDGRKADYVSCGVILFALLVGCALPPDD--DNLRQLLEKVKRGVFMHPHP 178
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Db 179 YASPEVSNPEPNGIKADWSGIIILYALVVGKLPYDENDDNRKLFNKIRPEPRIPRI 238
Qy 179 IPPDCQSLLRGMIEVDAAARLLTLEHIQKHIWYIGGKNEPEPEQPIPRKQIRSLP----- 233
Db 239 IHPDCRDLIRALLTNPQKRIIDKIKHPW---KSSPLPES---CRISQNLSFASVQ 292
Qy 234 SLEIDIDPVDLSMHSIGCFRDRNKLQDLSEENQEKMIYFLLDRKERYPSQEDDL 292
Db 293 NPISNPDPEITISFLPLQVQDKKTLGILSTKPSFLVLYRQLEWRKMKMDSVRSNLI 352
Qy 293 PPRNEIDPPRKRVDSPLNRHCK 315
Db 353 ---NEANPKKK-----LFKQSK 367

RESULT 4
JC1446
serine/threonine-specific protein kinase (EC 2.7.1.1-) AK21 - Arabidopsis thaliana
N:Alternate names: protein kinase SNF1 homolog
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text_change 11-Jun-1999
C:Accession: JC1446; S58266; S66334
R:LeGuen, L.; Thomas, M.; Bianchi, M.; Halford, N.G.; Kreis, M.
Gene 120, 249-254, 1992
A:Title: Structure and expression of a gene from Arabidopsis thaliana encoding a protein
A:Reference number: JC1446; MUID:93013041; PMID:1339373
A:Accession: JC1446
A:Molecule type: DNA
A:Residues: 1-512 <LEG>
A:Cross-references: EMBL:X869303; NID:gl66599; PIDN:AAA32736.1; PID:gl66600
R:Thuemmler, F.; Kirchner, M.; Teuber, R.; Ditttrich, P.
submitted to the EMBL Data Library, May 1995
A:Description: Differential accumulation of the transcripts of 22 novel protein kinase g
A:Reference number: S58266
A:Accession: S58266
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 144-198 <THU>
A:Cross-references: EMBL:X86966; NID:g928909; PIDN:CAA60529.1; PID:g928910
R:Thuemmler, F.; Kirchner, M.; Teuber, R.; Ditttrich, P.
Plant Mol. Biol. 29, 551-565, 1995
A:Title: Differential accumulation of the transcripts of 22 novel protein kinase genes i
A:Reference number: S66314; MUID:96123233; PMID:8534852
A:Accession: S66334
A:Molecule type: DNA
A:Residues: 144-198 <TH2>
A:Cross-references: EMBL:X86966; NID:g928909; PIDN:CAA60529.1; PID:g928910
C:Comment: This enzyme plays an important role in a signal transduction cascade regulati
C:Genetics:
A:Gene: AKin10; AK21
A:introns: 64/1; 125/3; 186/3; 230/3; 292/3; 322/3; 350/3; 396/3; 475/3
C:Function:
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
C:Superfamily: AMP-activated protein kinase; protein kinase homolog
C:Keywords: ATP; magnesium; phosphotransferase; serine/threonine-specific protein kinase
P:17-271/Domain: protein kinase homolog <kin>
F:125-33/Region: protein kinase Arg-binding motif
F:48,67,142,144/Active site: Lys, Glu, Asp, Lys #status predicted
F:147,151/Binding site: magnesium (Asn, Asp) #status predicted

Query Match 21.9%; Score 698; DB 1; Length 512;
Best Local Similarity 42.7%; Pred. No. 5.2e-22;
Matches 137; Conservative 70; Mismatches 90; Indels 24; Gaps 5;

Qy 2 KVEREIALKLEIHPHVLKLDVYENKYLVLVLEHVS GGELFDYLVKKGRLTTPKEARKF 61
Db 63 KVRREIKILRFMPHIIRLVEIETPTDYLVMVEYNSGGELFDYIVVEKGLQDEARNP 122
Qy 62 FROIISALDFCHSHSICHRLDKPENLLDKNINRIADFGMASLQVGDLSLETSCGSPHY 121
Db 123 FQIISGVEYCHRNWVVRDLKPNLLDLSKCNVKIADFGLSNIMRDGHFLKTS CGSPNY 182

RESULT 5
G01025
serine/threonine protein kinase - human
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1996 #sequence revision 06-Jun-1997 #text_change 16-Dec-1998
C:Accession: G01025
R:Navarro, E.
submitted to the EMBL Data Library, April 1996
A:Reference number: H00564
A:Accession: G01025
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-745 <NAV>
A:Cross-references: EMBL:X97630; NID:gl310674
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog
F:18-271/Domain: protein kinase homolog <kin>

Query Match 21.6%; Score 687.5; DB 2; Length 745;
Best Local Similarity 28.1%; Pred. No. 2e-21;
Matches 202; Conservative 108; Mismatches 225; Indels 183; Gaps 21;

Qy 2 KVEREIALKLEIHPHVLKLDVYENKYLVLVLEHVS GGELFDYLVKKGRLTTPKEARKF 61
Db 63 KLFREVRIMKVLNHPNIVKLFVETETKTLVLMVEYASGGVDFYLVAGHRMKEKARAK 122
Qy 62 FROIISALDFCHSHSICHRLDKPENLLDKNINRIADFGMASLQVGDLSLETSCGSPHY 121
Db 123 FROIISAVQYCHOKFIVHRDLKAEKLLDADNMKIADFGFSNEFTFGNKLDTFCGSPY 182
Qy 122 ACPEVIRGEKYDGRKADVWSCGVILFALLVGCALPFDDNLRQLLEKVKRGVFMHPPIPP 181
Db 183 ANPELFGKKYDGPVDVNSGLVILYLVSGSLPFFDQNLKELREVRVLRKYRIPFYMTST 242
Qy 182 DCQSLLRGMIEVDAAARLLTLEHIQKHIWYIGGKNEPEPEQPIPRKQIRSLPSLEDIDPD 241
Db 243 DCENLLKFLILNPKSKRGTLQIMKDRMVMVGHEDDE-----LKPVEPLPDYK--DPR 294
Qy 242 VLDSMHSIGCFRDRNKLQDLSEENQEKMIYFLLDRKERYPSQEDDLPRNEID-- 299
Db 295 RTELVMSMGVTRBE---IQSLVGQRYNEYMATYLLGLYKSSLEGGDTITLKPRPSADLT 351
Qy 300 -----PPRKEVDS-----PMLNRHKG-----RRPE-----R 320
Db 352 NSSAQFPESHKQSVSNPKQRFPSDQAGPAITPSNSYKKTQSNNAENKRPEDRESGR 411
Qy 321 KSM-----EVLVYTDG---GSPVPARRAIEMA--QHQRS 350
Db 412 KASSTAKVPASPLPGLERKKTITPTPSTNSVLSTSTNRNSPLLERASLQASIQNGKDS 471
Qy 351 RSTSG--ASSGLSTSPSSPRVTPH-----PSPRGSPLTPKGTVPHT 391
Db 472 LTMFGSRASASAGVSAARPRQHOKSMGSGVHPNKAAGLPPTESNCEVPRFSTAPQV 531
Qy 392 PKESPA-----GTNPNT-----PPSSSVGGV 413
Db 532 PVASPSAHNITSSSGGAPDRTNPRGVSSRSTFHAGQLRQVRDQONLPYGVTPASPSGHSQ 591
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Qy 122 ACPEVIRGEKYDGRKADVWSCGVILFALLVGCALPFDDNLRQLLEKVKRGVFMHPPIPP 181
Db 183 AAPEVISGKLYAGPEVDVWSCGVILYALLCCTLPFDDENIPNLFKIKGGIYTLPSHSLP 242
Qy 182 DCQSLLRGMIEVDAAARLLTLEHIQKHIWYIGGKNEPEPEQPIPRKQIRSLPSLEDI 238
Db 243 GARDLIPRLVVDPMKVTIPEIRQHWF-----QAHLPRYLAVPPDPTVQQAKKI 293
Qy 239 DPVDLSMHSIGCFRDRNKLQDLSEENQEKMIYFLLDRKERYPS-----QEDD 291
Db 294 DEELIQEVINMGF--DRNHLLIESLRNTQDGTVTYYILLDNRRFRASSGYLGASFQETME 351
Qy 292 LPPRNEIDPPRKRVDSPLNR 312
Db 352 GTPRMH---PAESVASPVSHR 369
```


Db 726 TEFO 729

RESULT 8

T52633

serine/threonine-specific protein kinase (EC 2.7.1.1) AKIN11 [validated] - Arabidopsis
 N:Alternate names: SNF1 protein kinase homolog AKIN11
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 03-Nov-2000

C:Accession: T52633

R:Bhalerao, R.P.; Salchert, K.; Bako, L.; Okresz, L.; Szabados, L.; Muranaka, T.; Machida

Proc. Natl. Acad. Sci. U.S.A. 96, 5322-7, 1999

A:Title: Regulatory interaction of PRU1 WD protein with Arabidopsis SNF1-like protein ki

A:Reference number: 225116; MUID:99238528; PMID:10220464

A:Accession: T52633

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-512 <BA>

A:Cross-references: EMBL:X99279; PIDN:CAA67671.1

A:Experimental source: cultivar Columbia

C:Genetics:

A:Gene: AKIN11

C:Function:

A:Description: EC 2.7.1.1; serine/threonine-specific protein kinase AKIN11 [validated, M

complements SNF1 mutations in yeast

C:Superfamily: AMP-activated protein kinase; protein kinase homolog

C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase

Query Match 21.4%; Score 681.5; DB 2; Length 512;

Best Local Similarity 39.5%; Pred. No. 2.4e-21;

Matches 140; Conservative 73; Mismatches 106; Indels 35; Gaps 6;

QY 2 KVEREIAIKLIEHPHVLKLDVYENKYLVLVLEHVSGLGELFDYLVKKGRLTPKEARKF 61

DB 64 KVRREIKLRLFMHPHIIRIQEVLETSDIVVWEYVKSGLFDYIVVEKGLQDEARNF 123

QY 62 FROIISALDFCHSHSICHRLDKPENLLDEKNNIRIADFGMASLQVGDLSLETSCGSPHY 121

DB 124 FQIISGVEYCHRNWVHRDLKPNLLDSCNLIKADFGSLNVRMDGHFLKTS CGSPNY 183

QY 122 ACPEVIRGEKYDGRKADVNSCGVILFALLVCGALPDDNLRQLLEKVKRGVFMHPHIPP 181

DB 184 AAPEVISGKLYAGPEVDVWVSCGVILYALLCGTLFPDENIPNLFKIKGGIYTLPSHLS 243

QY 182 DCQSLLRGMEVDAAARLTLEHIQKHIWYIGCKNEPEPEQIPRKVOIRSLPSLED--I 238

DB 244 EARDLIPRLMIVDPVKRITIEIRQHRNF-----QTHLPRLAVSPDPTVEQAKI 294

QY 239 DPVDLDSMHSILGCFDRNKLQDLSEENQEKMIYFLLDRKERYPSQEDDLPPENEI 298

DB 295 NEEIVQEVVNMGF--DRNQVLESRLNRNTQNDATVTYVLLDNRFRVPSGYLE-----SEF 347

QY 299 DPPRKVDSPMLNRHGRPERKPSNEVLSTVDGSPVPARAEIEMAQHGQSRSS 352

DB 348 QETDSSGNPW-----RTPEA-----GASPVGHWIPAHVDHYGLGARS 385

RESULT 9

S59941

serine/threonine-specific protein kinase (EC 2.7.1.1) BKIN2 - barley (fragment)

C:Species: Hordeum vulgare (barley)

C:Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 26-Feb-1999

C:Accession: S59941

R:Hannappel, U.; Vicente-Carbajosa, J.; Barker, J.H.A.; Shewry, P.R.; Halford, N.G.

Plant Mol. Biol. 27, 1235-1240, 1995

A:Title: Differential expression of two barley SNF1-related protein kinase genes.

A:Reference number: S59941; MUID:95284374; PMID:7766906

A:Accession: S59941

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-473 <BA>

A:Cross-references: EMBL:X82548

C:Genetics:

A:Gene: BKIN2

C:Function:

A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine
 C:Superfamily: AMP-activated protein kinase; protein kinase homolog

C:Keywords: ATP; magnesium; phosphotransferase; serine/threonine-specific protein kinase

F;1-244/Domain: protein kinase homolog (fragment) <KIN>

F;21,40,115,117/Active site: Lys, Glu, Asp, Lys #status predicted

F;120,124/Binding site: magnesium (Asn, Asp) #status predicted

Query Match 21.1%; Score 672.5; DB 1; Length 473;

Best Local Similarity 42.7%; Pred. No. 5.3e-21;

Matches 128; Conservative 69; Mismatches 82; Indels 21; Gaps 4;

QY 2 KVEREIAIKLIEHPHVLKLDVYENKYLVLVLEHVSGLGELFDYLVKKGRLTPKEARKF 61

DB 36 KVRREIKLRLFMHPHIIRLYEVIDTPADIYVWEYVKSGLFDYIVVEKGLQDEEARPF 95

QY 62 FROIISALDFCHSHSICHRLDKPENLLDEKNNIRIADFGMASLQVGDLSLETSCGSPHY 121

DB 96 FQIISGVEYCHRNWVHRDLKPNLLDSCNLIKADFGSLNVRMDGHFLKTS CGSPNY 155

QY 122 ACPEVIRGEKYDGRKADVNSCGVILFALLVCGALPDDNLRQLLEKVKRGVFMHPHIPP 181

DB 156 AAPEVISGKLYAGPEVDVWVSCGVILYALLCGTLFPDENIPNLFKIKGGIYTLPSHLS 215

QY 182 DCQSLLRGMEVDAAARLTLEHIQKHIWYIGCKNEPEPEQIPRKVOI---RSLPSLEDI 238

DB 216 LARDLIPRLMIVDPVKRITIEIRHSWF-----KARLPRLAVPPDPTAQVKKL 266

QY 239 DPVDLDSMHSILGCFDRNKLQDLSEENQEKMIYFLLDRKERYPS-----QEDD 291

DB 267 DDETLDNVKMGF--DKNQVLESRLNRNTQNDATVTYVLLDNRFRVPSGYLE-----SEF 324

RESULT 10

S59359

GIN4 protein - yeast (Saccharomyces cerevisiae)

N:Alternate names: protein YDR507c

C:Species: Saccharomyces cerevisiae

C:Date: 30-Nov-1995 #sequence_revision 01-Mar-1996 #text_change 24-Sep-1999

C:Accession: S59359; S59565

R:Longtine, M.S.; Pringle, J.R.

submitted to the EMBL Data Library, August 1995

A:Reference number: S59359

A:Accession: S59359

A:Molecule type: DNA

A:Residues: 1-1142 <ION>

A:Cross-references: EMBL:U33140; NID:g992650; PIDN:AAA75513.1; PID:g992651

R:Dietrich, F.S.

submitted to the EMBL Data Library, August 1995

A:Description: The sequence of S. cerevisiae cosmids 8166, 9787, 9717, and lambda 3073.

A:Reference number: S59553

A:Accession: S59565

A:Molecule type: DNA

A:Residues: 1-1142 <DIE>

A:Cross-references: EMBL:U33057; NID:g927764; PIDN:AAB64949.1; PID:g927777; MIPS:YDR507c

C:Genetics:

A:Gene: SGD:GIN4

A:Cross-references: SGD:S0002915; MIPS:YDR507c

A:Map position: 4R

C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog

C:Keywords: ATP

F;17-289/Domain: protein kinase homolog <KIN>

F;25-33/Region: protein kinase ATP-binding motif

Query Match 21.0%; Score 668.5; DB 2; Length 1142;

Best Local Similarity 34.1%; Pred. No. 1.8e-20;

Matches 183; Conservative 73; Mismatches 162; Indels 119; Gaps 16;

QY 3 VEREIAIKLIEHPHVLKLDVYENKYLVLVLEHVSGLGELFDYLVKKGRLTPKEARKPF 62

DB 78 IEREIIMKLNHPNVLRLVDWETNTDLYLVLEYAEKGLFNLLVERGSLPHEAIRFF 137

QY 63 RQIIISALDFCHSHSICHRLDKPENLLDDEKNNIRIADFGMASLQVDSGLLETSCGSPHYA 122
DB 138 RQIIIGVSYCHALGIVHRDLKPENLLDHDKNYKIADFGMAALETEGKLLLETSCGSPHYA 197
QY 123 CPEVIRGEKDGKADVWSCGVILFALLVGLALPPD--DNNRLQLLEKVKRGVFMHP--HF 178
DB 198 APEIVSGIPYCGFASDVWSCGVILFALLVGLALPPDDEEDGNIRTLTKLVKRGSEFMPDDE 257
QY 179 IPPDCQSLRGMIETDAARLLTLEHIQKHIWYIGGKNEPEPEPIPKV-----QIRS 231
DB 258 ISREAQDLIRKILTVDERIKTRDIKH-----PLQKYPISIRDSKSI 303
QY 232 LP-----SLEDIDPDVLSMHSGLCFDRNKLQDLISEENQKMIYFLLDDR 280
DB 304 LPREDTYLPLSENSSIDATILQNLVILWHGRDPEGIEKELREPGANAETKLYALLY-- 361
QY 281 KERYPSQDEEDLPRNEIDPPRKVDSPMLNRHCKRPERKSMVLSVTDGSGVPARRA 340
DB 362 --RPFKCDTQKELIKQQV-----KKGQSISVSVS-----PSKV 394
QY 341 IEMAQHGQRSISGASGLSTSPLSGRVTPHPSPRGSPLETPPKGTFFVHTPKESPAGTP 400
DB 395 STTPQRRNRRESLSVTS-----RKKPISFNKT-----ASSASS 431
QY 401 NPTPPSPSVGVPWRLNLSIKNSFLGSPRFRHKLQVTPPEMSNLTPESSPELAKKS 460
DB 432 NLTFPGSSK-----RL-----SKNFSSKK-----KLSTIVNQSSPTPASRN 467
QY 461 WFGNFISLEKEEQ---IFVVIKDKPLASIKADIHAFSLPSLSHVSISOTSPRAEY 514
DB 468 KRASVINVEKNQKRASIFSTTKKNKRSRS---IKRSLIPSMKRESVT-TKLMSTY 520

RESULT 11
A56009
serine/threonine-specific protein kinase (EC 2.7.1.-) NPXS - common tobacco
C/Species: Nicotiana tabacum (common tobacco)
C/Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 16-Jun-2000
C/Accession: A56009
Mol. Cell. Biol. 11, 2958-2965, 1994
R/Muranaka, T.; Banno, H.; Machida, Y.
A/Title: Characterization of tobacco protein kinase NPXS, a homolog of Saccharomyces cerevisiae.
A/Reference number: A56009; MUID:94217693; PMID:8164654
A/Accession: A56009
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-511 <MUR>
A/Cross-references: GB:D26602; NID:G496384; PIDN:BAA05649.1; PID:G496385
C/Function:
A/Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine-phosphate
C/Superfamily: AMP-activated protein kinase; protein kinase homology
C/Keywords: ATP; magnesium; phosphotransferase; serine/threonine-specific protein kinase
F:17-271/Domain: protein kinase homology <KIN>
F:25-33/Region: protein kinase ATP-binding motif
F:48,67,142,144/Active site: Lys, Glu, Asp, Lys #status predicted
F:147,151/Binding site: magnesium (Asn, Asp) #status predicted

Query Match 21.0%; Score 668; DB 1; Length 511;
Best Local Similarity 44.4%; Pred. No. 8.7e-21;
Matches 128; Conservative 61; Mismatches 85; Indels 14; Gaps 3;

QY 2 KVEREIALKLEIHPHVLKLDHVDYENKYLVLVLEHVSGLGELFDYLVKKGLRTPKEARKF 61
DB 63 KVRREIKILRFMHPHIIIRLYEVVETPSDIYVWVEYKVSGLGELFDYLVKKGLRTPKEARKF 122
QY 62 FROIISALDFCHSHSICHRLDKPENLLDDEKNNIRIADFGMASLQVDSGLLETSCGSPHY 121
DB 123 FQIIISGVEYCHRNWVHRDLKPENLLDSDKNVKNVADFGLSNIMRDGHFLKTSKSGSPNY 182
QY 122 ACPEVIRGEKDGKADVWSCGVILFALLVGLALPPDDNNRLQLLEKVKRGVFMHPHPTIP 181
DB 183 AAPEVISGLKLYAGPEVDVWSCGVILYALLCGTLPLPDDENIPNLFKKIKGMISLPSHLSA 242

QY 182 DCQSLLRGMIETDAARLLTLEHIQKHIWYIGGKNEPEPEPIPKVVOI---RSLPSLEDI 238
DB 243 GARDLIPMLIYVDPMKMTIPIRHPWF-----QAHLPRYLAVPPPTMQQAKKI 293
QY 239 DPVLDMSHSLGCFDRNKLQDLISEENQKMIYFLLDDRKERYPS 286
DB 294 DEDILQEVVKGRF--DRNSLVASLCNRVQNEGTVAAYLLENQFRASS 339

RESULT 12
T41587
probable carbon catabolite derepressing protein kinase - fission yeast (Schizosaccharomyces pombe)
C/Species: Schizosaccharomyces pombe
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Jan-2000
C/Accession: T41587
R/Murphy, L.; Harris, D.; Lyne, M.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, September 1998
A/Reference number: Z21968
A/Accession: T41587
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-576 <MUR>
A/Cross-references: EMBL:AL031543; PIDN:CAA20833.1; GSPDB:GN00068; SPDB:SPCC74.03c
A/Experimental source: strain 972h; cosmid c74
C/Genetics:
A/Gene: SPDB:SPCC74.03c
A/Map position: 3
A/Intons: 50/1; 127/3; 245/1
C/Superfamily: AMP-activated protein kinase; protein kinase homology

Query Match 20.8%; Score 662.5; DB 2; Length 576;
Best Local Similarity 37.3%; Pred. No. 1.6e-20;
Matches 146; Conservative 76; Mismatches 114; Indels 55; Gaps 10;

QY 1 MKVEREIALKLEIHPHVLKLDHVDYENKYLVLVLEHVSGLGELFDYLVKKGLRTPKEARK 60
DB 77 MRVEREISYLVKLRHPHIIIRLYEVVETPSDIYVWVEY-AGGELFDYLVKKGLRTPKEARK 135
QY 61 FROIISALDFCHSHSICHRLDKPENLLDDEKNNIRIADFGMASLQVDSGLLETSCGSPH 120
DB 136 FQIIISGVEYCHRNWVHRDLKPENLLDSDKNVKNVADFGLSNIMRDGHFLKTSKSGSPN 195
QY 121 YACPEVIRGEKDGKADVWSCGVILFALLVGLALPPDDNNRLQLLEKVKRGVFMHPHPTIP 180
DB 196 YAAPEVINGKLYAGPEVDVWSCGVILYVGLRPLPDDDEFIPNLFKKVNSCVVMPDFLS 255
QY 181 DCQSLLRGMIETDAARLLTLEHIQKHIWYIGGKNEPEPEPIPKVQIERSLPSLEDDIP 240
DB 256 PGAQSLIRRMIVADPMQRTIQEIRDPWF--NVNLPDYLRP-----MEEVQG 301
QY 241 DVLDSDM-----HSLGCFDRNKLQDLISEENQKMIYFLLDDRKERYPSQEDDLPP 294
DB 302 SYADSRIVSKLGEAMGFSED--YIVELASDENNEVKEAYNLL--HENQVIOEKSHL-- 354
QY 295 RNEIDPPRKVDSD-----PMLNRHGRKRRPERKSMVLSVTDG-----SPVPARRAI 341
DB 355 -----SKSKVDVSLVSPAPFSEYTSLEQKSKBELIDPTLEGPRWTVDPPTYAKQTI 409
QY 342 E-----MAHQGQRSISGASGLSTS 363
DB 410 DSNICVLVPTAEKNKLEMTLADASAADVTS 440

RESULT 13
I48609
Probable serine/threonine-specific protein kinase (EC 2.7.1.-) kem - mouse
C/Species: Mus musculus (house mouse)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 04-Mar-2000
C/Accession: I48609; S31333
R/Ingalls, J.D.; Lee, M.; Hill, R.E.
Mamm. Genome 4, 401-403, 1993
A/Title: Emk, a protein kinase with homologs in yeast maps to mouse chromosome 19.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 26, 2003, 11:50:16 ; Search time 10.0063 Seconds
(without alignments)
2857.432 Million cell updates/sec

Title: US-10-054-579-4

Perfect score: 3188

Sequence: 1 MKVERETAILKLIBHVLK.....TNCMMMTGRLSKGIIPKS 608

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	722	22.6	1518	1 KKK1 YEAST	P34244 saccharomyc
2	698	21.9	512	1 K110 ARATH	Q38997 arabidopsis
3	685.5	21.5	775	1 CDR2 SCHPO	P87050 schizosacch
4	675.5	21.2	752	1 MRK4 HUMAN	Q96134 homo sapien
5	668.5	21.0	1142	1 G1N4 YEAST	Q12263 saccharomyc
6	662.5	20.8	576	1 SNF1 SCHPO	O74536 schizosacch
7	661.5	20.7	774	1 MRK2 MOUSE	Q05512 mus musculu
8	655	20.5	915	1 KCC4 YEAST	P25389 saccharomyc
9	645	20.2	786	1 SN1L HUMAN	P57059 homo sapien
10	638	20.0	776	1 SN1L RAT	Q97155 rattus norv
11	637	20.0	776	1 MRK3 HUMAN	P27448 homo sapien
12	636	19.9	552	1 AAK2 RAT	Q09137 rattus norv
13	632	19.8	552	1 AAK2 HUMAN	P54646 homo sapien
14	631.5	19.8	548	1 AAK1 RAT	P54645 rattus norv
15	631	19.8	779	1 SN1L MOUSE	Q60670 mus musculu
16	627.5	19.7	550	1 AAK1 HUMAN	Q13131 homo sapien
17	620.5	19.5	619	1 SNF1 CANTR	O94168 candida tro
18	616	19.3	633	1 SNF1 YEAST	P06782 saccharomyc
19	611.5	19.2	502	1 RK11 SECCO	Q02723 secale cere
20	609.5	19.1	611	1 SNF1 CANAL	Q03372 candida gla
21	596.5	18.7	620	1 SNF1 SCHPO	P52497 candida alb
22	585.5	18.4	891	1 KIN1 SCHPO	P22987 schizosacch
23	556	17.4	622	1 YNA3 CAEEL	P45894 caenorhabdi
24	546.5	17.1	1064	1 KIN1 YEAST	P13185 saccharomyc
25	546	17.1	661	1 Y537 HUMAN	O60285 homo sapien
26	533	16.7	593	1 CDR1 SCHPO	P07334 schizosacch
27	500	15.7	1147	1 KIN2 YEAST	P13186 saccharomyc
28	493	15.5	800	1 KIN4 YEAST	Q01919 saccharomyc
29	461.5	14.5	353	1 ASK2 ARATH	P43292 arabidopsis
30	458.5	14.4	363	1 ASK1 ARATH	P43291 arabidopsis
31	447	14.0	714	1 HUNK HUMAN	P57058 homo sapien
32	444.5	13.9	714	1 HUNK MOUSE	O88866 mus musculu
33	433.5	13.6	664	1 KCCB HUMAN	Q13554 homo sapien

RESULT 1

KKK1 YEAST
ID _KKK1 YEAST STANDARD; PRT; 1518 AA.
AC P34244;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Probable serine/threonine-protein kinase YKL101W (EC 2.7.1.1.-).
GN YKL101W OR YKL453.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=94078677; PubMed=8256524;
RA Pallier C., Valens M., Fuzos V., Fukuhara H., Cheret G., Sor F.,
RA Bolotin-Fukuhara M.;
RT "DNA sequence analysis of a 17 kb fragment of yeast chromosome XI
physically localizes the MRB1 gene and reveals eight new open reading
frames, including a homologue of the KIN1/KIN2 and SNF1 protein
kinases".
RL Yeast 9:1149-1155(1993).
RL - SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC NIM1 SUBFAMILY.

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EMBL; X71133; CAA50456.1; --
EMBL; Z28101; CAA81941.1; --
PIR; S37928; S37928.
HSSP; Q63450; 1A06.
SGD; S0001584; HSL1.
GO; GO:0005935; C:bud neck; IDA.
GO; GO:0005940; C:septin ring; IDA.
GO; GO:0000086; P:G2/M transition of mitotic cell cycle; IGI.
GO; GO:0006468; P:protein amino acid phosphorylation; IDA.
GO; GO:0000074; P:regulation of cell cycle; IMP.
GO; GO:0000135; P:septin checkpoint; IGI.
InterPro; IPR000719; Prot_kinase.
InterPro; IPR002290; Ser_Chk_kinase.
InterPro; IPR001245; Tyr_kinase.
Pfam; PF00069; kinase; 1.
PRINTS; PR00109; TYRKINASE.
ProDom; PD000001; Prot_kinase; 1.
SMART; SM00220; S_TKC_1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR

ALIGNMENTS

34	433	13.6	370	1	KCC1_HUMAN
35	433	13.6	374	1	KCC1_MOUSE
36	433	13.6	374	1	KCC1_RAT
37	424	13.3	472	1	KCCG_HUMAN
38	423	13.3	332	1	AAIP_WHEAT
39	417.5	13.1	433	1	STKB_HUMAN
40	413	13.0	1050	1	ULK1_HUMAN
41	411.5	12.9	499	1	KCCD_HUMAN
42	411.5	12.9	533	1	KCCD_RAT
43	410	12.9	473	1	PK2_DICDI
44	406.5	12.8	527	1	KCCG_RAT
45	406.5	12.8	529	1	KCCG_MOUSE

KW Hypothetical protein; Transferase; Serine/threonine-protein kinase;
KW ATP-binding. 81 369 PROTEIN KINASE.
FT NP BIND 87 95 ATP (BY SIMILARITY).
FT BINDING 110 110 ATP (BY SIMILARITY).
FT ACT SITE 239 239 BY SIMILARITY.
SQ SEQUENCE 1518 AA; 169592 MW; 803F84F7531241DD CRC64;

Query Match 22.6%; Score 722; DB 1; Length 1518;
Best Local Similarity 30.4%; Pred. No. 8.8e-30;
Matches 216; Conservative 98; Mismatches 250; Indels 146; Gaps 19;

QY 3 VEREIALKLTIEHPVLKLDHVVNKKYLVLEHVGSGELFDYLVKKGLTPEAKRFF 62
DB 161 IEREIVTKLISHNVNVALFEWENKSELVLYLEVVGSELFDYLVSKGLPREAIHYF 220
QY 63 RQISALDPCHSHISCHRDLPENLLDEKN-NRIADFGWASLVQSDSLLETSCGSPHY 121
DB 221 KQIVEGVSYCHSFNICHRLDKPENLLDKNRRIKIADFGWAALEPNKLLKTS CGSPHY 280
QY 122 ACPEVIRGEKYDGRKADVWSCGVTLFALLGALPPDDNLRQLLEKYKRGVFMHPHIPP 181
DB 281 ASPVIMVGRPVHGGPSDVWSCGVTLFALLGALPPDDNLRQLLEKYKRGVFMHPHIPP 340
QY 182 DCOSLLRGMEVDAAERLTLEHIOKHWYGGKNEPEQPIPRKVO----- 228
DB 341 EARDLISKILVIDEKAITTOELKH--PLIKKYDDLVPVNVKLRKONWARKGNSDL 398
QY 229 -----IRSLPSLEDIPDVLDSMHSIGCFDRNKLQDLLSEENGEKMIYFLLD 279
DB 399 HLLNNVSPSIVTLHSGKEIDSLRSQILWHGVSRRLITAKLLQKPMSEKLFYSILLQ 458
QY 280 RKERY-----PSQDEDLPRNEIDPRKRVDSPLNHRHGKRPER--KSMVLSV-TDG 331
DB 459 YKQHSISLSSSENKKSATESVNEPRIEYASKTANTNGLRSENNVDKTLHSLHSEID 518
QY 332 GSPVPARRAE-----MAHQGRSRS-----ISGASSG 359
DB 519 TSTVNQNAITGVNTEINAPVLAQKQSFINTLSQPSDKAEAVTLPPAIPFNASS 578
QY 360 -----LSTPSLSPRVTPHSPRGSPPLTPKPGTVHTPKESPAGTP 400
DB 579 RIFRNSYTSISRRSRRLSLNSRLSASTSRETVDHNEPLPQ-LPKSPRSYLSRRA 637
QY 401 NPTPPSPSGVGPWRARLNSIKNSFLGSPFRHRRKLQVPTPEMSNLTPESSPELAKS 460
DB 638 IHASPTKSIH-----KSLSRNIAATVAARTIQ-----NSAKRSLYLSQISKRS 685
QY 461 WFGNFI SLEKEEQIFVVIKDKPLSSIKADIHAFSLPSLSHVISQTSFRA----- 512
DB 686 -----LNLND-----LLVFDPLPSKPKPASENVNKSEP---HSLSDSDFEILCDQILFG 732
QY 513 -----EYKATGGPAVQKPKVQVDIITYTGEQAQKEN-----GIYSVTFT 553
DB 733 NALDRILEEEDNEKEDRTQROQNDTKSSADTTTISGVSTNKENEGPEYPTKIKNQFN 792
QY 554 LLSGSPRRFKV-----VETIOAQLSTHDPAAQHLSDTTCNMEMM 595
DB 793 MSYKPSNMNGLSGFPPEKEKNTLSSYLEEQKPRAA-LSDIITNSFNKM 841

RESULT 2

KI10 ARATH
ID KI10 ARATH STANDARD; PRT; 512 AA.
AC Q38997; O04728; Q39076;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE SNF1-related protein kinase KIN10 (EC 2.7.1.-) (AKIN10).
GN KIN10 OR SKIN10 OR AT3GG1090 OR T4P13.22.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurooids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=93013041; PubMed=1339373;
RA le Guen L., Thomas M., Bianchi M., Halford N.G., Kreis M.;
RT "Structure and expression of a gene from Arabidopsis thaliana
encoding a protein related to SNF1 protein kinase.";
RL Gene 120:249-254(1992).
RN (2)
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Lessard P., Kreis M., Thomas M.;
RN Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
RN (3)
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=21016720; PubMed=11130713;
RA Salanoubat M., Lemcke K., Rieger M., Ansoorge W., Unseld M.,
FArtmann B., Valle G., Bloeker H., Perez-Alonso M., Obermaier B.,
RDelaney M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,
De Simone V., Choisne N., Artiguenave F., Robert C., Brottier P.,
Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
R Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
Wurmback E., Drzonek H., Erfle H., Jordan N., Bangert S.,
R Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
R Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simonati B.,
R Conrad A., Hornischer K., Kauer G., Loehner T.-H., Nordsiek G.,
R Reichelt J., Schaefer M., Schoen O., Barges M., Terol J., Climent J.,
R Navarro J., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,
R Cooke R., Laudie M., Berger-Llauro C., Purnelle B., Masuy D.,
R de Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casasuberta E.,
R Monfort A., Agirion A., Flores M., Liguori R., Vitale D.,
R Mannhaupt G., Haase D., Schoof H., Rued S., Zaccaria P., Mewes H.-W.,
R Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
R Rooney T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S.,
R Pai G., Miltscher J., Sellers P., Gill J.E., Feldblyum T.V.,
R Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,
R Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
R Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,
R Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
R Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T.,
R Watanabe A., Yamada M., Yasuda M., Tabata S.;
RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis
thaliana.";
RL Nature 408:820-822(2000).
RN (4)
RP SEQUENCE OF 1-19 FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=95115691; PubMed=7816049;
RA le Guen L., Thomas M., Kreis M.;
RT "Gene density and organization in a small region of the Arabidopsis
thaliana genome.";
RL Mol. Genet. 245:390-396(1994).
CC -1- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN A SIGNAL TRANSDUCTION
CASCADE REGULATING GENE EXPRESSION AND CARBOHYDRATE METABOLISM IN
HIGHER PLANTS
CC -1- TISSUE SPECIFICITY: EXPRESSED IN ROOTS, SHOOTS AND LEAVES.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC SNF1 SUBFAMILY.
CC -1- SIMILARITY: Contains 1 UBA domain.
CC -----
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send an email to license@ebi.ac.uk).
CC -----
DR EMBL; M93023; AAA32736.1; --
DR EMBL; X79707; CAA56146.1; --


```
DR PROSITE; PS0108; PROTEIN KINASE ST; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
FT Domain 10 262 PROTEIN KINASE (BY SIMILARITY).
FT NP_BIND 16 24 ATP (BY SIMILARITY).
FT ACT_SITE 133 133 BY SIMILARITY.
FT BINDING 39 39 ATP (BY SIMILARITY).
SQ SEQUENCE 775 AA; 85971 MW; 2EE2EBCA8A4FAC CRC64;

Query Match 21.5%; Score 685.5; DB 1; Length 775;
Best Local Similarity 29.3%; Pred. No. 3e-28;
Matches 212; Conservative 99; Mismatches 210; Indels 203; Gaps 26;

Qy 2 KVEREIALKLEHPVHLKLDVVENKYYLVYLVHVSQGLFDFVYLVKKGRLTPKEARKF 61
Db 54 RIEGELVLLRIEHPNVQLIDVISAQQLFVVEYMPGGLFCMLKRGSTFQDTAKF 113

Qy 62 FQIISALDFCHSHSICHRDLKPNLLDEKXNIRIADFGMASIQVGDLSLETSCGSPHY 121
Db 114 LWQILGLECHKLHICHRDLKPNLYLDAGHSIKIGFGMASIQQPKLLQTSQCGSPHY 173

Qy 122 ACPEVIREKYGDKADVWSCGVILFALLVQALPDDNLRQLLEKVKRGVFNHPHIPP 181
Db 174 ASPEILMGSRSDGCSADISWCGIIFALLTGKLPDDNIRSLLLKVCQGFQFEMPSNISP 233

Qy 182 DCQSLRGMIEDVDAARLLTLEHIOKHWIYGGKNEP-----EPEQIPRKVQIRSLPSL 235
Db 234 QAQHLLYMLVDSDSTRITMQIREH-----PFLSCFVHNISIP-----IISAP-I 279

Qy 236 EDIDPDVLDMSHL-GCFDRNRKLLQDLLSEENQEKMIYFLLLDRKERYSPQDEDLPP 294
Db 280 QPIDPLIVQHLSLVPRCDDPMPLEYKLASQSLVEKLTLYLL-SRHLHP-----PS 330

Qy 295 RNEIDPPKRVDSPM--LNRHKRPRPKSEVLSVTGGSPVPARRAIEAQAQGRSRS 352
Db 331 SAAVDNRNAVVDLLGTAAASQQQWDEEIEQAINIPT-LAPYPTSYAAESVPRPATAS 389

Qy 353 -----ISGA--SSGLSTSLSSPRVTPHSPRGSPLP-TPKG-TP-VHTPKESPAGTP 400
Db 390 PFLTPTVTSGTFNYFSNATNQS---ILQRATTSSAVPQLPKSVTPCLAYPHDSMLSS 446

Qy 401 NPTPPSS-----PSV-----GGV 413
Db 447 NYRPPSALSPRNFNVSINDPEVQLSRRATSLDMSNDFRMNENDPSIVGNLAASNPTGMG 506

Qy 414 PWRARLNSIKNSFLG-----SPRFR-----434
Db 507 PRKRVTRMSHETGNRVVSPRGSFAFNRVTRFVNGNEQFSNNIDNNYQPYANATMN 566

Qy 435 --RKLQVTPTE-----EMSNLTPE-----SPELAKKSW 461
Db 567 NSRRLTSGERSMRADLSQSPASYDSLNVPKHRRRQSLFSPSSTKKLSGSPFPQKESF 626

Qy 462 -----FGNFISLEKEQIFVVKDKPLSSIK-ADIVHAFSLSPSLSHSVIS 506
Db 627 LRRFLSFPSCKCVVASLVSLEHLEILVRWQLLGIGADIYDVS-ASISARIKR 685

Qy 507 QTSFRAEYKATGPAVFOKPKVFOVDITVTEGEAQKNGIYSVTFTLLSGPSRRFKEVW 566
Db 686 QNSLNL-----KPVFRISVLAEFPGS-----QAVFVLESSTTFDHLA 725

Qy 567 ETIQ 570
Db 726 TEFG 729

RESULT 4
MRK4 HUMAN
ID MRK4 HUMAN STANDARD; PRT; 752 AA.
AC Q96L34; Q96JG7; Q9YB8;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
```

```
DE MAP/microtubule affinity-regulating kinase 4 (EC 2.7.1.27)
DE (MAP/microtubule affinity-regulating kinase like 1).
GN MARK4 OR MARKL1 OR KIAA1860.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Brain;
RA Drewes G., Mandelkow E.M.;
RT "MARK4, homologue of MARK1, MARK2 and MARK3.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Brain;
RA MEDLINE=21226021; PubMed=11326310;
RA Kato T., Satoh S., Okabe H., Kitahara O., Ono K., Kihara C.,
RA Tanaka T., Tsunoda T., Yamaoka Y., Nakamura Y., Furukawa Y.;
RT "Isolation of a novel human gene, MARKL1, homologous to MARK3 and its
RT involvement in hepatocellular carcinogenesis.";
RL Neoplasia 3:4-9(2001).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Brain;
RA Beghini A., Magnani I., Roversi G., Piepoli T., DiTerlizzi S.,
RA Pallo B., Conti A.M.F., Cowell J.K., Finocchiaro G., Larizza L.;
RT "Neural progenitor-restricted isoform of MARKL1 gene is upregulated by
RT 19q13 amplification in human glioblastoma.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Brain;
RA MEDLINE=21245130; PubMed=11347906;
RA Nagase T., Nakayama M., Nakajima D., Kikuno R., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XX.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro.";
RL DNA Res. 8:95-95(2001).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Thyroid;
RA Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,
RA Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoform=2;
CC Name=1;
CC IsoId=Q96L34-1; Sequence=Displayed;
CC Name=2; Synonyms=MARKL1S;
CC IsoId=Q96L34-2; Sequence=VSP_004946;
CC -!- TISSUE SPECIFICITY: Ubiquitous. Isoform 2 is brain-specific.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. MARK
CC SUBFAMILY.
CC -!- SIMILARITY: Contains 1 kinase-associated (KAI) domain.
CC -!- SIMILARITY: Contains 1 UBA domain.
CC
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CC
CC EMBL; AY057448; AAL23683.1; -.
CC EMBL; AB049127; BAB39380.1; -.
CC EMBL; AY120867; AAM55491.1; -.
CC
CC DR
CC DR
CC DR
```

DR EMBL; AK075272; BAC11510.1; --
 DR EMBL; AB058763; BAB47489.1; ALT_INIT.
 DR HSSP; O63450; 1A06.
 DR Genew; HGNC:13538; MARK4.
 DR MIM; 606495; --
 DR InterPro; IPR001772; Kinase_Cterm.
 DR InterPro; IPR000719; Prot_Kinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR InterPro; IPR00449; UBA_domain.
 DR Pfam; PF02149; KAI; 1.
 DR Pfam; PF00069; pkinase; 1.
 DR Pfam; PF00627; UBA; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_Kinase; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS00030; UBA; 1.
 DR Transferase; Serine/threonine-protein kinase; ATP-binding;
 KW Alternative splicing.
 FT DOMAIN 59 310 PROTEIN_KINASE.
 FT DOMAIN 324 368 UBA.
 FT DOMAIN 703 752 KAI.
 FT NP_BIND 65 73 ATP (BY SIMILARITY).
 FT BINDING 88 88 ATP (BY SIMILARITY).
 FT ACT_SITE 181 181 BY SIMILARITY.
 FT VARSPIC 628 752 ADEPERIGPEVTSCHLPDQDTAPRLRPFWSVKLTSSR
 PFEALMALRQNTAAARCRQPPQFLACLHGGAGPEPL
 SHFEVECOLPRGLRGVLFRRVAGTALAFRLTVTRISNDL
 EL -> TLDPKRONKRCVSGSLPQGSKIRSNLRESG
 DLRSQVATYLGIRKPPGCSDSGV (in isoform
 2).
 FTID=VSP 004946.
 FT CONFLICT 70 70 F -> S (IN REF. 2).
 FT SEQUENCE 752 AA; 82519 MW; 4B430FDD2B150E7A CRC64;
 Query Match 21.2%; Score 675.5; DB 1; Length 752;
 Best Local Similarity 29.3%; Pred. No. 9.5e-28;
 Matches 205; Conservative 94; Mismatches 223; Indels 177; Gaps 22;
 QY 2 KVERIAIKLIEHPVHLKHDVYENKYLVLVHVGSGELFDVLVKKGLRTPKEARKF 61
 DB KLFEVRIMKGLNHPNVLKFEVETKTLVLMVEYASAGEVDFVLVHGMRKEARAK 161
 QY 62 PQIISALDFCHSHICHRLDKPENLLDKNNIRIADFGMASLQVGSLLTSCGSPHY 121
 DB FQIIVSAVHYCHQKIVHRDLKAEALLDLDAENIKIADFGFSNEFTLGSKLDTFCGSPPY 221
 QY 122 ACEVIRGEKDYGRKADVMSCCVILFALLVGLPFDNDNLRLLEKVRGVFMHPHTPP 181
 DB AAPELFQKKYDGPEDVINSGLVILTVLSGLPFDGHNKLRERVLKGYRPFYMYST 281
 QY 182 DCQSLLRGMIEVDARRLTLEHIQKHW----YIGGKNP--EPQPIPRKVQIRSLPSL 235
 DB DCESTLRFLVLPNPKRKTLEQIMKDKMINIGYEGLKPYTEP----- 326
 QY 236 EDI-DPDVLDSMHSIGCFDRNKLQDLLSEENQKMIYFLLDLRKERYPSQEDDLP 294
 DB EDFGTGKRIEVMVGYYTRKIK--ESLTSQKYNVTATY--LLGRK-----TEEGD--- 376
 QY 295 RNEIDPPKRVDSPLNLRHG----KRRPERKSMELVSVT-----DGGSPVPARRA 340
 DB RGAPGLALARVAPSDTYTNGTSSSGKTSKSGQSSSTYHQRHSDFCGSPAPLHPK 436
 QY 341 IEMAHQGQ-----RSRISGASGLSTPSLSSRVTPHPSPRSPPLTPKGTVPVH 390
 DB RSPTSTGEALKEERLPGRKASCSTAGSGRLPFPSPVMSAHPNKAETIPERRKDS 496
 QY 391 TP-----KESPACTNPPTPPSPS-----VGG 412
 DB TPNNLPSPMMTRRTYVCTERPGAERPSLLPNKNGNSGTPR--VPPASPSHSLAPPSGE 555

RESULT 5

GIN4 YEAST
 ID GIN4 YEAST STANDARD; PRT; 1142 AA.
 AC Q12263;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Serine/threonine-protein kinase GIN4 (EC 2.7.1.1-).
 GN GIN4 OR YDR507C OR D9719.13.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99030835; PubMed=9813093;
 RA Longtine M.S., Fares H., Pringle J.R.;
 RT "Role of the yeast Gln4 protein kinase in septin assembly and the
 RL relationship between septin assembly and septin function."; J. Cell Biol. 143:719-736(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Dietrich F.S., Mulligan J., Allen E., Araujo R., Aviles E., Berno A.,
 RA Carpenter J., Chen E., Cherry J.M., Chung E., Duncan M.,
 RA Hunnicke-Smith S., Hyman R., Komp C., Lashkari D., Lew H., Lin D.,
 RA Mosedale D., Nakahara K., Namath A., Osfner P., Oh C., Petel F.X.,
 RA Roberts D., Schramm S., Schroeder M., Shogren T., Shroff N.,
 RA Winant A., Yelton M., Botstein D., Davis R.W.;
 RA Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: MAY PLAY A ROLE IN SEPTIN ASSEMBLY.
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC NIM1 SUBFAMILY.
 CC
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 CC
 CC EMBL; U33140; AAA75513.1; --
 CC EMBL; U33057; AAB64949.1; --
 DR PIR; S59359; S59359.
 DR HSSP; O63450; 1A06.
 DR SGD; S0002915; GIN4.
 DR GO; GO:0005935; C:bud neck; IDA.
 DR GO; GO:0007117; P:bud growth; IGI.
 DR GO; GO:0000094; P:septin assembly and septum formation; IGI.
 DR GO; GO:0001135; P:septin checkpoint; IGI.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00069; pkinase; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.

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DR SMART; SMO0220; S TKC; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding.
FT DOMAIN 19 289 PROTEIN KINASE.
FT NP BIND 25 33 ATP (BY SIMILARITY).
FT BINDING 48 48 ATP (BY SIMILARITY).
FT ACT SITE 156 156 BY SIMILARITY.
SQ SEQUENCE 1142 AA; 129857 MW; EC16PF4B849DD811 CRC64;

Query Match 21.0%; Score 668.5; DB 1; Length 1142;
Best Local Similarity 34.1%; Pred. No. 3.5e-27;
Matches 183; Conservative 73; Mismatches 162; Indels 119; Gaps 16;

QY 3 VEREIAIKLIEHPVHLKLDHVDYENKYLVLVLEHVS GGELFDYLVKKGRLTPKEARKFP 62
DB 78 IEREIIIMKLNHPNVLRLVDVWETNTDYLVLVEYAEKGFNLLVERGLPHEAIRFP 137
QY 63 RQIISALDFCHSHSICHRLDKPENLLDEKNNIRIADFGMASLQVGSLLLETSCGSPHYA 122
DB 138 RQIIGVSYCHALGIVHRDLKPENLLDHKNYKIADFGMAALETGKLLTSCGSPHYA 197
QY 123 CPVIRGEKDGKADVWSCGVILFALLVGLALPPD--DDNLRLEKVKRGVFMPP--HF 178
DB 198 APEIVSGIPYQGFASDVWSCGVILFALLTGRLPDEEDGNIRTLKLVQKGEPEMPSDDE 257
QY 179 IPPDCQLLGMIEVDAAERLTLEHIOKHTWYIGKNKEPEQPIPKV-----QIRS 231
DB 258 ISREAQLIRKILVDPERIKTRDIUKH-----PLIQKPSIRDSKSIRG 303
QY 232 LP-----SLEIDIPDVLDSMSLSCGFRDNKLLQDLSEENQEKMIYFLLDR 280
DB 304 LPREDTYLPLSESSSIDATILQNVLVHGRDPEGIKELREPANAETKLYALLY-- 361
QY 281 KERYPSQDEEDLPPRNEIDPPKRVDSFMLNRHGRKRPKRSMEVLSTVDTGGSPVPARRA 340
DB 362 --RPFKCDTQELIKQQQV-----KKRQSISVSVS-----PSKV 394
QY 341 IEMAHQGRSISGASGLSTSLSPRVTPHPSPRGSPPLTPKGTVPVHTPKESPAGTP 400
DB 395 STTPQRRNRRESLISVTS-----RKPFISFNKFT-----ASSASS 431
QY 401 NPTPPSPSVGGVPPWRLNLSIKNSFLGSPRFRHKLQVTPPEMSNLTPESSPELAKS 460
DB 432 NLTPGSSK-----RL-----SKNFSSK-----KLSTIVNQSSFTPASRN 467
QY 461 WFGNFISLEKEQ---IFVVIKQPLSSIKADIVHAFSLSPSLSHSVISQTSFRAEY 514
DB 468 KRASVINVEKQKRASIFSTTKQKRSRS---IKRMSLIPSMKRESVT-TKLMSY 520

RESULT 6
SNFL_SCHPO STANDARD; PRT; 576 AA.
AC O74536;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE SNF1-like protein kinase (EC 2.7.1.1-).
GN SPC74.03C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RC MEDLINE=21848401; PubMed=118593360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
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RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitz E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Welljens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Leirach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forburg S.L.,
RA Cerretti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RL "The genome sequence of Schizosaccharomyces pombe.";
Nature 415:871-880(2002).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC -!- SUBFAMILY.
CC -!- SIMILARITY: Contains 1 UBA domain.
CC -----
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CC -----
DR EMBL; AL031543; CAA20833.1; -.
DR F1R; T41587; T41587.
DR HSSP; Q63450; 1A06.
DR GeneDB SPombe; SPC74.03C; -.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002230; Ser_thr_kinase.
DR InterPro; IPR000449; UBA_domain.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SMO0220; S TKC; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
DR PROSITE; PS00030; UBA; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding.
FT DOMAIN 34 285 PROTEIN KINASE.
FT NP BIND 304 345 UBA.
FT BINDING 63 63 ATP (BY SIMILARITY).
FT ACT SITE 156 156 BY SIMILARITY.
SQ SEQUENCE 576 AA; 65996 MW; E5857E8F171E7B50 CRC64;

Query Match 20.8%; Score 662.5; DB 1; Length 576;
Best Local Similarity 37.3%; Pred. No. 3.2e-27;
Matches 146; Conservative 76; Mismatches 114; Indels 55; Gaps 10;

QY 1 MKVEREIAIKLIEHPVHLKLDHVDYENKYLVLVLEHVS GGELFDYLVKKGRLTPKEARK 60
DB 77 MRVEREISVLKLRHPIIKLYDVITPTDVIWVIEY-AGGELFDYIVKRGKRWTEDEGR 135
QY 61 FFRQIISALDFCHSHSICHRLDKPENLLDEKNNIRIADFGMASLQVGSLLLETSCGSPH 120
DB 136 FFOQIICAIEYCHRRKLVHRDLKPENLLDHKNYKIADFGNLSNIMTMDGNFLKTCGSPN 195
QY 121 YACPEVIRGEKDGKADVWSCGVILFALLVGLALPPDNDNLRLEKVKRGVFMHPHFIP 180
DB 196 YAAPEVINGKLYAGPEVDVWSCGVILVLMVGLPFDDEDFIPNLFKYNVCVYVMPDFLS 255
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QY 181 PDCQSLRGMIEVDAAARLTLEHIOKHIIWYIGCKNEPEQPIPRKVOIRSLPSLEDIDP 240
 Db 256 PQAQSLIRMIIVADPMQRIIOEIRDPWF--NVNLPDYLRP-----MEEVQG 301
 QY 241 DVLDSM-----HSLGCFRDRNKLQDLISEBENCCKMYIFLLDRKERYPSQDEDLPP 294
 Db 302 SVADSRIVSKLGEANGFSED--YIVAEALSDENNEVKEAYNLL---HENQVIOEKSHL-- 354
 QY 295 RNEIDPPKRVDS-----PMLNRHGKRRPERKSMIEVLSVTDG-----SPVPARRAI 341
 Db 355 -----SKKRVDSFLSVSPAPSEYTSSELOKSKQELIDPTLEGPRWTVPDPPTVAKQTI 409
 QY 342 E-----MAHQGQRSISGASGLSTS 363
 Db 410 DSNICVLPTAEKNKLEMKRTLAASAVIDTS 440

RESULT 7

ID_MRK2 MOUSE STANDARD; PRT; 774 AA.
 AC Q05512;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE MAP/microtubule affinity-regulating kinase 2 (EC 2.7.1.27)
 DE (Serine/threonine-protein Kinase Emk).
 GN MARK2 OR EMK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Embryo;
 RC MEDLINE=93364122; PubMed=8358177;
 RA Inglis J.D., Lee M., Hill R.E.;
 RT "Emk, a protein kinase with homologs in yeast maps to mouse
 chromosome 19.";
 RL Mamm. Genome 4:401-403 (1993).
 CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC MARK SUBFAMILY.

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 or send an email to license@isb-sib.ch).

CC EMBL; X70764; CAA50040.1; --
 DR PIR; I48609; I48609.
 DR HSP; O63450; 1A06.
 DR MGD; MGI:99638; Mark2.
 DR InterPro; IPR001772; Kinase_Cterm.
 DR InterPro; IPR000719; Prot_Kinase.
 DR InterPro; IPR002290; Ser_Thr_kinase.
 DR InterPro; IPR001245; Tyr_kinase.
 DR Pfam; PF02149; KAI; 1.
 DR Pfam; PF00069; pkinase; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00220; S_TK; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR Transfrase; Serine/threonine-protein kinase; ATP-binding.
 KW DOMAIN 53 304 PROTEIN_KINASE.
 FT NP_BIND 59 67 ATP (BY SIMILARITY).
 FT BINDING 82 82 ATP (BY SIMILARITY).
 FT ACT_SITE 175 175 BY SIMILARITY.
 SQ SEQUENCE 774 AA; 85874 MW; 02BF8D7BF443483A CRC64;

Query Match 20.7%; Score 661.5; DB 1; Length 774;
 Best Local Similarity 27.2%; Pred. No. 5.1e-27;
 Matches 195; Conservative 111; Mismatches 227; Indels 183; Gaps 19;

QY 2 KVEREIALKLIHPIVHLKLDHYVYENKYLVLVLEHVYGGGELFDYLVKKGLTKEARKP 61
 Db 96 KLFREVRIMKVLNPNIVKLFVETETKTLVMEYASGGVEFDYLVAHGMRKKEARAK 155
 QY 62 FROIISALDFCHSHSICHRLKPNLLLDKNNIRIADFGMASLQVGSLELETSCGSPHY 121
 Db 156 FROIVLHVQIHOXKFIHVHDLKAENLLLDADNMKIADFGSNEFTFGNKLDTFCGSPY 215
 QY 122 ACPEVIRGEKYDKKADVMSCGVILFALLVGLPDDNLRQLLEKVKRGVFMHPTTP 181
 Db 216 AAPLFOGKKIDGPEVDVMSGLVLYTLVSGSLPFDGQNLKELRERVLRGKYRPFYFYST 275
 QY 182 DCQSLRGMIEVDAAARLTLEHIOKHIIWYIGCKNEPEQPIPRKVOIRSLPSLEDIDP 241
 Db 276 DCENLLKKFLILNPSKRGTLLEQIMKDRMNVGHDEDLKPYVE-----PLTTGPRD 327
 QY 242 VLSMHSLGCFRDRNKLQDLISEBENCCKMYIFLLDRKERYPSQDEDLPPRNEID-- 299
 Db 328 RVDGVNGL-----HTEIQDSLVCQRYNEVMATYLLGLYKSSSEPGDTITLKPRPSADLT 382
 QY 300 -----PPRKRVDS-----PMLNRHGK-----RRPERK----- 321
 Db 383 NSSAPSPSHKQVRSVSNPKQRSSDQAVPAIPTSNSYSKKTQSNNAENKPEBETGRKA 442
 QY 322 -----SMEVLVTDG---GSPVPARRAEMA---OHQQRSS 352
 Db 443 SSTAKVPASPLFGLDRKKTTPAPSTNSVLSTNRSNSPLLDRAISLGQASIQNGKOSLT 502
 QY 353 ISG--ASSGLSTSPSLSPRVTPH-----PSPRGSLPTPKGTVPVHTPK 393
 Db 503 MGSRASTASASAASAAARPRHQKMSASVHPNKAQSLPTESNCEVPRSTAPQRPV 562
 QY 394 ESP-----AGTPNPT-----PPSSPSVGGVPM 415
 Db 563 ASPSAHNISSSSGAPDRTNFPRGVSSRSTFHAGQLQRVDRQDQNLPGVTPASPSSGHSQR 622
 QY 416 RARLNSIKNSFLGSPFRHRRKLOVP--TPEEMSLTP-----ESSPELAK 458
 Db 623 RGASGSIFSKP--TSKVRRLNLEPESKRVETURPHVVGSGGTDKKEEFREAKPSLR 680
 QY 459 KSW--FGNFISLEKEEQIFVVIKDKPLSSIKADIHAFILSPISLSHSVISQTSFRAEYKAT 517
 Db 681 FTWSMKTSSNEPMEMREIRKVLDSNCSQSELHERYMLL--CVHGTTPGHENF----- 731
 QY 518 GGPAVQKPKVQVDITYTTEGGEAKENGIVSVTFTLLSGSPRRPKRVETVETIQAL 573
 Db 732 -----VQWEMEV-----KLPRLSLNGVRFKRISGTSMAFKNIASKIANEL 772

RESULT 8

ID_KCC4_YEAST STANDARD; PRT; 915 AA.
 AC P25389; P87005;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Probable serine/threonine-protein kinase YCL24W (EC 2.7.1.1-).
 GN YCL024W OR YCL24W.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE OF 1-569 FROM N.A.
 RA Duesterhoeft A., Hegemann J., Philippsen P.,
 RA Schweitzer B., Spiegelberg R.;
 RL Submitted (MAR-1992) to the EMBL/GenBank/DBJ databases.
 RN [2]

RP SEQUENCE OF 567-915 FROM N.A.
 RA Oliver S.G., Anwar R., Brown A., Gent M.E., Indge K.J., James C.M.,
 RA Staveva L.I.,
 RL Submitted (MAR-1992) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP REVISIONS.
 RA Gromadka R.;
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC NIM1 SUBFAMILY.

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CC EMBL; X59720; CAA42361.1; -.
 DR PIR; S74283; S74283.
 DR HSSP; O63450; 1A06.
 DR SGD; S0000529; YCL024W.
 DR GO; GO:0005935; C:bud neck; IDA.
 DR GO; GO:0003700; F:transcription factor activity; IDA.
 DR GO; GO:0007117; P:bud growth; IGI.
 DR GO; GO:0000094; P:septin assembly and septum formation; IGI.
 DR GO; GO:0000135; P:septin checkpoint; IGI.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002230; Ser_thr_kinase.
 DR InterPro; IPR001245; Tyr_kinase.
 DR Pfam; PF00069; pkinase; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00220; S_TKC_1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 KW Hypothetical protein; Transferase; Serine/threonine-protein kinase;
 KW ATP-binding.
 FT DOMAIN 21 285 PROTEIN KINASE.
 FT NP_BIND 27 35 ATP (BY SIMILARITY).
 FT BINDING 50 50 ATP (BY SIMILARITY).
 FT ACT_SITE 152 152 BY SIMILARITY.
 SQ SEQUENCE 915 AA; 102688 MW; BFB01C8CA43AC181 CRC64;

Query Match 20.5%; Score 655; DB 1; Length 915;
 Best Local Similarity 34.2%; Pred. NO. 1.3e-26;
 Matches 177; Conservative 73; Mismatches 177; Indels 90; Gaps 13;
 3 VEREIAIKLIEHPHVLKLDHYENKKYLYLVLEHVGGEFDYLVKKGRLPPEARKFF 62
 74 IEREIVIMKLLHPNVLSDYVWETNNLYLILEVAEKGEFLNLLVDHGPPEARINCF 133
 63 ROIISALDFCHSHSCHRDLKPEKLLDKNNIRIADFQMSALQVDSLETSCSPHYA 122
 134 ROIITGISYCHALGIVHRLKPEKLLDFFYNIKIADFQMAALQTDADLETSCSPHYA 193
 123 CPEVIRGEYDGRKADWCSGVLPFALLVGPFDGDD--NLRLLEKVKRGVFMH--F 178
 194 AFEIVSGLYPEFASDVWCSGVLPFALLVGRPFDEENGVDLLKVGQGFENPDTE 253
 179 IPPDCQSLRGMIEVDAARRLTLEHTQKHIWIGGKNEPEPEQPIPRKVQ--IRSLPSLED 237
 254 ISRDAQDLGKILVDPQRKIRKIDLSH-----PLLKVKYQTIKDSKIKD 299
 238 -----IDPDVLDMSHSLGCFRDNKLLQDLLESEENQKMIPL 276
 300 LPRENTYLPADSNHNTGASIDDSILQNLVLMHGRHADDIVSKLKENGNTKEXILYAL 359
 277 LLDRKERYPSQEDDLPPNEIDPPRKRYDPSMLNRHGRKRRPERKSMVELSVTDGSGPVP 336
 360 LY--RFKLDVSGSNKKNRNKIKTKTKNKRSTLSSSSILLNKRISQ-----STP 408

QY 337 ARRAIEAQAHQGRSRISGASGLSTSPVTPHPSP-RGSPLPKGTVPVHTPKES 395
 DB 409 RRTSK-----RHSRSEFS-SSRRKSSFLSSNTDSSPIPLRSKRITHINVASANTQAT 462
 QY 396 PAGTPNPTPPSPSVGVGVPWRARLNSIKNSIFLGSPPHRRKLVQVTPPEMSNNTPESSPE 455
 DB 463 PSQVPPN-----HKNSKKRSKRSLSYMPNTPKRSS 492
 QY 456 LAKSNFGNFISEKEEQIFWIKD-KPLSSIKADIV 491
 DB 493 LTSKS-LSNFTNLIDDDDDWEYIEKDAKRTSSNFATLI 528

RESULT 9

ID SNIL_HUMAN STANDARD; PRT; 786 AA.
 AC PS7059;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Probable serine/threonine protein kinase SNF1LK (EC 2.7.1.-).
 DE SNF1LK.
 GN Homo sapiens (Human).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20289795; PubMed=10830953;
 RA Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
 RA Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Groner Y.,
 RA Soeda E., Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K.,
 RA Polley A., Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
 RA Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W.,
 RA Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,
 RA Shantani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,
 RA Minoshima S., Shimizu N., Nordstiek G., Hornischer K., Brandt P.,
 RA Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloeker H.,
 RA Ramser J., Beck A., Klages S., Hennig S., Rieselmann L., Dagand E.,
 RA Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
 RA Lehrach H., Reinhardt R., Yaspo M.-L.; -.
 RT "The DNA sequence of human chromosome 21."
 RL Nature 405:311-319(2000).
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC SNF1 SUBFAMILY.
 CC -!- SIMILARITY: Contains 1 UBA domain.
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 CC or send an email to license@isb-sib.ch).

EMBL; AP001751; BAA95536.1; -.
 HSSP; P24941; 1A01.
 DR Genew; HGNC:11142; SNF1LK.
 DR MIM; 605705; -.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR InterPro; IPR001245; Tyr_kinase.
 DR InterPro; IPR000449; UBA domain.
 DR Pfam; PF00069; pkinase; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00220; S_TKC_1.
 DR SMART; SM00165; UBA; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS00030; UBA; 1.

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KW Transferase; Serine/threonine-protein kinase; ATP-binding.
FT DOMAIN 27 281
FT NP BIND 306 346
FT BINDING 33 41
FT ACT SITE 149 149
SQ SEQUENCE 786 AA; 85252 MW; FB44EE7CAF87CB1A CRC64;

Query Match
Best Local Similarity 20.2%; Score 645; DB 1; Length 786;
Matches 203; Conservative 84; Mismatches 238; Indels 134; Gaps 24;

QY 2 KVEREIALKLIETHPVHLKLDVYENKYLVLVLEHVSQGGELFDYLVKKGRLTPKEARKF 61
DB 70 KIYREVQLMKNLHNPHIILKQVMEKMDLYIVTEFAKNGEMFDYLTNGHLSNEARKK 129
QY 62 FQIITISALDFCHSHSICHRLDKPENLLDEKKNIRIADFGMASLQVDSLETSCGSPHY 121
DB 130 FWOILSAVEYCHNEHIVHRLDKNLLENLDGNDIKLADFGFNGFYKPGELSTWCGSPY 189
QY 122 ACPEVIRGEKVDGRKADVWVSCGVILFALLVGLALPDDNLLRQLLEKVKRGVFMHPHTPP 181
DB 190 AAPEVFEKGEYEGPOLDIWSLGVILVLCVCSLPFDGPNLPTLRQVRLEGRFRIFFMSQ 249
QY 182 DCQSLLRGMIEVDAAARLTLLEHIOKHIWYIGGKNEPEP---EQIPRQVIRSLPSLEDI 238
DB 250 DCEITLREMLVVDPAKRTITIAIRQHRW---QADPTLLQDDDPAFSMQGYTSNLGDY 304
QY 239 DPVDLDSMHSIGCFDRDNKLLQDLLESEENKMIYFILLDR---KERYPSQDEDELP 294
DB 305 NEQVLGIMQALGI--DRQRTVESLQNSYNHFAIYLLERLREHRSRTPSPSRATPAPA 362
QY 295 R-----NEI---DPRKEVDSPM-----LNRRKGRP----- 318
SEQUENCE FROM N.A.

STRAIN=Sprague-Dawley; TISSUE=Adrenal gland;
MEDLINE=9930184; PubMed=1040390;
Wang Z., Takemori H., Halder S.K., Nonaka Y., Okamoto M.;
"Cloning of a novel kinase (SIK) of the SNF1/AMPK family from high
salt diet-treated rat adrenal.";
FEBS Lett. 453:135-139 (1999).
[2]
SEQUENCE FROM N.A.
RA Feldman J.D., Vician L., Crispino M., Hoe W., Baudry M.,
Herschman H.R.;
"The Kid2 gene encodes a protein kinase induced by depolarization in
brain.";
Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
SNF1 SUBFAMILY.
-1- SIMILARITY: Contains 1 UBA domain.
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
EMBL; AB020480; BAAB2673.1; -
EMBL; AF106937; AAF14191.1; -
HSSP; P24941; 1A01.
InterPro; IPR000719; Prot_kinase.
InterPro; IPR0002290; Ser_Thr_kinase.
InterPro; IPR000449; UBA_domain.
Pfam; PF00069; pkinase; 1.
ProDom; PD000001; Prot_kinase; 1.
SMART; SM00220; S_TKc; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS00030; UBA; 1.
Transferrase; Serine/threonine-protein kinase; ATP-binding.
KW TRANSFERASE; Serine/threonine-protein kinase; ATP-binding.
FT DOMAIN 27 278
FT NP BIND 303 343
FT BINDING 33 41
FT ACT SITE 149 149
FT CONFLICT 473 473
SQ SEQUENCE 776 AA; 84908 MW; 7BF745AF28F17E6E CRC64;

Query Match
Best Local Similarity 20.0%; Score 638; DB 1; Length 776;
Matches 187; Conservative 79; Mismatches 200; Indels 156; Gaps 20;

QY 2 KVEREIALKLIETHPVHLKLDVYENKYLVLVLEHVSQGGELFDYLVKKGRLTPKEARKF 61
DB 70 KIYREVQLMKNLHNPHIILKQVMEKMDLYIVTEFAKNGEMFDYLTNGHLSNEARKK 129
QY 62 FQIITISALDFCHSHSICHRLDKPENLLDEKKNIRIADFGMASLQVDSLETSCGSPHY 121
DB 130 FWOILSAVEYCHNEHIVHRLDKNLLENLDGNDIKLADFGFNGFYKPGELSTWCGSPY 189
QY 122 ACPEVIRGEKVDGRKADVWVSCGVILFALLVGLALPDDNLLRQLLEKVKRGVFMHPHTPP 181
DB 190 AAPEVFEKGEYEGPOLDIWSLGVILVLCVCSLPFDGPNLPTLRQVRLEGRFRIFFMSQ 249
QY 182 DCQSLLRGMIEVDAAARLTLLEHIOKHIWYIGGKNEPEP---EQIPRQVIRSLPSLEDI 238
DB 250 DCEITLREMLVVDPAKRTITIAIRQHRW---QADPTLLQDDDPAFSMQGYTSNLGDY 304
QY 239 DPVDLDSMHSIGCFDRDNKLLQDLLESEENKMIYFILLDR---KERYPSQDEDELP 294
DB 305 NEQVLGIMQALGI--DRQRTVESLQNSYNHFAIYLLERLREHRSRTPSPSRATPAPA 362
QY 295 R-----NEI---DPRKEVDSPM-----LNRRKGRP----- 318
SEQUENCE FROM N.A.
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Db 363 RQPOLRNDLSLEVPQELPDCPFRPSLLCPQALQAQSLQAEICDLHSLQLPFFP 422
Qy 319 -----ERKSEVLVSVTGGSPVPARRAIEAHOGRSRISGASSGLST----- 362
Db 423 LDTNCSGVFRHRSISPSLLDTAISEARQPSLEEEQVEPFGTGRHTLAEVSTH 482
Qy 363 -SPSSSRVTPHPGPRGSPPLTPKGT-----VHTPKESPAG-----TPNPTPPSPSV 410
Db 483 FSLNPPCCIIVSSAAVSP-----SEGTSSDSCLPFSASEGPAGLGGGLATPGLTGTSSP-- 537
Qy 411 GGVPWRRLNLSIKNSFLGSPFRHKLQVPPPEMSN-----LTPESSE----- 455
Db 538 -----VRLAS-----PFLGS-----QSATPVIQSQAAGLGTALPPVSPFOGRRASDTS 580
Qy 456 -----LAKSWFGNFISLEKEQIFWIKDKPLSLIKADIVHAFILSIPSLSHSV 504
Db 581 LTQGLKAFRQQLKRNARKYKGLNKK-----INGLARQV 614
Qy 505 ISQTSFRAEYKATGPAVFQKP 526
Db 615 -QSSSIRG---SRGGMSTFHTP 632

RESULT 11
MRK3_HUMAN
ID MRK3_HUMAN STANDARD; PRT; 776 AA.
AC P27448; O60219; Q8TB41; Q8WX83; Q96RG1; Q9UMY9; Q9UN34;
DT 01-AUG-1992 (Rel. 23, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE MAP/microtubule affinity-regulating kinase 3 (EC 2.7.1.27) (Cdc25C-associated protein kinase 1) (CTAK1) (C-TAK1) (Serine/threonine protein kinase p78) (Ser/Thr protein kinase PAR-1) (Protein kinase STK10).
DE MARK3 OR CTAK1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RX MEDLINE=98202387; PubMed=9543386;
RA Peng C.Y., Graves P.R., Ogg S., Thoma R.S., Byrnes M.J. III, Wu Z., Stephenson M.T., Pivnick-Worms H.;
RT "C-TAK1 protein kinase phosphorylates human Cdc25C on serine 216 and promotes 14-3-3 protein binding."
RL Cell Growth Differ. 9:197-208(1998).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RA Waggoner S.N., Stephen R., Farrar W.L., Howard O.M.Z.;
RT "Human serine/threonine protein kinase cTAK1/Kp78/Mark3: Identification of a novel splice variant and a larger 5'UTR."
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 4).
RX MEDLINE=21326471; PubMed=11433294;
RA Sun T.O., Lu B., Feng J.J., Reinhard C., Jan Y.N., Fantl W.J., Williams L.T.;
RT "PAR-1 is a Dishevelled-associated kinase and a positive regulator of Wnt signalling."
RL Nat. Cell Biol. 3:628-636(2001).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 5).
RA Drewes G.;
RT "Characterization of an alternatively spliced form of MARK3 from human brain."
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 6).
RA Maheshwari K.K., Som S., Parsa I.;
RL Submitted (JAN-1992) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM 3).

TISSUE=Cervix;
RC MEDLINE=22388257; PubMed=12477932;
RX Srausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shennen C.M., Schuler G.D., Altschul S.F., Jordan B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Zordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Spatlenko M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J., Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahy J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [7]
RP SEQUENCE OF 323-775 FROM N.A. (ISOFORM 7).
RC TISSUE=Urinary bladder;
RA Reynolds C.H., Patel U.A., Anderton B.H.;
RT "Homo sapiens mRNA partial sequence for a protein kinase, STK10, similar to p78/C-TAK1."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Involved in the specific phosphorylation of microtubule-associated proteins for tau, MAP2 and MAP4. Phosphorylated Cdc25C on Ser-216.
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=7;
CC Names=1;
CC IsoId=P27448-1; Sequence=Displayed;
CC Names=2; Synonyms=CTAK75a;
CC IsoId=P27448-2; Sequence=VSP_004944;
CC Names=3;
CC IsoId=P27448-3; Sequence=VSP_004942, VSP_004944;
CC Names=4;
CC IsoId=P27448-4; Sequence=VSP_004942, VSP_004945;
CC Names=5;
CC IsoId=P27448-5; Sequence=VSP_004942;
CC Names=6; Synonyms=p58;
CC IsoId=P27448-6; Sequence=VSP_004942, VSP_004943, VSP_004944;
CC Names=7;
CC IsoId=P27448-7; Sequence=VSP_004943;
CC -1- TISSUE SPECIFICITY: Ubiquitous.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. MARK SUBFAMILY.
CC -1- SIMILARITY: Contains 1 kinase-associated (KAI) domain.
CC -1- SIMILARITY: Contains 1 UBA domain.
CC -----
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CC -----
CC EMBL; U64205; AAC15093.1; -;
DR EMBL; AF159295; AAD48007.1; -;
DR EMBL; AF387637; AAK82367.1; -;
DR EMBL; AF465413; AAL69982.1; -;
DR EMBL; M80359; AAA59991.1; -;
DR EMBL; BC024773; AAD24773.1; -;
DR EMBL; AF170723; AAD51631.1; -;
DR HSP; Q63450; IAO6.
DR Genew; HGNC:6897; MARK3.
DR MIM; 602678; -;

CC isoid=009137-2; Sequence=VSP 004949, VSP 004950;
CC Note=Lacks the sequence parts essential for kinase activity and
CC is therefore inactive;
CC -1- TISSUE SPECIFICITY: SKELETAL MUSCLE, LOWER LEVELS IN LIVER, HEART,
CC AND KIDNEY.
CC -1- INDUCTION: BY AMP.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. SNF1
CC SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z29486; CAA82620.1; -;
DR EMBL; U12149; AAB85033.1; -;
DR PIR; A53621; A53621.
DR HSSP; Q63450; 1A06.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR Transfaser; Serine/threonine-protein kinase; Fatty acid biosynthesis;
KW Phosphorylation; ATP-binding; Multigene family; Alternative splicing.
FT DOMAIN 16 268 PROTEIN KINASE.
FT NP_BIND 22 30 ATP (BY SIMILARITY).
FT BINDING 45 45 ATP (BY SIMILARITY).
FT ACT_SITE 139 139 BY SIMILARITY.
FT MOD_RES 172 172 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT VARSPLOC 32 388 Missing (in isoform Short).
FT VARSPLOC 392 552 /FTId=VSP 004949.
FT VARSPLOC 392 552 Missing (in isoform Short).
FT CONFLICT 355 355 /FTId=VSP 004950.
FT CONFLICT 462 462 M -> S (IN REF. 2).
SQ SEQUENCE 552 AA; 62257 MW; 2829E07F674D89B1 CRC64;

Query Match 19.9%; Score 636; DB 1; Length 552;
Best Local Similarity 28.4%; Pred. No. 7e-26;
Matches 174; Conservative 95; Mismatches 202; Indels 142; Gaps 21;

QY 2 KVEREIALKLEHPHVLKLDVYENKYLVLVLEHVGSGELFDYLVKGRITPKARKF 61
Db 60 KIKREIQNLKLFRRHHIILKLVQVISTPTDFFWMEYVSGELFDYKCHGRVEVEARRL 119
QY 62 FQIILALDFCHSHSICHRLDKPENLLDEKKNIRIADFGWASLQVGSLETSCGSPHY 121
Db 120 FQIILSAVDYCHRHVVRDLKPNVLLDAQWNAKIADFGLSNMMSDGEFLRTSCGSPNY 179
QY 122 ACPEVIRGEKDGKADYVSCGVILFALLVGLALPDNDNLRLLEKVKRGVFMHPHFIPP 181
Db 180 APEVIRGLVAGPBDVILWSCGVILVLLCGLFPDDEHVPFLFKIRGVFIPIELNLR 239
QY 182 DCQSLRGMIEYDAARRLTLEHIOKHIWYIGGKNEPEPEQIPRKVQIRLSFLSDIDPD 241
Db 240 STATLLMHLQVDPKRAIKIDIREHEWF-----KQDLPSYL-----FPEDPSYDAN 286
QY 242 VLDS-----MHSICCFDRNKLQDLIS-EEENQEKMIYFLLLDRKERYSQDE----- 290
Db 287 VIDDEAVKEVCKFCFC--TESEWNLSYSGDPQDQLAVAYHLIIDNR-RIMNQASEFYLA 343
QY 291 DLPPRNEIDPPKRVDSFPMNRHGRKRRKSMVLSVTDGSGPVPARRATEMAHQGQRS 350
Db 344 SSPPTG-----SFWD-----DMAMH----- 358

RESULT 13

AAK2 HUMAN STANDARD; PRT; 552 AA.
ID AAK2 HUMAN
AC P54646; Q9HLE8; Q9UD43;
DT 01-OCT-1996 (Rel. 34, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 5'-AMP-activated protein kinase, catalytic alpha-2 chain (EC 2.7.1.1-)
DE (AMPK alpha-2 chain).
GN PRKAA2 OR AMPK2 OR AMPK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=95047501; Pubmed=7959015;
RA Aguan K., Scott J., See C.G., Sarkar N.H.;
RT "Characterization and chromosomal localization of the human homologue
RT of a rat AMP-activated protein kinase-encoding gene: a major
RT regulator of lipid metabolism in mammals.";
RL Gene 149:345-350(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=95080410; Pubmed=7988703;
RA Beri R.K., Marley A.E., See C.G., Sopwith W.F., Aguan K., Carling D.,
RA Scott J., Carey F.;
RT "Molecular cloning, expression and chromosomal localisation of human
RT AMP-activated protein kinase.";
RL FEBS Lett. 356:117-121(1994).
RN [3]
RP SEQUENCE OF 33-552 FROM N.A.
RA Cobley V.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: RESPONSIBLE FOR THE REGULATION OF FATTY ACID SYNTHESIS
CC BY PHOSPHORYLATION OF ACETYL-COA CARBOXYLASE. IT ALSO REGULATES
CC CHOLESTEROL SYNTHESIS VIA PHOSPHORYLATION AND INACTIVATION OF
CC HORMONE-SENSITIVE LIPASE AND HYDROXYMETHYLGLOUTARYL-COA REDUCTASE.
CC APPEARS TO ACT AS A METABOLIC STRESS-SENSING PROTEIN KINASE
CC SWITCHING OFF BIOSYNTHETIC PATHWAYS WHEN CELLULAR ATP LEVELS ARE
CC DEPLETED AND WHEN 5'-AMP RISES IN RESPONSE TO FUEL LIMITATION
CC AND/OR HYPOXIA. THIS IS A CATALYTIC SUBUNIT.
CC -1- SUBUNIT: HETEROTRIMER OF A CATALYTIC SUBUNIT, A BETA AND A GAMMA
CC NON-CATALYTIC SUBUNIT.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC SNF1 SUBFAMILY.
CC -----
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CC -----
DR EMBL; U06454; AAA64745.1; -.
DR EMBL; AL035705; CAC17574.1; -.
DR PIR; S51025; S51025.
DR HSP; Q63450; IA06.
DR Genew; HGNC:9377; PRKAA2.
DR MIM; 600497; -.
DR GO; GO:0006468; P:protein amino acid phosphorylation; TAS.
DR GO; GO:0007165; P:sigal transduction; TAS.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TK; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR Transferrase; Serine/threonine-protein kinase; Fatty acid biosynthesis;
KW Phosphorylation; ATP-binding; Multigene family.
FT DOMAIN 16 268
FT NP_BIND 22 30 ATP (BY SIMILARITY).
FT BINDING 45 45 ATP (BY SIMILARITY).
FT ACT_SITE 139 139 BY SIMILARITY.
FT MOD_RES 172 172 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT CONFLICT 180 180 A -> T (IN REF. 1).
FT CONFLICT 271 271 D -> G (IN REF. 1).
FT CONFLICT 403 404 HL -> RO (IN REF. 1).
SQ SEQUENCE 552 AA; 62319 MW; C46AARCI05104975 CRC64;

Query Match 19.8%; Score 632; DB 1; Length 552;
Best Local Similarity 27.9%; Pred. No. 1.1e-25;
Matches 171; Conservative 94; Mismatches 206; Indels 142; Gaps 20;

Qy 2 KVEREATLKLEHPHVLKLDVYENKYLVLVLEHVSGBGLFDYLVKKGLRTPKEARKP 61
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 60 KIKREIQNLKFRPHHIKLVQVISTPTDFPMVBYVSGGLFDYCKHGRVEMEARRL 119
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 62 FQIISALDFCHSHSICHRDLKPNLLLDKNNIRIADFGMSAQVDSILLETSCSPHY 121
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 120 FQQLSAYDVCHRWVHRDLKPNVLLDAHNAKIADFGLSNMWSDGEFLRTSCGSPNY 179
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 122 ACPEVIREKTDGRKADVWCGVILFALLVGPDPDDNLRLQLLEKVKRGVFMHPTFP 181
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 180 AAPEVISGRLYAGPEVDIWSGCVILYALLCGTLPPDDEHVPTLFKIRGGVFYIPEYLN 239
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 182 DCQSLLRGWIEVDARRLTLEHQHVIWYIGKNEPEPEQIPRKVQIRSLPSLEDIDPD 241
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 240 SVATLLMHLQVDPDKRATIKDIREHEWF-----KQDLPSYL-----FPDPSYDAN 286
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 242 VLDS-----MHSGLCFDRNKLQDLLS--BEENQKMIYFLLDRKERYPSQDE---- 290
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 287 VIDDEAVKEVCEKEFC--TESEVMNLSYSGFPQDLAVAYHLIDNR-RIMNQASEFYLA 343
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 291 DLPPRNEIDPPKRKRVDSPLNLRHGRKRRPERKSMELSVLSDGSPVPARRAIEAQMGRS 350
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 344 SSPSPSGSF-----MDDSAMHIP----- 360
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 351 RSISGASSGLSTSLSSPRVTPHPSRGSPL--PTPKGTPTVHTPKESPAGTPTPTSPSP 408
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 361 -----PGLKPHPE-RMPPLIADSPKA-----RCPLDALNTTKPKSL 395
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 409 SVGGVPMRRLNLSIKNSFLGSPRFRHRLQVPTPEMSNL-----TPSGSPELAKKSWFGN 464
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 396 AVKAKWHLGIRSQSKPDIAMAEVTRAMKQLDFEKKVNVAYHLVRKXNPT-----GN 449
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 465 FLSLEKEQIFVVIKDKPLSSIKADIVHAFISIPLSHVSISQTSFRABRYKATGPAVFQ 524
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 450 YKMSLA--QLYLIV-----DNRSYLLDFKSIDDEWVEQRSGSSTPQRSASAGLH 496
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

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Qy 525 KPVKQVDITYTEGGEAQAQKNGIYVTFLLSGPSRRFRKRVETIQALQLSTHDDPPAAQH 584
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 497 RP-RSSFDSTAESH-----LSG-----SLTGLSTGLTSLSSVSPRLGSH 535
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 585 LSDTTN-CMEMMT 596
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 536 TMDFFENCASLIIT 548
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
RESULT 14
AAKL RAT STANDARD; PRT; 548 AA.
AC PS4645; 1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 5'-AMP-activated protein kinase, catalytic alpha-1 chain (EC 2.7.1.-)
DE (AMPK alpha-1 chain).
DE PRKAA1 OR AMPK1.
DE Rattus norvegicus (Rat).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=Sprague-Dawley; TISSUE=Hypothalamus, and Liver;
RX MEDLINE=96132781; PubMed=8557660;
RA Stapleton D., Mitchell K.I., Gao G., Widmer J., Michell B.J.,
RA Teh T., House C.M., Fernandez C.S., Cox T., Witters L.A.,
RA Kemp B.E.;
RT "Mammalian AMP-activated protein kinase subfamily.";
RL J. Biol. Chem. 271:611-614 (1996).
[2]
PARTIAL SEQUENCE.
RC STRAIN=Sprague-Dawley; TISSUE=Hypothalamus, and Liver;
RX MEDLINE=95050763; PubMed=7961907;
RA Stapleton D., Gao G., Michell B.J., Widmer J., Mitchell K.,
RA Teh T., House C.M., Witters L.A., Kemp B.E.;
RT "Mammalian 5'-AMP-activated protein kinase non-catalytic subunits are
homologs of proteins that interact with yeast Snf1 protein kinase.";
RL J. Biol. Chem. 269:29343-29346 (1994).
CC -1- FUNCTION: RESPONSIBLE FOR THE REGULATION OF FATTY ACID SYNTHESIS
BY PHOSPHORYLATION OF ACETYL-COA CARBOXYLASE. IT ALSO REGULATES
CHOLESTEROL SYNTHESIS VIA PHOSPHORYLATION AND INACTIVATION OF
HORMONE-SENSITIVE LIPASE AND HYDROXYMETHYLGUTARYL-COA REDUCTASE.
APPEARS TO ACT AS A METABOLIC STRESS-SENSING PROTEIN KINASE
SWITCHING OFF BIOSYNTHETIC PATHWAYS WHEN CELLULAR ATP LEVELS ARE
DEPLETED AND WHEN 5'-AMP RISES IN RESPONSE TO FUEL LIMITATION
AND/OR HYPOXIA. THIS IS A CATALYTIC SUBUNIT.
CC -1- SUBUNIT: HETEROTRIMER OF A CATALYTIC SUBUNIT, A BETA AND A GAMMA
NON-CATALYTIC SUBUNITS.
CC -1- TISSUE SPECIFICITY: LOW EXPRESSION IN KIDNEY, LIVER, LUNG, HEART,
AND BRAIN.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
SNF1 SUBFAMILY.
CC -----
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DR GO: 0017148; P: negative regulation of protein biosynthesis; NAS.
DR GO: 0045768; P: positive regulation of anti-apoptosis; ISS.
DR GO: 0045542; P: positive regulation of cholesterol biosynthesis; ISS.
DR GO: 0046321; P: positive regulation of fatty acid oxidation; NAS.
DR GO: 0045722; P: positive regulation of gluconeogenesis; NAS.
DR GO: 0046326; P: positive regulation of glucose import; NAS.
DR GO: 0006468; P: protein amino acid phosphorylation; NAS.
DR GO: 0001666; P: response to hypoxia; ISS.
DR InterPro: IPR000719; Prot. kinase.
DR InterPro: IPR002290; Ser. Thr. kinase.
DR Pfam: PF00069; pkinase; 1.
DR PRINTS: PR00109; TYRKINASE.
DR ProDom: PD000001; Prot. kinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE: PS00108; PROTEIN KINASE ST; 1.
DR PROSITE: PS00111; PROTEIN KINASE DOM; 1.
DR Transferrase; Serine/threonine-protein kinase; Fatty acid biosynthesis;
KW phosphorylation; ATP-binding; Multigene family.
FT DOMAIN 16 268 PROTEIN KINASE
FT NP_BIND 22 30 ATP (BY SIMILARITY).
FT BINDING 45 45 ATP (BY SIMILARITY).
FT ACT_SITE 139 139 BY SIMILARITY.
FT MOD_RES 172 172 PHOSPHORYLATION (AUTO-) (POTENTIAL).
SQ SEQUENCE 548 AA; 62599 MW; 5CCAC3281C195F867 CRC64;

Query Match 19.8%; Score 631.5; DB 1; Length 548;
Best Local Similarity 40.7%; Pred. No. 1.2e-25;
Matches 134; Conservative 57; Mismatches 103; Indels 35; Gaps 8;

QY 2 KVEREIALKLEIHPHVLKHDVYENKYLVLVLEHVSOGELFDYLVKGRGLTPKEARKF 61
DB 60 KIRREIQNLKFRPHIHLKQVISTPDSDFWMEYVSGGELFDYICKNGELDEKERRL 119
QY 62 FROIISALDFCHSHSICHRDLKPNLLDKENIRIADFGMASIQVDSLETSCGSPHY 121
DB 120 FQQLSGVDYCHRWVHVRDLKPNLLDAHNAKIADFGLSNMMSDGEFLRTSCGSPNY 179
QY 122 ACPEVIRGEKVDGRKADVWSCGVILFALLVGLPDDDLNLRQLLEKVKRGVFMHPHIPP 181
DB 180 AAPEVIRGLVAGPEVDVWSSGVILYALLCGTLFPDDHVTLPKIKCDGFIYTPQVLP 239
QY 182 DCQSLRGMIEVDAAARLLTSHIQHWIYIGGKNEPEPEQIPRKVQIRSLPSLED--ID 239
DB 240 SVISILKHLQVDPKRAIKDIREHEWF-----KQDLP-KYLPPEPSYSTWID 289
QY 240 PDVLDSDM-----HSLGCFRDRNKLQDLLEENQEKMIYFLLDRKERYPSQDE 290
DB 290 DEALKEVCEKEFECSEEVLSCLYRNH--QDPLA-----VAYHLIIDNRIMNEAKDF 340
QY 291 DLPRNEIDPPRKRVDSPLNAR-HGKRPP 318
DB 341 YL-----ATSPDPSFLDDHHLTRPHERVP 365

RESULT 15
ID SNIL_MOUSE STANDARD; PRT; 779 AA.
AC Q60670;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Probable serine/threonine protein kinase SNFLK (EC 2.7.1.1-) (HRT-20)
DE (Myocardial SNF1-like kinase).
GN SNFLK OR MSK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND REVISIONS TO 8; 16-18; 44-45; 316 AND 435.
RC TISSUE=Embryo;

RA Ruiz J.C.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 1-435 FROM N.A., AND TISSUE SPECIFICITY.
RX TISSUE=Embryo;
RC MEDLINE=95200798; PubMed=7893599;
RA Ruiz J.C., Conlon P.L., Robertson E.J.;
RT "Identification of novel protein kinases expressed in the myocardium
of the developing mouse heart";
RL Mech. Dev. 48:153-164 (1994).
CC -1- TISSUE SPECIFICITY: EXPRESSED IN LUNG, SKIN, OVARY, HEART AND
STOMACH. NO EXPRESSION IN BRAIN, LIVER OR SKELETAL MUSCLE.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC SNF1 SUBFAMILY.
CC -1- SIMILARITY: Contains 1 UBA domain.
CC
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CC
CC EMBL; U11494; AAA67926.2; -.
DR HSP; P24941; 1AQL.
DR MGD; MGI:104754; Snflk.
DR InterPro: IPR000719; Prot. kinase.
DR InterPro: IPR002290; Ser. Thr. kinase.
DR InterPro: IPR000449; UBA domain.
DR Pfam: PF00069; pkinase; 1.
DR ProDom: PD000001; Prot. kinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE: PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE: PS00108; PROTEIN KINASE ST; 1.
DR PROSITE: PS00030; UBA; 1.
KW Transferrase; Serine/threonine-protein kinase; ATP-binding.
FT DOMAIN 27 278 PROTEIN KINASE.
FT NP_BIND 303 343 UBA.
FT BINDING 33 41 ATP (BY SIMILARITY).
FT ACT_SITE 149 149 BY SIMILARITY.
SQ SEQUENCE 779 AA; 85027 MW; 7B08131BC46D9C4E CRC64;

Query Match 19.8%; Score 631; DB 1; Length 779;
Best Local Similarity 32.7%; Pred. No. 1.9e-25;
Matches 163; Conservative 74; Mismatches 170; Indels 92; Gaps 14;

QY 2 KVEREIALKLEIHPHVLKHDVYENKYLVLVLEHVSOGELFDYLVKGRGLTPKEARKF 61
DB 70 KIYREVQLMKLLNHPNIIKLYQVMEKDMLYIVTEFAQNGEMFDYLTNGHLSNEARQK 129
QY 62 FROIISALDFCHSHSICHRDLKPNLLDKENIRIADFGMASIQVDSLETSCGSPHY 121
DB 130 FQQLSVAVEYCHNHHIVHRDLKTENLLDSDNMDIKLADFGFNGFYPGEFLSTCVGSPPY 189
QY 122 ACPEVIRGEKVDGRKADVWSCGVILFALLVGLPDDDLNLRQLLEKVKRGVFMHPHIPP 181
DB 190 AAPEVIRGEKVDGRKADVWSCGVILFALLVGLPDDDLNLRQLLEKVKRGVFMHPHIPP 249
QY 182 DCQSLRGMIEVDAAARLLTSHIQHWIYIGGKNEPEPEQIPRKVQIRSLPSLEDI 238
DB 250 DCETLIRMLVDPKRAITIAQIRQHRW-----QADPTLLQDDPAPDMQVTSNLGDY 304
QY 239 DPVLDSDMHSILGCFRDRNKLQDLLEENQEKMIYFLLDRKERY-----PSQDEDLPP 294
DB 305 NEQVLGIMQALGI--DRQRTIESLQNSYNHFAIYLLERLKEHRSAPSSRPTAPT 362
QY 295 R-----NEI--DPPRKRVDSM-----LNHRGKRPP--- 318
DB 363 RQQLRSSDLSLEVPOEILPCDPFRPSLLCPQALAQSVLQAEIDCDLHSLQLPLFP 422

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 26, 2003, 11:51:21 ; Search time 32.4013 Seconds
(without alignments)
4842.281 Million cell updates/sec

Title: US-10-054-579-4

Perfect score: 3188

Sequence: 1 MKVERETAILKLEHPPHVLK.....TNCMEMTGRSLKCGIIPKS 608

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 23.4

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_oraganelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3182	99.8	668	Q81WQ3	Q81WQ3 homo sapien
2	3015	94.6	603	O60843	O60843 homo sapien
3	2545.5	79.8	715	Q96JL4	Q96JL4 homo sapien
4	2545.5	79.8	768	Q8ND00	Q8ND00 homo sapien
5	2545.5	79.8	778	Q8TDC2	Q8TDC2 homo sapien
6	2545.5	79.8	794	Q8TDC3	Q8TDC3 homo sapien
7	1712	53.7	793	Q9VUV4	Q9VUV4 drosophila
8	1596.5	50.1	698	O61298	O61298 halocynthia
9	1536	48.2	914	Q19469	Q19469 caenorhabdi
10	1439.5	45.2	473	Q96AV4	Q96AV4 homo sapien
11	1248	39.1	701	Q95T82	Q95T82 drosophila
12	769.5	24.1	833	Q8SXS5	Q8SXS5 dictyosteli
13	718	22.5	170	Q8TB60	Q8TB60 homo sapien
14	698	21.9	401	Q98SC8	Q98SC8 guillardia
15	698	21.9	535	Q8RW22	Q8RW22 arabidopsis
16	688.5	21.6	745	Q15524	Q15524 homo sapien

17	688.5	21.6	755	4	Q96HB3	Q96hb3 homo sapien
18	686.5	21.5	691	4	Q96RG0	Q96rg0 homo sapien
19	686	21.5	504	10	P93113	P93113 cucumis sat
20	684.5	21.5	722	11	O08679	O08679 rattus norv
21	683.5	21.4	888	11	Q8BR95	Q8br95 mus musculu
22	681.5	21.4	512	10	P92968	P92968 arabidopsis
23	681.5	21.4	512	10	P92958	P92958 arabidopsis
24	680	21.3	149	4	O95099	O95099 homo sapien
25	680	21.3	505	10	Q92RJ1	Q92rj1 cryza sativ
26	679	21.3	514	10	Q9XF25	Q9xf25 glycine max
27	676.5	21.2	785	13	Q8QGV3	Q8qgv3 xenopus lae
28	675.5	21.2	752	4	Q8NG37	Q8ng37 homo sapien
29	672.5	21.1	484	10	Q43475	Q43475 hordeum vul
30	672.5	21.1	926	4	Q9H0K1	Q9h0k1 homo sapien
31	671.5	21.1	729	11	Q9JKE4	Q9jke4 mus musculu
32	671.5	21.1	744	11	Q9JKE5	Q9jke5 mus musculu
33	670.5	21.0	795	4	Q9P0L2	Q9p0l2 homo sapien
34	670	21.0	514	10	Q9M726	Q9m726 lycopersico
35	668	21.0	511	10	Q40544	Q40544 nicotiana t
36	668	21.0	931	11	Q8CFH6	Q8cfh6 mus musculu
37	667.5	20.9	752	11	Q8CIP4	Q8cip4 mus musculu
38	665.5	20.9	671	3	Q96WI7	Q96wi7 trichoderma
39	663.5	20.8	626	5	Q95Q04	Q95zq4 caenorhabdi
40	660.5	20.7	624	5	Q22068	Q22068 caenorhabdi
41	658.5	20.7	797	11	Q8VHF0	Q8vhf0 rattus norv
42	657.5	20.6	793	11	O08678	O08678 rattus norv
43	657.5	20.6	795	11	Q8VHJ5	Q8vhj5 mus musculu
44	657.5	20.6	1371	4	Q9Y2K2	Q9y2k2 homo sapien
45	655	20.5	1037	3	Q8NKJ8	Q8nkj8 saccharomyc

ALIGNMENTS

RESULT 1

Q81WQ3	PRELIMINARY;	PRT;	668 AA.
ID	Q81WQ3		
AC	Q81WQ3;		
DT	01-MAR-2003 (TrEMBLrel. 23, Created)		
DT	01-MAR-2003 (TrEMBLrel. 23, Last sequence update)		
DT	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)		
DE	Serine/threonine protein kinase isoform.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Brain tumor;		
RA	Guo J.H., Yu L.		
RL	Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AY166857; AAN87839.1; -		
KW	Kinase.		
SQ	SEQUENCE 668 AA; 74714 MW; 6AF8CB84FC48C07 CRC64;		

Query Match	99.8%;	Score 3182;	DB 4;	Length 668;
Best Local Similarity	99.8%;	Pred. No. 2.1e-229;		
Matches 607;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
Qy	1	MKVERETAILKLEHPPHVLKHDVYENKKYLVLVLEHVS	GGELFDYLVKKGRLTPKEARK	60
Db	61	MKVERETAILKLEHPPHVLKHDVYENKKYLVLVLEHVS	GGELFDYLVKKGRLTPKEARK	120
Qy	61	FFRQITSAIDFCHSHSICHRDLKPENLLDEKKNIRIAD	FGMASLQVDSILLETSCSGPH	120
Db	121	FFRQITSAIDFCHSHSICHRDLKPENLLDEKKNIRIAD	FGMASLQVDSILLETSCSGPH	180
Qy	121	YACPEVIRGSKYDGRKADVWSCGVILFALAVGALP	FDNRLQLLEKVGVFHMFIP	180
Db	181	YACPEVIRGSKYDGRKADVWSCGVILFALAVGALP	FDNRLQLLEKVGVFHMFIP	240
Qy	181	PDQCSLLRGMIEVDAARRLTLEHIQHIWYIGGKNEP	PEPQIPRKVIQIRSLPSLEIDP	240

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Db 241 PDCQSLRGMSVDAARELTLEHIQKHIWIYGGKNEPEPEQIPRKQVIRSLPSLEIDP 300
Qy 241 DVLDSMSLGCGRDRNKLQDLLEENQEKMIYFLLLDKRYPSQEDDLPPRNEIDP 300
Db 301 DVLDSMSLGCGRDRNKLQDLLEENQEKMIYFLLLDKRYPSQEDDLPPRNEIDP 360
Qy 301 PRKRVDSPLNRHGKRRRPERKSMELSVTDGGSVPARRAIEAQAQHGORSISGASGL 360
Db 361 PRKRVDSPLNRHGKRRRPERKSMELSVTDGGSVPARRAIEAQAQHGORSISGASGL 420
Qy 361 STPSLSSPRVTPHSPRGSPLETPKGTVPVHTPKSPAGTNPPTPSSPSVGGVPMRRLN 420
Db 421 STPSLSSPRVTPHSPRGSPLETPKGTVPVHTPKSPAGTNPPTPSSPSVGGVPMRRLN 480
Qy 421 SIKNSFLGSPFRHRKLOVPTPEMSNLTPSSPELAKKSWFGNFI SLEKEEQIFVVIKD 480
Db 481 SIKNSFLGSPFRHRKLOVPTPEMSNLTPSSPELAKKSWFGNFI SLEKEEQIFVVIKD 540
Qy 481 KPLSSIKADIHVAFLSIPSLSHSVISQTSFRAEYKATGPAVFOKPVKFQVDITVTEGGE 540
Db 541 KPLSSIKADIHVAFLSIPSLSHSVISQTSFRAEYKATGPAVFOKPVKFQVDITVTEGGE 600
Qy 541 AQKENGIVSVTFTLLSGSPSRFRVETIQALLSTHDPAAQHLSDTTNCMWMTCRLS 600
Db 601 AQKENGIVSVTFTLLSGSPSRFRVETIQALLSTHDPAAQHLSDTTNCMWMTCRLS 660
Qy 601 KCGIIPKS 608
Db 661 KCGIIPKS 668

RESULT 2
O60843 PRELIMINARY; PRT; 603 AA.
AC O60843;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative serine/threonine protein kinase (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=21064499; PubMed=11124703;
RA Stanchi F., Bertocco E., Toppo S., Dioguardi R., Simionati B.,
RA Cannata N., Zimbello R., Lanfranchi G., Valle G.;
RT "Characterization of 16 novel human genes showing high similarity to
RT yeast sequences."
RL Yeast 18:69-80(2001).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AJ006701; CAA07196.1; -.
DR Genew; HGNC:11405; STK29.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot kinase; 1.
DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
FT NON_TER 1
SQ SEQUENCE 603 AA; 67401 MW; B02C5D678F8EE96 CRC64;

Query Match 94.6%; Score 3015; DB 4; Length 603;
Best Local Similarity 99.7%; Pred. No. 5.5e-217;
Matches 574; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 12 LIEHPVLKLDVYENKYLVLVLEHVSQGLFDYLKVKGRTPKARKFFRQIISALDF 71
Db 1 LIEHPVLKLDVYENKYLVLVLEHVSQGLFDYLKVKGRTPKARKFFRQIISALDF 60

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Qy 72 CHSHSICHSDIKPENLILDEKNNIRIADFGMASLOVDSILLETSCGSPHYACPEVIRGEK 131
Db 61 CHSHSICHSDIKPENLILDEKNNIRIADFGMASLOVDSILLETSCGSPHYACPEVIRGEK 120
Qy 132 YDGRKADVMSGCVILFALLVGLPFDNDRQLLEKVKRGVFMHPHFIPDQCQSLRGMI 191
Db 121 YDGRKADVMSGCVILFALLVGLPFDNDRQLLEKVKRGVFMHPHFIPDQCQSLRGMS 180
Qy 192 EVDAARRLTLEHIQKHIWIYGGKNEPEPEQIPRKQVIRSLPSLEIDPDLVDSMSLGC 251
Db 181 EVDAARRLTLEHIQKHIWIYGGKNEPEPEQIPRKQVIRSLPSLEIDPDLVDSMSLGC 240
Qy 252 FDRNKLQDLLEENQEKMIYFLLLDKRYPSQEDDLPPRNEIDPDKRVDSPLMN 311
Db 241 FDRNKLQDLLEENQEKMIYFLLLDKRYPSQEDDLPPRNEIDPDKRVDSPLMN 300
Qy 312 RHGKRPERKSMELSVTDGGSVPARRAIEAQAQHGORSISGASGLSTPSLSPRVT 371
Db 301 RHGKRPERKSMELSVTDGGSVPARRAIEAQAQHGORSISGASGLSTPSLSPRVT 360
Qy 372 PHSPRGSPLETPKGTVPVHTPKSPAGTNPPTPSSPSVGGVPMRRLNSIKNSFLGSPR 431
Db 361 PHSPRGSPLETPKGTVPVHTPKSPAGTNPPTPSSPSVGGVPMRRLNSIKNSFLGSPR 420
Qy 432 FHRKLOVPTPEMSNLTPSSPELAKKSWFGNFI SLEKEEQIFVVIKDPLSSIKADI 491
Db 421 FHRKLOVPTPEMSNLTPSSPELAKKSWFGNFI SLEKEEQIFVVIKDPLSSIKADI 480
Qy 492 HAFSLPSLSHVISQTSFRAEYKATGPAVFOKPVKFQVDITVTEGGEAQKENGIVSVT 551
Db 481 HAFSLPSLSHVISQTSFRAEYKATGPAVFOKPVKFQVDITVTEGGEAQKENGIVSVT 540
Qy 552 FTLLSGSPSRFRVETIQALLSTHDPAAQHLSD 587
Db 541 FTLLSGSPSRFRVETIQALLSTHDPAAQHLSE 576

RESULT 3
Q96JL4
ID Q96JL4 PRELIMINARY; PRT; 715 AA.
AC Q96JL4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein KIAA1811 (Fragment).
GN KIAA1811.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=21245130; PubMed=11347906;
RA Nagase T., Nakayama M., Nakajima D., Kikuno R., Ohara O.;
RA "Prediction of the coding sequences of unidentified human genes. XX.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro."
RL DNA Res. 8:85-95(2001).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AB058714; BAB47440.1; -.
DR HSSP; P24941; 18UH.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW Hypothetical protein; ATP-binding; Kinase;
KW Serine/threonine-protein kinase; Transferase.

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FT NON_TER 1 1
 SQ SEQUENCE 715 AA; 78499 MW; B90F6EBE115C418A5 CRC64;
 Query Match 79.8%; Score 2545.5; DB 4; Length 715;
 Best Local Similarity 75.6%; Pred. No. 8.8e-182;
 Matches 495; Conservative 51; Mismatches 44; Indels 65; Gaps 7;
 QY 1 MKVEREAILKLEIHPHVLKLDVYENKYLVLVLEHVSOGGELFDYLVKGRGLTPKEARK 60
 Db 13 MKVEREAILKLEIHPHVLKLDVYENKYLVLVLEHVSOGGELFDYLVKGRGLTPKEARK 72
 QY 61 FFRQIISALDFCHSHSICHRLDKPENLLDEKNNIRIADFGMASLOVGDLSLETSCGSPH 120
 Db 73 FFRQIVSALDFCHSYCHRLDKPENLLDEKNNIRIADFGMASLOVGDLSLETSCGSPH 132
 QY 121 YACPEVIRGEKYDGRKADVMSGCVILFALLVGVLPDDNNLRQLLEKVKRGVFMHPHIP 180
 Db 133 YACPEVIRGEKYDGRADVMSGCVILFALLVGVLPDDNNLRQLLEKVKRGVFMHPHIP 192
 QY 181 PDCQSLLRGMIEVDAAARLTLEHIQKHWYIGGKNEPEP-EQPIP-RKVOIRSLPSLEDI 238
 Db 193 PDCQSLLRGMIEVEPEKRLSLQIQKHPWYLGKHEPDPCLEPAPGRRVAMRSLPSNGEL 252
 QY 239 DPVLDLSMHSICGFRDRNKLLODLSSEENQEKMIYFLLDRKERYPSQEDDLPPRNEI 298
 Db 253 DPVLDLSMHSICGFRDRNKLLODLSSEENQEKMIYFLLDRKERYPSQEDDLPPRNDV 312
 QY 299 DPPRKRVDSPLNLRHGRKRRPERKSMVLSVTD---GGSPVPARRAIEMAHQGRSRSISG 355
 Db 313 DPPRKRVDSPLNLRHGRKRRPERKSMVLSITDAGGGSPVTRALEMAHQGRSRSVSG 372
 QY 356 ASSGLSTSPSSPR-----VTPHP 374
 Db 373 ASTGLSSPLSSPRSPVFSPEPGAGDEARGGSGPTSKTQTLPSRPGGGAGQPPPP 432
 QY 375 SPRGSLPTPKG-----TPVHTPKESPAGTNPPTPSSP--SVGGVPMRRLNS 421
 Db 433 SARSTPLPGPPSPRSSGGTPLHSPHTPRASPTGTPTTTPPPSGGGVGAAMRSLNS 492
 QY 422 IKNSFLGSPRFRHRRKQVPTPEMSNLTPESSPELAKKSWFNGFNISLEKEQIFVVIKDK 481
 Db 493 INNSFLGSPRFRHRRKQVPTAEEMSLTPESSPELAKKSWFNGFNISLEKEQIFVVIKDK 552
 QY 482 PLSSIKADIVHAFISLPSLSHVSISQTSFRAEYKATGGPAVKFQVQDITTEGGEA 541
 Db 553 PLSSIKADIVHAFISLPSLSHVSISQTSFRAEYKASGGSPVFKPVRFOVDISSEGEPEP 612
 QY 542 QKE-----NGIYSVTFTLLSGPSRRFRKRVVETIQALLSTHDPAAQHLSDTTN 590
 Db 613 SPRDGGGGGIYSVTFTLLSGPSRRFRKRVVETIQALLSTHDPQSVQALADEKN 667

RESULT 4

Q8ND00 ID Q8ND00 PRELIMINARY; PRT; 768 AA.
 AC Q8ND00;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein (Fragment).
 GN DKF2547E1613.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Koehler K., Beyer A., Mewes H.W., Weil B., Wiemann S.;
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL834275; CAD38950.1; --
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_kinase.

DR InterPro; IPR001245; Tyr_kinase.
 DR InterPro; IPR000449; UBA domain.
 DR Pfam; PF0069; kinase; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR SMART; SM00219; TyrKc; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00101; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
 KW Hypothetical protein; ATP-binding; Transferase.
 FT NON_TER 1 1
 SQ SEQUENCE 768 AA; 83962 MW; 1P954ADFF62B889A CRC64;
 Query Match 79.8%; Score 2545.5; DB 4; Length 768;
 Best Local Similarity 75.6%; Pred. No. 9.7e-182;
 Matches 495; Conservative 51; Mismatches 44; Indels 65; Gaps 7;
 QY 1 MKVEREAILKLEIHPHVLKLDVYENKYLVLVLEHVSOGGELFDYLVKGRGLTPKEARK 60
 Db 42 MKVEREAILKLEIHPHVLKLDVYENKYLVLVLEHVSOGGELFDYLVKGRGLTPKEARK 101
 QY 61 FFRQIISALDFCHSHSICHRLDKPENLLDEKNNIRIADFGMASLOVGDLSLETSCGSPH 120
 Db 102 FFRQIVSALDFCHSYCHRLDKPENLLDEKNNIRIADFGMASLOVGDLSLETSCGSPH 161
 QY 121 YACPEVIRGEKYDGRKADVMSGCVILFALLVGVLPDDNNLRQLLEKVKRGVFMHPHIP 180
 Db 162 YACPEVIRGEKYDGRADVMSGCVILFALLVGVLPDDNNLRQLLEKVKRGVFMHPHIP 221
 QY 181 PDCQSLLRGMIEVDAAARLTLEHIQKHWYIGGKNEPEP-EQPIP-RKVOIRSLPSLEDI 238
 Db 222 PDCQSLLRGMIEVEPEKRLSLQIQKHPWYLGKHEPDPCLEPAPGRRVAMRSLPSNGEL 281
 QY 239 DPVLDLSMHSICGFRDRNKLLODLSSEENQEKMIYFLLDRKERYPSQEDDLPPRNEI 298
 Db 282 DPVLDLSMHSICGFRDRNKLLODLSSEENQEKMIYFLLDRKERYPSQEDDLPPRNDV 341
 QY 299 DPPRKRVDSPLNLRHGRKRRPERKSMVLSVTD---GGSPVPARRAIEMAHQGRSRSISG 355
 Db 342 DPPRKRVDSPLNLRHGRKRRPERKSMVLSITDAGGGSPVTRALEMAHQGRSRSVSG 401
 QY 356 ASSGLSTSPSSPR-----VTPHP 374
 Db 402 ASTGLSSPLSSPRSPVFSPEPGAGDEARGGSGPTSKTQTLPSRPGGGAGQPPPP 461
 QY 375 SPRGSLPTPKG-----TPVHTPKESPAGTNPPTPSSP--SVGGVPMRRLNS 421
 Db 462 SARSTPLPGPPSPRSSGGTPLHSPHTPRASPTGTPTTTPPPSGGGVGAAMRSLNS 521
 QY 422 IKNSFLGSPRFRHRRKQVPTPEMSNLTPESSPELAKKSWFNGFNISLEKEQIFVVIKDK 481
 Db 522 IRNSFLGSPRFRHRRKQVPTAEEMSLTPESSPELAKKSWFNGFNISLEKEQIFVVIKDK 581
 QY 482 PLSSIKADIVHAFISLPSLSHVSISQTSFRAEYKATGGPAVKFQVQDITTEGGEA 541
 Db 582 PLSSIKADIVHAFISLPSLSHVSISQTSFRAEYKASGGSPVFKPVRFOVDISSEGEPEP 641
 QY 542 QKE-----NGIYSVTFTLLSGPSRRFRKRVVETIQALLSTHDPAAQHLSDTTN 590
 Db 642 SPRDGGGGGIYSVTFTLLSGPSRRFRKRVVETIQALLSTHDPQSVQALADEKN 696

RESULT 5

Q8TDC2 ID Q8TDC2 PRELIMINARY; PRT; 778 AA.
 AC Q8TDC2;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Protein kinase-like protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA She X.Y., Yu L., Guo J.H.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AF479827; AAL87698.1; -
DR HSSP; P24941; 1BUH.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD00001; Prot kinase; 1.
DR SMART; SM00220; S_TK; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 778 AA; 85086 MW; 8D1818D4E54398BB CRC64;

Query Match 79.8%; Score 2545.5; DB 4; Length 778;
Best Local Similarity 75.6%; Pred. No. 9.9e-182;
Matches 495; Conservative 51; Mismatches 44; Indels 65; Gaps 7;

QY 1 MKVERETAILKLIHHPVHLKLDVYENKKYLYLVLEHVSGLGELFDYLVKKGRITPKEARK 60
DB 76 MKVERETAILKLIHHPVHLKLDVYENKKYLYLVLEHVSGLGELFDYLVKKGRITPKEARK 135

QY 61 FFRQIISALDFCHSHSICHRLDKPENLLLDKKNIRIADFGMASLQVGDLSLETSCGSPH 120
DB 136 FFRQIVSALDFCHSYISICHRLDKPENLLLDKKNIRIADFGMASLQVGDLSLETSCGSPH 195

QY 121 YACPEVIRGEKYDGRADVNSCGVILFALLVGLALPDNDNLRQLLEKVKRGVFMHPHFIP 180
DB 196 YACPEVIRGEKYDGRADVNSCGVILFALLVGLALPDNDNLRQLLEKVKRGVFMHPHFIP 255

QY 181 PDCQSLLRGMIEVDARLTLHETQKHIWYIGKNEPEP-EQPIP-RKVQIRSLPSLEDI 238
DB 256 PDCQSLLRGMIEVPEKRLSLEQIQKHPYLGKHEPDPCLEPAPGRVAMRSLPSNGEL 315

QY 239 DPDLVDSMHSILGCFDRNKLQDLISEENQEKMIYFLLLDKRYEYPSQEDDLPPNEI 298
DB 316 DPDLVDSMHSILGCFDRNKLQDLISEENQEKMIYFLLLDKRYEYPSQEDDLPPNEI 375

QY 299 DPPRKRVDSPLNRHGRKRRPERKSMVLSVTD---GGSPVPARRAIEMAHQGRSRSISG 355
DB 376 DPPRKRVDSPLNRHGRKRRPERKSMVLSVTDAGGGGSPVPTRRALLEMAHQGRSRSVSG 435

QY 356 ASSGLSTSPSSPR-----VTTPHP 374
DB 436 ASTGLSSPLSSPRSPVFSFSPGAGDEARGGSGTSTQTTLPSRPGGGAGEQPPPP 495

QY 375 SPRGSLPTPKG-----TPVHTPKESPACTNPTPPSP--SVGGVPMRRLNS 421
DB 496 SARSTPLPGPPGPRSSGGTPLHSPHTPRASPTGTPTTTPPSPGGVGGAAWRSLNS 555

QY 422 IKNSFLGSPRFRHRRKLVQPTPEEMSNLTPESSPELAKSWFNGFISLEKEEQIFVWIKDK 481
DB 556 IRNSFLGSPRFRHRRKLVQPTPEEMSNLTPESSPELAKSWFNGFISLEKEEQIFVWIKDK 615

QY 482 PLSSIKADIVHAFISIPSLSHSVISQTSFRAEYKATGGPAVFQKPVKQFVDITYTEGEA 541
DB 616 PLSSIKADIVHAFISIPSLSHSVISQTSFRAEYKATGGPAVFQKPVKQFVDITYTEGEA 675

QY 542 QKE-----NGIYSVTFTLLSGPSRRFRKRVVETIQALLSTHDPAPAAHLSDTTN 590
DB 676 SPRDGGGGGGIYVFTLLSGPSRRFRKRVVETIQALLSTHDPAPAAHLSDTTN 730

RESULT 6

Q8TDC3

ID Q8TDC3

AC Q8TDC3;

PRELIMINARY; PRT; 794 AA.

DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Putative serine/threonine protein kinase.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA She X.Y., Guo J.H., Yu L.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AF479826; AAL87697.1; -
DR HSSP; P24941; 1BUH.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD00001; Prot kinase; 1.
DR SMART; SM00220; S_TK; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 794 AA; 86753 MW; 5DD395B0E61AEF77 CRC64;

Query Match 79.8%; Score 2545.5; DB 4; Length 794;
Best Local Similarity 75.6%; Pred. No. 1e-181;
Matches 495; Conservative 51; Mismatches 44; Indels 65; Gaps 7;

QY 1 MKVERETAILKLIHHPVHLKLDVYENKKYLYLVLEHVSGLGELFDYLVKKGRITPKEARK 60
DB 92 MKVERETAILKLIHHPVHLKLDVYENKKYLYLVLEHVSGLGELFDYLVKKGRITPKEARK 151

QY 61 FFRQIISALDFCHSHSICHRLDKPENLLLDKKNIRIADFGMASLQVGDLSLETSCGSPH 120
DB 152 FFRQIVSALDFCHSYISICHRLDKPENLLLDKKNIRIADFGMASLQVGDLSLETSCGSPH 211

QY 121 YACPEVIRGEKYDGRADVNSCGVILFALLVGLALPDNDNLRQLLEKVKRGVFMHPHFIP 180
DB 212 YACPEVIRGEKYDGRADVNSCGVILFALLVGLALPDNDNLRQLLEKVKRGVFMHPHFIP 271

QY 181 PDCQSLLRGMIEVDARLTLHETQKHIWYIGKNEPEP-EQPIP-RKVQIRSLPSLEDI 238
DB 272 PDCQSLLRGMIEVPEKRLSLEQIQKHPYLGKHEPDPCLEPAPGRVAMRSLPSNGEL 331

QY 239 DPDLVDSMHSILGCFDRNKLQDLISEENQEKMIYFLLLDKRYEYPSQEDDLPPNEI 298
DB 332 DPDLVDSMHSILGCFDRNKLQDLISEENQEKMIYFLLLDKRYEYPSQEDDLPPNEI 391

QY 299 DPPRKRVDSPLNRHGRKRRPERKSMVLSVTD---GGSPVPARRAIEMAHQGRSRSISG 355
DB 392 DPPRKRVDSPLNRHGRKRRPERKSMVLSVTDAGGGGSPVPTRRALLEMAHQGRSRSVSG 451

QY 356 ASSGLSTSPSSPR-----VTTPHP 374
DB 452 ASTGLSSPLSSPRSPVFSFSPGAGDEARGGSGTSTQTTLPSRPGGGAGEQPPPP 511

QY 375 SPRGSLPTPKG-----TPVHTPKESPACTNPTPPSP--SVGGVPMRRLNS 421
DB 512 SARSTPLPGPPGPRSSGGTPLHSPHTPRASPTGTPTTTPPSPGGVGGAAWRSLNS 571

QY 422 IKNSFLGSPRFRHRRKLVQPTPEEMSNLTPESSPELAKSWFNGFISLEKEEQIFVWIKDK 481
DB 572 IRNSFLGSPRFRHRRKLVQPTPEEMSNLTPESSPELAKSWFNGFISLEKEEQIFVWIKDK 631

QY 482 PLSSIKADIVHAFISIPSLSHSVISQTSFRAEYKATGGPAVFQKPVKQFVDITYTEGEA 541
DB 632 PLSSIKADIVHAFISIPSLSHSVISQTSFRAEYKATGGPAVFQKPVKQFVDITYTEGEA 691

QY 542 QKE-----NGIYSVTFTLLSGPSRRFRKRVVETIQALLSTHDPAPAAHLSDTTN 590

Db 692 SPRDGGGGGIYVFTLLTIGSRFRKRVSTIQALLSTLHDQPSVALADEKN 746

RESULT 7

Q9VUV4 PRELIMINARY; PRT; 793 AA.

ID Q9VUV4

AC Q9VUV4

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE CG6114 protein.

DE CG6114

GN CG6114

OS Drosophila melanogaster (Fruit fly).

OS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

OX [1]

RP SEQUENCE FROM N.A.

RP STRAIN=Berkeley;

RC MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards M.D., Zhang Q., Chen L.X.,

RA Sutton G.G., Wortman J.R., Vandeell M.D., Zhang Q., Chen L.X.,

RA Brannon R.C., Rogers Y.-H.C., Blazell R.G., Champe M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlike C., Davenport L.B., Davies P.,

RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Dodeon K., Doup L.E., Downes N., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

RA Foster C., Gabrielian A.B., Garg N.S., Gelbart W.M., Glasser K.,

RA Glöck A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

RA Talali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kechum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., MCPerson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupek M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,

RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,

RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.:

RT "The genome sequence of *Drosophila melanogaster*."

RT Science 287:2185-2195 (2000).

RL [2]

RP SEQUENCE FROM N.A.

RP Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,

RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,

RA Banzon J., An H., Baldwin D., Sanson J., Beeson K.Y., Busam D.A.,

RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

RA Dodeon K., Dorsett E., Doup L.E., Doyle C., Drensek D., Farfan D.,

RA Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A.,

RA Gonzales M., Houck J., Hoskins R.A., Hostin D., Howard T.J.,

RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,

RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,

RA Pacle J., Paragas V., Park S., Patel S., Patel S., Pfeiffer B.,

RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,

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QY 389 -----VHTPKESPAGTNPPT-----PSSP--SVGGVPMARLNSIKNSPL 427
DB 478 NSGTIALSMFHDSDNSVNPNGSPMWNSSPGMPSGCPNPGQQLWKRLTNIKNSPL 537
QY 428 GSPRFRKRLQVPTPEMSNLTPESSPELAKXWFGNFISLEKEEQIFVWIKDKPLSSIK 487
DB 538 GSPRFRKRMQVSADE--VHLTPSSPELTKRSGWFGNLITTEKDETFTILVKGKPIATVK 595
QY 488 ADIVHAFSLISLSHSVTSQTSFRAEYKATG- GPAVFQKPVKFOVDIT--YTEGGEAQKE 544
DB 596 AHLTHAFSLMAELSHSVVSPTSFVVEYKRNNGSPVFMQRHYKFOVDISAICKQGDIA DM- 654
QY 545 NGIYSVTFTLLSGSPRRFRKRVETITQALLSTH-----DPP-----AAQHLSDTTNMEMM 595
DB 655 --LPAITFTLLSGNRRFRICEHIQSQVCKRFGPSSPTVTSVTAQVSESSCGSVS 712
QY 596 TGRULS 600
DB 713 SERLS 717

RESULT 8
ID O61298 PRELIMINARY; PRT; 698 AA.
AC O61298;
DT 01-AUG-1998 (Tremblrel. 07, Created)
DT 01-AUG-1998 (Tremblrel. 07, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE HRPPOK-1 protein.
GN HRPPOK-1.
OS Halocynthia roretzi (Sea squirt).
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
OC Stolidobranchia; Pyridae; Halocynthia.
OX NCBI_TaxID=7729;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Egg;
RX MEDLINE=98404280; PubMed=9767157;
RA Sasakura Y., Ogasawara M., Makabe K.W.;
RT "Maternally localized RNA encoding a serine/threonine protein kinase
in the ascidian, Halocynthia roretzi."
RL Mech. Dev. 76:161-163(1998).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AB014885; BAA28663.1; -.
DR HSSP; O63450; 1A06.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00069; kinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 698 AA; 78607 MW; B29B1751B83200BF CRC64;

Query Match 50.1%; Score 1596.5; DB 5; Length 698;
Best Local Similarity 53.5%; Pred. No. 7.7e-111;
Matches 329; Conservative 98; Mismatches 121; Indels 67; Gaps 16;

QY 2 KVEREIALKLEHPHVLKLDVYENKYLVLVLEHVSGLGFYLVKKGRLTTPKEARKF 61
DB 57 KVEREIALKLEHPHVLKLDVYENKYLVLVLEHVSGLGFYLVKKGRLTTPKEARKF 116
QY 62 FQRIISALDFCHSHSICHRDLKPNLLDDEKNNIRIADFGMASLQVGSLLTSCGSPHY 121
DB 117 FQRIISAVDYCHNHVCHRLKPNLLDDEKNNIKVADFGMASLQPEGLLETSCGSPHY 176
QY 122 ACPEVIREKTDGRKADYVSCGVILFALLVGLALPFDDNLRLLEKVKRGVYHFMPIPP 181

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DB 177 ACPEVIRGERYDGRADYVSCGVILFALLVGLALPFDDNLRLLEKVKRGVYHFMPIPP 236
QY 182 DCOSILRGMEIVDAARLTLLEHIQKHIWYIGKNE-----PEPEQIPRKVQIRSLPS 234
DB 237 DAQNLLRGIMIDVRPDKRLSLQVLOHPWMPRPGNSVEGVLVTPDPVVPV---IDCVPLPE 293
QY 235 LEDIDPDVLDSMHSLSGCFRDRNKLQDLLESEBENQEKMIYFLILLDRKERYPS-QEDEDLP 293
DB 294 EESVDPDLVSLMTSLGCFCKEKLAKNLITEQNTKVVVYVYMLLRKKRYPSPFDDADSL 353
QY 294 PRNEIDPPKRVQD--SPMLNRHG-----KRRPERK-SMEVLSTVDCGSPVPARAEIMAQ 345
DB 354 PCCHPDAPKRVDSSTSLSSNGDDCVNPIPKRMASLCLTDSSESLSRK--KSTE 411
QY 346 HGORSSISGASSGL-----STSPLSRPTVPHSPRGSPLTPKGTGVH--TPKESP 396
DB 412 THORSLSLGSNSRLVCNISDTKAEKSRI-----NGTPVRGTTCCSN 457
QY 397 AGTPNPTPPSPSVGGVPMARLNSIKNSFLGSPRFRKRLQVPTPEMSNLTPESSPEL 456
DB 458 QVPVQINTPASPN---PWRQLASLKNFTMGSPRFRKRMQAPSSDEVN-QGNSSEL 512
QY 457 AKKSWFGNFISLE-----KEEQIFVWIKDKPLSSIKADIVHAFSLISLSHSVTSQTS 509
DB 513 SKRSWFGNFMSSRYSTHCHDELFPYAIAYKNRTLSNVKSELVHAFSLIPNLTHSMVSPTR 572
QY 510 FRAEYKATG- GPAVF- QKPVKFOVDITVTEGGEAQEN-----GIYSVTFLLSGP 558
DB 573 FRCDYKSSGTSTTSVFHQRSIKQVDIIQHSLSLDROENGKKPSSQTVGFTIAFSLISGP 632
QY 559 SRRFRKRVETITQAL 573
DB 633 IRRYKRVLELLQOM 647

RESULT 9
Q19469 PRELIMINARY; PRT; 914 AA.
ID Q19469;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-OCT-2001 (Tremblrel. 18, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE F15A2.6 protein (Serine/threonine kinase SAD-1).
GN F15A2.6.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Gregory J.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
investigating biology."
RL Science 282:2012-2018(1998).
RN [3]
RP SEQUENCE FROM N.A.
RA Crump J.G., Zhen M., Jin Y., Bargmann C.;
RT "The SAD-1 kinase regulates presynaptic vesicle clustering."
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; Z70207; CAA94127.2; -.
DR EMBL; AF316542; AAG50270.1; -.
DR HSSP; Q63450; 1A06.
DR WormPep; F15A2.6; CE28218.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR006025; Zn_Wipeptase.
DR Pfam; PF00069; kinase; 1.

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DR InterPro: IPR000719; Prot_kinase.
DR Pfam: PF00069; pkinase; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Transferase.
SQ SEQUENCE 701 AA; 76973 MW; 87B30879883B2425 CRC64;

Query Match 39.1%; Score 1248; DB 5; Length 701;
Best Local Similarity 44.9%; Pred. No. 8.8e-85;
Matches 284; Conservative 76; Mismatches 131; Indels 142; Gaps 19;

QY 102 MASLQVGSLSLETSCGSPHYACPEVIRGEKYDGRKADVMSGCVILFALLVGLALPFDDNL 161
Db 1 MASLQVGSLSLETSCGSPHYACPEVIRGEKYDGRKADVMSGCVILFALLVGLALPFDDNL 60

QY 162 ROLLEKVKRGVEMPHPIPDCCSLRGLMTEVDAARELTLEHIQKHLY-IGCKNPEPE 220
Db 61 ROLLEKVKRGVEMPHPIPDCCSLRGLMTEVDAARELTLEHIQKHLY-IGCKNPEPE 120

QY 221 QPIPRKQVIRSLSELDIDPDVLDMSHSLGCFDRNKLQDLLESEENQEKMIYFLLDR 280
Db 121 LPMMEVQTHVPTATVDPVLAICSLGCFEKEKLIQELSSSHNTKVIYFLLER 180

QY 281 KERYPSQDEED-LPRNE-IDPPRKRVDSPLN----- 311
Db 181 KRRRPALEDDEDEIAQKSRSELDAVDPPRKRLDTCRINGTNAPSYGQISEGSLTPRRQAF 240

QY 312 -----RHGKRPRKSNVSLVTDGSGVPVARRAIEMAQ----- 345
Db 241 NFRSYSTRNHQRSPPTVTSVRS-SYHSPTRCNSPMSSAQQAIAISRPSPAGTR 299

QY 346 ---HGQSRISISGASGLSTSPSS-----PRVTPHPSR-----GSP--- 380
Db 300 HSTYGDRLR-SGHSSVSRTSPSSQKSLGDDVVVREPRIERDLSLQERGSGSPDR 357

QY 381 --LTPKGT-----VHTPKSPAGTNPT----- 404
Db 358 GDCGIPGSPGSGSGTSASPSVHRANSQPTIAISWFHDPSNSVVPNGSPMMNSS 417

QY 405 ---PSSP-SVGVGVPMRRLNSIKNSFLGSPRRHRRKLOVPTPEMSNLTPESSPELAKK 459
Db 418 PGMGSPCNTGGQLWKRLTNIKNSFLGSPRRHRRKQVSADE-VHLPESPFLTKR 475

QY 460 SWFGNFISSLEKEQIFVYIKDKPLSSIKADIVHAFSLPSLSHSVISQTSFRAEYKATG- 518
Db 476 SWFGNLIITEKDEFTILVKGPATVKAHILHAFSLMAELSHSVSPTSFVEYKENG 535

QY 519 GPVAFQPKVQVDIT--YTGGEAQKENGYSVTFLLSGPSRRPKRVETVIAQLLST 576
Db 536 GPVAFQPKVQVDISAIKQGDADM--LFALTFTLLSGNIRPRRICEHIOQVCSK 592

QY 577 H-----DPP-----AAQHLSDTTNCWEMMTGRLS 600
Db 593 RPPGSPSPPTVTSVTAQVSSSSCGSVSSRLS 625

RESULT 12
Q8SSX5 PRELIMINARY; PRT; 833 AA.
AC Q8SSX5;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative serine/threonine protein kinase.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RA Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P.,
RA Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,
RA Tunngal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;

RT "Sequence and Analysis of Chromosome 2 of Dictyostelium.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: AC115685; AAL92711.1; -.
DR HSSP: P24941; IBOH.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_Thr_kinase.
DR Pfam: PF00069; pkinase; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS01008; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 833 AA; 93467 MW; 51B64036C90CF94 CRC64;

Query Match 24.1%; Score 769.5; DB 5; Length 833;
Best Local Similarity 29.5%; Pred. No. 6.6e-49;
Matches 190; Conservative 88; Mismatches 154; Indels 211; Gaps 15;

QY 2 KVEREIALKLIEHPVLKLDHVENKKYLVLEHVSQGLFDYLVKKGRLTPKEARXP 61
Db 54 KIEREIVLKLIDHPNAMQVEYETSKYLFILVEVGGELFDYLVKKGLESGEALFF 113

QY 62 FQITISALDFCHSHSICHRLDLPENLLDEKNIRIADPGMASLQVGSLSLETSCSPHY 121
Db 114 FQITIIIGLEYCHSRNICHRDLXPNLLSGDKRIKIADFGMSIVRKOMLLHTSCSPHY 173

QY 122 ACEPVIRGEKYDGRKADVMSGCVILFALLVGLALPFDDNLRLLEKVRGVPMHPIFP 181
Db 174 ASPEVVGSDYDQKADVMSGCVILYALTUTKLPDDENIRLLNKKVKGATSMPPYIHK 233

QY 182 DQOSLRGMIEVDAARLTLEHIQKHLYIGCKNPEPEQPIPRKQVIRSLSELDIDPD 241
Db 234 DAQDLITKMLTVDPKRSIKSIKEHPWFVSNFQKATPV-EEINASPLVDYSQIDED 292

QY 242 VLDMSHSLGCFDRNKLQDLLESEENQEKMIYFLLDRKRY----- 284
Db 293 IFRSLMALG-VGTIDEVKQOLVSNQKS-ATLIYRLLERKKKFDSDVNKYGYKPKETRN 350

QY 285 ----- 284
Db 351 SLSDMSLKKIFSGSNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 410

QY 285 -----PSQEDDLP 293
Db 411 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 470

QY 294 PRNEIDPPKRVDSPLNHRGKERP-----ERKSMEVLSVTDGSGSPV 336
Db 471 PSNSAN--NMAIQOPTIINNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 525

QY 337 ARRAIEMAQHGQSRISIG-----ASSGLSTPSLSPRVTPHPSPRGSPPLP 382
Db 526 LKQALQO-HHQOQQOQFNGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 584

QY 383 TPKGTVHTPKESPAG--TPNPTPPSPSPVGVVPMRRLNSIKNSFLGSPRRHRRKLOVP 440
Db 585 SPQLSAIKPDHYQRRGSMTASTNPATSPMS-----HRGKTSSP 623

QY 441 -----TPEMSNTLPE-----SPELAKKSWFGNFIS 467
Db 624 IEITSKVRKLKISEQSN-TPNSPIIGSSP---KXSWFSYFFS 662

RESULT 13
Q8TB60 PRELIMINARY; PRT; 170 AA.
AC Q8TB60;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Similar to serine/threonine kinase 29.
OS Homo sapiens (Human).
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(1) NCBI_TaxID=9606;

RP SEQUENCE FROM N.A.

RC TISSUE=Eye;

RA Strausberg R.;

RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC024291; AAB4291.1; -

KW Kinase.

SQ SEQUENCE 170 AA; 18488 MW; 55D569F31F5E651A CRC64;

Query Match 22.5%; Score 718; DB 4; Length 170;

Best Local Similarity 99.3%; Pred. No. 5.6e-46;

Matches 142; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 445 MSNLTPESSPELAKSWFGNFTLSKEQIFVVIKDKPLSSIKADIVHAFISIPLSHSV 504

DB 1 MSNLTPESSPELAKSWFGNFTLSKEQIFVVIKDKPLSSIKADIVHAFISIPLSHSV 60

QY 505 ISQTSFRAEYKATGGPAVFKQVQVDTYTEGGEAKENGIVSVTTLTSGPSRRPKR 564

DB 61 ISQTSFRAEYKATGGPAVFKQVQVDTYTEGGEAKENGIVSVTTLTSGPSRRPKR 120

QY 565 VVETIQALLSTHDPAPAAQHS 587

DB 121 VVETIQALLSTHDPAPAAQHS 143

RESULT 14

Q98SC8

ID Q98SC8 PRELIMINARY; PRT; 401 AA.

AC Q98SC8;

DT 01-OCT-2001 (TrEMBLrel. 18, Created)

DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE SNF1-related protein kinase.

GN KIN(SNF2).

OS Guillardia theta (Cryptomonas phi).

OC Nucleomorph.

OC Eukaryota; Cryptophyta; Cryptomonadaceae; Guillardia.

OX NCBI_TaxID=55529;

(1)

RP SEQUENCE FROM N.A.

RX MEDLINE=21223349; PubMed=11323671;

RA Douglas S., Zauner S., Fraunholz M., Beaton M., Penny S., Deng L.T.,

RA Wu X., Reith M., Cavalier-Smith T., Maier U.G.;

RT "The highly reduced genome of an enslaved algal nucleus.";

RL Nature 410:1091-1096(2001).

CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

DR EMBL; AF083031; AAK39655.1; -

DR InterPro; IPR000719; Prot_kinase.

DR InterPro; IPR002290; Ser_thr_kinase.

DR InterPro; IPR001245; Tyr_kinase.

DR Pfam; PF00069; kinase; 1.

DR PRINTS; PR00109; TYRKINASE.

DR ProDom; PD000001; Prot_kinase; 1.

DR SMART; SM00220; S_TKc; 1.

DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

DR ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.

KW SEQUENCE 401 AA; 46888 MW; 282CE9E6677CSD4E CRC64;

Query Match

Best Local Similarity 21.9%; Score 698; DB 8; Length 401;

Matches 138; Conservative 77; Mismatches 86; Indels 22; Gaps 6;

QY 1 MKVEREAILKLEIHPHYLVKLDVYVYENKKYLYLVLEHVSGGELFDYLVKGRITPKARK 60

DB 59 LKIQREISVKMLFPHYKIVYDVLDSKYLFLIEYASKGELFNLYVEKKLENREALK 118

QY 61 FFRQIISALDFCHSHSICHRLDKPENLLLDKNNIRIADFGWASIQVDSLSLETSCGSPH 120

DB 119 FFHEIISGLEVYCHKHCHRICRDLKLENILLDKLQIKIADFGWASISIPNIMLTKFCGSPH 178

QY 121 YACPEVIRGEKYDKRKADVSCGVILFALLVGLPFD--DNLRLLEKVKRGVFMHPHF 178

DB 179 YASPEVVSNEFYNGIKADIWSCGIIYALVVGKLPYDEENDNMKLFNKIRFEPPIPRI 238

QY 179 IPPQCQILLRGMIEVDAARLLTLEHIQKIWIYIGCKNEPEPEQIPRKVQIRSLP----- 233

DB 239 IHPDRLIRALLTINPKQITIDKIKHPY---KSPLPES---CRISQNLSPASVQ 292

QY 234 -SLEDIDPDVLSMHSIGCFRDRNKLQDLSEENQKMYFYLLDRKERYPQEDDL 292

DB 293 NPISNPDEIISFLLQLVKDKKTLGCLSTKPSFLVLYRQLEKMKMDSVRSNLI 352

QY 293 PPRNEIDPPKRVDSPLNRHKK 315

DB 353 ---NEANFKRKK-----LFQGGK 367

RESULT 15

Q8RWD2

ID Q8RWD2 PRELIMINARY; PRT; 535 AA.

AC Q8RWD2;

DT 01-JUN-2002 (TrEMBLrel. 21, Created)

DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Putative SNF1-related protein kinase.

GN AT3G01090.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI_TaxID=3702;

(1)

RP SEQUENCE FROM N.A.

RA Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,

RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,

RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,

RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,

RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,

RA Ecker J., Theologis A., Davis R.W.;

RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

DR EMBL; AY093170; AAM13169.1; -

DR HSSP; P24941; 1BUH.

DR InterPro; IPR001772; Kinase Cterm.

DR InterPro; IPR000719; Prot_kinase.

DR InterPro; IPR002290; Ser_thr_kinase.

DR InterPro; IPR000449; UBA_domain.

DR Pfam; PF02149; KAI; 1.

DR Pfam; PF00069; kinase; 1.

DR Pfam; PF00627; UBA; 1.

DR ProDom; PD000001; Prot_kinase; 1.

DR SMART; SM00220; S_TKc; 1.

DR SMART; SM00165; UBA; 1.

DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.

SQ SEQUENCE 535 AA; 61181 MW; FFFC383223FD8317 CRC64;

Query Match 21.9%; Score 698; DB 10; Length 535;

Best Local Similarity 42.7%; Pred. No. 8.1e-44;

Matches 137; Conservative 70; Mismatches 90; Indels 24; Gaps 5;

QY 2 KVEREAILKLEIHPHYLVKLDVYVYENKKYLYLVLEHVSGGELFDYLVKGRITPKARKF 61

DB 86 KVRREIKILFLWHPHPIRLYVEVETPTDYLWYVNSGELFDYIIVEKQLQDEARNF 145

QY 62 FQRIISALDFCHSHSICHRLDKPENLLLDKNNIRIADFGWASIQVDSLSLETSCGSPHY 121

DB 146 FQRIISGVEYCHRMVYVHRLDKPENLLLDKNNIRIADFGWASIQVDSLSLETSCGSPHY 205

Qy	122	ACPEVIRGEKYDGRKADVWSCGVILFALLVGALPDDDNRLQLLEKVKRGVFHMPHFIPP	181
Dd	206	AAPENVISGKLTYAGPEVDWWSGCVLYIYALLCGTLFPDDDENINLNFKKIKGGIYTLPShLSP	265
Qy	182	DCQSLLRGMLEVDAARLTLEHIQKHITWYIGGNKEPEEQIPRKVOI---RSPLSLEDI	238
Dd	266	GARDLIIPMLVDPMKRVTPTEIQHPWF-----QAHLPRYLAVPPDPTVOQAOKKI	316
Qy	239	DPDVLDMSHSLGCPRDRNKILQDLLSBEENEKMIFLLLRDKERYPS-----QEDED	291
Dd	317	DEEILQEVINGGF--DRNHLESLNRTONDGTYYIYLIDNRFRASSGYLGAEFFQETWE	374
Qy	292	LPPRNEIDPPRRKRVDSPLNLR	312
Dd	375	GTPRMH---PAESVASPVSHR	392

Search completed: November 26, 2003, 12:01:54
Job time : 34.4013 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 26, 2003, 12:01:57 ; Search time 25.7304 Seconds
(without alignments)
4358.326 Million cell updates/sec

Title: US-10-054-579-4

Perfect score: 3188

Sequence: 1 MKVREITAILKLIHHPVLK.....TNCMEMTGRSLKCGIIPKS 608

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 673684 seqs, 184443283 residues

Total number of hits satisfying chosen parameters: 673684

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications AA:*
- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
 - 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
 - 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
 - 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
 - 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
 - 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
 - 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
 - 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
 - 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
 - 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
 - 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
 - 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
 - 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
 - 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
 - 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
 - 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
 - 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
 - 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3188	100.0	608	14	US-10-054-579-4
2	3188	100.0	664	12	US-10-288-798-18
3	3188	100.0	668	14	US-10-054-579-2
4	3188	100.0	668	15	US-10-195-072-2
5	3188	100.0	668	15	US-10-195-071-2
6	3071	96.3	674	15	US-10-283-247-2
7	3065	96.1	614	15	US-10-283-247-9
8	3065	96.1	614	15	US-10-283-247-10
9	3065	96.1	674	10	US-09-842-582-2
10	3065	96.1	674	15	US-10-283-247-7
11	3065	96.1	674	15	US-10-283-247-8
12	3050	95.7	636	15	US-10-283-247-5
13	3028	95.0	585	15	US-10-195-072-4
14	3028	95.0	585	15	US-10-195-071-4
15	3015	94.6	603	15	US-10-195-072-17

16	3015	94.6	603	15	US-10-195-071-17	Sequence 17, Appl
17	2545.5	79.8	703	12	US-10-116-326-6	Sequence 6, Appl
18	2545.5	79.8	778	12	US-10-354-358-92	Sequence 92, Appl
19	2545.5	79.8	778	12	US-10-116-326-2	Sequence 2, Appl
20	2386.5	74.9	762	12	US-10-116-326-4	Sequence 4, Appl
21	722	22.6	1518	10	US-09-801-368-152	Sequence 152, App
22	688.5	21.6	745	12	US-10-161-565-24	Sequence 24, Appl
23	688.5	21.6	745	15	US-10-195-101-36	Sequence 36, Appl
24	686.5	21.5	691	10	US-09-919-585-6	Sequence 6, Appl
25	686.5	21.5	724	10	US-09-919-585-9	Sequence 9, Appl
26	682.5	21.4	722	8	US-08-817-8328-32	Sequence 32, Appl
27	680	21.3	149	12	US-10-102-548-2	Sequence 2, Appl
28	680	21.3	149	15	US-10-102-558-2	Sequence 2, Appl
29	680	21.3	149	15	US-10-195-072-18	Sequence 18, Appl
30	680	21.3	149	15	US-10-195-071-18	Sequence 18, Appl
31	675.5	21.2	752	10	US-09-835-081-2	Sequence 2, Appl
32	671.5	21.1	688	12	US-10-161-565-28	Sequence 28, Appl
33	671.5	21.1	688	12	US-10-161-565-29	Sequence 29, Appl
34	671.5	21.1	744	10	US-09-835-081-4	Sequence 4, Appl
35	670.5	21.0	795	10	US-09-919-585-12	Sequence 12, Appl
36	670.5	21.0	795	12	US-10-161-565-25	Sequence 25, Appl
37	670.5	21.0	795	15	US-10-142-356-9	Sequence 9, Appl
38	667	20.9	1369	12	US-10-288-798-7	Sequence 7, Appl
39	663.5	20.8	729	12	US-10-161-565-26	Sequence 26, Appl
40	663.5	20.8	729	15	US-10-142-356-11	Sequence 11, Appl
41	663.5	20.8	729	15	US-10-195-101-33	Sequence 33, Appl
42	662.5	20.8	783	9	US-09-815-915-2	Sequence 2, Appl
43	662.5	20.8	783	11	US-09-823-187-90	Sequence 90, Appl
44	662.5	20.8	783	12	US-10-393-316-2	Sequence 2, Appl
45	657.5	20.6	744	10	US-09-919-585-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1

US-10-054-579-4
; Sequence 4, Application US/10054579
; Publication No. US20020137913A1
GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Brian
; TITLE OF INVENTION: No. US20020137913A1el Human Kinases and Polynucleotides Encoding t
; FILE REFERENCE: LEX-0300-USA
; CURRENT APPLICATION NUMBER: US/10/054,579
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/263,378
; PRIOR FILING DATE: 2001-01-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 608
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-054-579-4

Query Match	100.0%;	Score 3188;	DB 14;	Length 608;
Best Local Similarity	100.0%;	Pred. No. 2.5e-196;		
Matches	608;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
Qy	1	MKVREITAILKLIHHPVLKLDVYENKYLVLVLEHVS	GGELFDYLVKKGRLLTPKEARK	60
Db	1	MKVREITAILKLIHHPVLKLDVYENKYLVLVLEHVS	GGELFDYLVKKGRLLTPKEARK	60
Qy	61	FFROIISALDPCSHSICHRLDKPENLLDDEKNIRIADFG	MASLQVGDLSLETSCGSPH	120
Db	61	FFROIISALDPCSHSICHRLDKPENLLDDEKNIRIADFG	MASLQVGDLSLETSCGSPH	120
Qy	121	YACFEVIRGEYDKGRKADVWMSCGVILFALLVGLALP	FFDDNLRQLLEKVKRGVFFHMFIP	180
Db	121	YACFEVIRGEYDKGRKADVWMSCGVILFALLVGLALP	FFDDNLRQLLEKVKRGVFFHMFIP	180
Qy	181	PDQSLLRGMTEVDARRRLTLEHIQKHWITGGKNEPEPE	QPIPRKVOIRSLPSLEDIDP	240

181 PDQCSLLRGMI EVDAAARLTLEHIQKHWIYGGKNEPEPEPIPRKQVIRSLPSLEIDP 240
241 DVLDMSHSLGCFRDRNKLQDLSEENQKMIYFLLIDRKERYPSQEDDLPNEIDP 300
241 DVLDMSHSLGCFRDRNKLQDLSEENQKMIYFLLIDRKERYPSQEDDLPNEIDP 300
301 PRKRVDSPLNLRHGRKRPKRSMEVLSVTDGSGSPVARRAIEMAHQGQSRSSISGASSGL 360
301 PRKRVDSPLNLRHGRKRPKRSMEVLSVTDGSGSPVARRAIEMAHQGQSRSSISGASSGL 360
361 STSPLSSPRVTPHPSPRGSPPLTPKGTPTVHTPKESPAGTNPPTPPSSPSVGGVPMRRLN 420
361 STSPLSSPRVTPHPSPRGSPPLTPKGTPTVHTPKESPAGTNPPTPPSSPSVGGVPMRRLN 420
421 SIKNSFLGSPFRHRRKLVQVPTPEMSNLTPSSPELAKKSWFGNFISLEKEEQIFVVIKD 480
421 SIKNSFLGSPFRHRRKLVQVPTPEMSNLTPSSPELAKKSWFGNFISLEKEEQIFVVIKD 480
481 KPLSSIKADIVHAFSLSPSLSHSVISQTSFRAEYKATGGPAVFOKPVKFOVDITYTEGGE 540
481 KPLSSIKADIVHAFSLSPSLSHSVISQTSFRAEYKATGGPAVFOKPVKFOVDITYTEGGE 540
541 AQKNGIYSVTFTLLSGPSRRFRKRVVETIQALLSTHDPAAQHLSDTTNCMEMMTGRLS 600
541 AQKNGIYSVTFTLLSGPSRRFRKRVVETIQALLSTHDPAAQHLSDTTNCMEMMTGRLS 600
601 KCGIIPKS 608
601 KCGIIPKS 608

RESULT 2

US-10-288-798-18

; Sequence 18, Application US/10288798

; Publication No. US20030207299A1

; GENERAL INFORMATION:

; APPLICANT: BANDMAN, Olga; NGUYEN, Danniell B;
; APPLICANT: WALIA, Naxinder K.; HAPALIA, April J.A.;
; APPLICANT: YAO, Monique G.; GANDHI, Ameena R.;
; APPLICANT: GURURAJAN, Rajagopal; DING, Li;
; APPLICANT: PATTERSON, Chandra; YUE, Henry;
; APPLICANT: BAUGHN, Marian R.; TRIBOULEY, Catherine M.;
; APPLICANT: THORNTON, Michael; ELLIOTT, Vicki S.;
; APPLICANT: LU, Yan; ISON, Craig H.;
; APPLICANT: AU-YOUNG, Janice; TANG, Y. Tom;
; APPLICANT: AZIMZAI, Valda; BURRILL, John D.;
; APPLICANT: MARCUS, Gregory A.; ZINGLER, Kurt A.;
; APPLICANT: LU, Dying Aina M.; LAL, Preeti G.;
; APPLICANT: RAMKUMAR, Jayalaxmi; WARREN, Bridget A.;
; APPLICANT: KEARNEY, Liam; POLICKY, Jennifer L.;
; APPLICANT: THANGAVELU, Kavitha; BURFORD, Neil

; TITLE OF INVENTION: HUMAN KINASES

; FILE REFERENCE: PI-0209 USA

; CURRENT APPLICATION NUMBER: US/10/288,798

; CURRENT FILING DATE: 2002-11-01

; PRIOR APPLICATION NUMBER: PCT/US01/27219

; PRIOR FILING DATE: 2001-08-31

; PRIOR APPLICATION NUMBER: US 60/240,542

; PRIOR FILING DATE: 2000-10-13

; PRIOR APPLICATION NUMBER: US 60/238,389

; PRIOR FILING DATE: 2000-10-06

; PRIOR APPLICATION NUMBER: US 60/236,499

; PRIOR FILING DATE: 2000-09-29

; PRIOR APPLICATION NUMBER: US 60/234,902

; PRIOR FILING DATE: 2000-09-22

; PRIOR APPLICATION NUMBER: US 60/232,654

; PRIOR FILING DATE: 2000-09-14

; PRIOR APPLICATION NUMBER: US 60/231,357

; PRIOR FILING DATE: 2000-09-08

; PRIOR APPLICATION NUMBER: US 60/229,873

; PRIOR FILING DATE: 2000-08-31

; NUMBER OF SEQ ID NOS: 48

; SOFTWARE: PERL Program

; SEQ ID NO 18

; LENGTH: 664

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; OTHER INFORMATION: Incyte ID No. US20030207299A1 4022651CD1

US-10-288-798-18

Query Match

Best Local Similarity 100.0%; Score 3188; DB 12; Length 664;

Matches 608; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKVEREIALKLIIEPHVLKLDVVENKKYLVLEHVSGGELFDYLVKKGRLTPKEARK 60
DB 57 MKVEREIALKLIIEPHVLKLDVVENKKYLVLEHVSGGELFDYLVKKGRLTPKEARK 116
QY 61 FFRQIISALDFCHSHSICHRLDKPENLLDKNNIRIADFGMASIQVDSLLETSCGSPH 120
DB 117 FFRQIISALDFCHSHSICHRLDKPENLLDKNNIRIADFGMASIQVDSLLETSCGSPH 176
QY 121 YACPEVIRGEKYDGRKADVWSCGVILFALLVGLPDDDNLRQLLEKVKRGVFMHPHFIP 180
DB 177 YACPEVIRGEKYDGRKADVWSCGVILFALLVGLPDDDNLRQLLEKVKRGVFMHPHFIP 236
QY 181 PDCQSLLRGMI EVDAAARLTLEHIQKHWIYGGKNEPEPEPIPRKQVIRSLPSLEIDP 240
DB 237 PDCQSLLRGMI EVDAAARLTLEHIQKHWIYGGKNEPEPEPIPRKQVIRSLPSLEIDP 296
QY 241 DVLDMSHSLGCFRDRNKLQDLSEENQKMIYFLLIDRKERYPSQEDDLPNEIDP 300
DB 297 DVLDMSHSLGCFRDRNKLQDLSEENQKMIYFLLIDRKERYPSQEDDLPNEIDP 356
QY 301 PRKRVDSPLNLRHGRKRPKRSMEVLSVTDGSGSPVARRAIEMAHQGQSRSSISGASSGL 360
DB 357 PRKRVDSPLNLRHGRKRPKRSMEVLSVTDGSGSPVARRAIEMAHQGQSRSSISGASSGL 416
QY 361 STSPLSSPRVTPHPSPRGSPPLTPKGTPTVHTPKESPAGTNPPTPPSSPSVGGVPMRRLN 420
DB 417 STSPLSSPRVTPHPSPRGSPPLTPKGTPTVHTPKESPAGTNPPTPPSSPSVGGVPMRRLN 476
QY 421 SIKNSFLGSPFRHRRKLVQVPTPEMSNLTPSSPELAKKSWFGNFISLEKEEQIFVVIKD 480
DB 477 SIKNSFLGSPFRHRRKLVQVPTPEMSNLTPSSPELAKKSWFGNFISLEKEEQIFVVIKD 536
QY 481 KPLSSIKADIVHAFSLSPSLSHSVISQTSFRAEYKATGGPAVFOKPVKFOVDITYTEGGE 540
DB 537 KPLSSIKADIVHAFSLSPSLSHSVISQTSFRAEYKATGGPAVFOKPVKFOVDITYTEGGE 596
QY 541 AQKNGIYSVTFTLLSGPSRRFRKRVVETIQALLSTHDPAAQHLSDTTNCMEMMTGRLS 600
DB 597 AQKNGIYSVTFTLLSGPSRRFRKRVVETIQALLSTHDPAAQHLSDTTNCMEMMTGRLS 656
QY 601 KCGIIPKS 608
DB 657 KCGIIPKS 664

RESULT 3

US-10-054-579-2

; Sequence 2, Application US/10054579

; Publication No. US20020137913A1

; GENERAL INFORMATION:

; APPLICANT: Mathur, Brian

; APPLICANT: Turner, C. Alexander Jr.

; TITLE OF INVENTION: No. US20020137913A1 Human Kinases and Polynucleotides Encoding t

; FILE REFERENCE: LEX-0300-USA

; CURRENT APPLICATION NUMBER: US/10/054,579

; CURRENT FILING DATE: 2002-01-22

; PRIOR APPLICATION NUMBER: US 60/263,378

; PRIOR FILING DATE: 2001-01-23

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 668
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-054-579-2

Query Match 100.0%; Score 3188; DB 14; Length 668;
Best Local Similarity 100.0%; Pred. No. 2.8e-196;
Matches 608; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKVEREAILKLEHHPHVLKLDHVVYENKYLVLVLEHVSGLDFYLVKKGRLTPKEARK 60
DB 61 MKVEREAILKLEHHPHVLKLDHVVYENKYLVLVLEHVSGLDFYLVKKGRLTPKEARK 120

QY 61 FFRQIISALDFCHSHSICHRDLKPENLLDEKNIRIADFGWASLQVGSLLTSCGSPH 120
DB 121 FFRQIISALDFCHSHSICHRDLKPENLLDEKNIRIADFGWASLQVGSLLTSCGSPH 180

QY 121 YACPEVIRGEKYDGRKADWMSCGVILFALLVGLPDDNLRQLLEKVKRGVFMHPHPI 180
DB 181 YACPEVIRGEKYDGRKADWMSCGVILFALLVGLPDDNLRQLLEKVKRGVFMHPHPI 240

QY 181 PDCOSLLRGMIEVDAARLTLEHIQKHIWYIGGKNEPEPEQIPRKQVIRSLPSLEDIDP 240
DB 241 PDCOSLLRGMIEVDAARLTLEHIQKHIWYIGGKNEPEPEQIPRKQVIRSLPSLEDIDP 300

QY 241 DVLDMSHSLGCFRDRNKLQDLLSEENQEKMIYFLLDDRKYRPSQDEDLPPRNEIDP 300
DB 301 DVLDMSHSLGCFRDRNKLQDLLSEENQEKMIYFLLDDRKYRPSQDEDLPPRNEIDP 360

QY 301 PRKRVDSFPLNHRHGKRRPERKSMELSVTDGGSVPARRAEMAQHQRSISGASSGL 360
DB 361 PRKRVDSFPLNHRHGKRRPERKSMELSVTDGGSVPARRAEMAQHQRSISGASSGL 420

QY 361 STSPLSSPRVTPHPSRGSPLTPKGTVPHTPKESPAAGTNPPTSSPSVGVGVPWRARLN 420
DB 421 STSPLSSPRVTPHPSRGSPLTPKGTVPHTPKESPAAGTNPPTSSPSVGVGVPWRARLN 480

QY 421 SIKNSFLGSPRFRHRKLOVTPTEMSNLTPSSPELAKKSWFGNFI SLEKEQIFVVIKD 480
DB 481 SIKNSFLGSPRFRHRKLOVTPTEMSNLTPSSPELAKKSWFGNFI SLEKEQIFVVIKD 540

QY 481 KPLSSIKADIVHAFSLPSLSHVSISQTSFRAEYKATGPAVFKPVKQFVDITVTEGGE 540
DB 541 KPLSSIKADIVHAFSLPSLSHVSISQTSFRAEYKATGPAVFKPVKQFVDITVTEGGE 600

QY 541 AQKENGIVSVTFTLLSGPSRRKRVVETIQALLSTHDPAAQHLSDTTNCMMMTGRSL 600
DB 601 AQKENGIVSVTFTLLSGPSRRKRVVETIQALLSTHDPAAQHLSDTTNCMMMTGRSL 660

QY 601 KCGIIPKS 608
DB 661 KCGIIPKS 668

RESULT 4

US-10-195-072-2
; Sequence 2, Application US/10195072
; Publication No. US20030092036A1
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies
; TITLE OF INVENTION: Full-length Serine Protein Kinase in Brain and Pancreas
; FILE REFERENCE: 16U 101 C2
; CURRENT APPLICATION NUMBER: US/10/195,072
; PRIOR FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: US 09/930,181
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 668
; TYPE: PRT

; ORGANISM: Homo sapiens
US-10-195-072-2

Query Match 100.0%; Score 3188; DB 15; Length 668;
Best Local Similarity 100.0%; Pred. No. 2.8e-196;
Matches 608; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKVEREAILKLEHHPHVLKLDHVVYENKYLVLVLEHVSGLDFYLVKKGRLTPKEARK 60
DB 61 MKVEREAILKLEHHPHVLKLDHVVYENKYLVLVLEHVSGLDFYLVKKGRLTPKEARK 120

QY 61 FFRQIISALDFCHSHSICHRDLKPENLLDEKNIRIADFGWASLQVGSLLTSCGSPH 120
DB 121 FFRQIISALDFCHSHSICHRDLKPENLLDEKNIRIADFGWASLQVGSLLTSCGSPH 180

QY 121 YACPEVIRGEKYDGRKADWMSCGVILFALLVGLPDDNLRQLLEKVKRGVFMHPHPI 180
DB 181 YACPEVIRGEKYDGRKADWMSCGVILFALLVGLPDDNLRQLLEKVKRGVFMHPHPI 240

QY 181 PDCOSLLRGMIEVDAARLTLEHIQKHIWYIGGKNEPEPEQIPRKQVIRSLPSLEDIDP 240
DB 241 PDCOSLLRGMIEVDAARLTLEHIQKHIWYIGGKNEPEPEQIPRKQVIRSLPSLEDIDP 300

QY 241 DVLDMSHSLGCFRDRNKLQDLLSEENQEKMIYFLLDDRKYRPSQDEDLPPRNEIDP 300
DB 301 DVLDMSHSLGCFRDRNKLQDLLSEENQEKMIYFLLDDRKYRPSQDEDLPPRNEIDP 360

QY 301 PRKRVDSFPLNHRHGKRRPERKSMELSVTDGGSVPARRAEMAQHQRSISGASSGL 360
DB 361 PRKRVDSFPLNHRHGKRRPERKSMELSVTDGGSVPARRAEMAQHQRSISGASSGL 420

QY 361 STSPLSSPRVTPHPSRGSPLTPKGTVPHTPKESPAAGTNPPTSSPSVGVGVPWRARLN 420
DB 421 STSPLSSPRVTPHPSRGSPLTPKGTVPHTPKESPAAGTNPPTSSPSVGVGVPWRARLN 480

QY 421 SIKNSFLGSPRFRHRKLOVTPTEMSNLTPSSPELAKKSWFGNFI SLEKEQIFVVIKD 480
DB 481 SIKNSFLGSPRFRHRKLOVTPTEMSNLTPSSPELAKKSWFGNFI SLEKEQIFVVIKD 540

QY 481 KPLSSIKADIVHAFSLPSLSHVSISQTSFRAEYKATGPAVFKPVKQFVDITVTEGGE 540
DB 541 KPLSSIKADIVHAFSLPSLSHVSISQTSFRAEYKATGPAVFKPVKQFVDITVTEGGE 600

QY 541 AQKENGIVSVTFTLLSGPSRRKRVVETIQALLSTHDPAAQHLSDTTNCMMMTGRSL 600
DB 601 AQKENGIVSVTFTLLSGPSRRKRVVETIQALLSTHDPAAQHLSDTTNCMMMTGRSL 660

QY 601 KCGIIPKS 608
DB 661 KCGIIPKS 668

RESULT 5

US-10-195-071-2
; Sequence 2, Application US/10195071
; Publication No. US20030096271A1
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies
; TITLE OF INVENTION: Full-length Serine Protein Kinase in Brain and Pancreas
; FILE REFERENCE: 16U 101 C1
; CURRENT APPLICATION NUMBER: US/10/195,071
; PRIOR FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: US 09/930,181
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 668
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-195-071-2

Query Match 100.0%; Score 3188; DB 15; Length 668;

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Qy 181 PDCQSLRLGMIEVDAAARLTLEHIOKHIWYIGGKNEPEPEQIPRKVQIRSLPSLEDIDP 240
Db 181 PDCQSLRLGMIEVDAAARLTLEHIOKHIWYIGGKNEPEPEQIPRKVQIRSLPSLEDIDP 240
Qy 241 DVLDSMHSGLCFDRDNKLLQDLLSEENQEKMIYFLLDRKERYPSQDEDLPRNEIDP 300
Db 241 DVLDSMHSGLCFDRDNKLLQDLLSEENQEKMIYFLLDRKERYPSQDEDLPRNEIDP 300
Qy 301 PRKRVDSFPLNRHGRKRRPERKSMELSVTDGSGVPARRAEMAHOGRSISGASSGL 360
Db 301 PRKRVDSFPLNRHGRKRRPERKSMELSVTDGSGVPARRAEMAHOGRSISGASSGL 360
Qy 361 STPSLSSPRVTPHPSRGSPPLTPKGTVPHTPKESPAGTNPPTPPSSPSVGVVPMWRARLN 420
Db 361 STPSLSSPRVTPHPSRGSPPLTPKGTVPHTPKESPAGTNPPTPPSSPSVGVVPMWRARLN 420
Qy 421 SIKNSFLGSPRFRHRKLOVPTPEMSNLTPSSSPELAKKSWFGNFISLEKEEQIFVVIKD 480
Db 421 SIKNSFLGSPRFRHRKLOVPTPEMSNLTPSSSPELAKKSWFGNFISLEKEEQIFVVIKD 480
Qy 481 KPLSSIKADIHAFLSIPSLSHSVISQTSFRAEYKATGGPAVFOKPVKFOVDIITYTEGGE 540
Db 481 KPLSSIKADIHAFLSIPSLSHSVISQTSFRAEYKATGGPAVFOKPVKFOVDIITYTEGGE 540
Qy 541 AQKENGISYVFTLLSGPSRRFRKRVVETIQALLSTHDPAPAAQLHSD 587
Db 541 AQKENGISYVFTLLSGPSRRFRKRVVETIQALLSTHDPAPAAQLHSD 587

RESULT 8
US-10-283-247-10
; Sequence 10, Application US/10283247
; Publication No. US20030119037A1
; GENERAL INFORMATION:
; APPLICANT: NEELAM, Beena et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001304
; CURRENT APPLICATION NUMBER: US/10/283,247
; CURRENT FILING DATE: 2002-10-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 614
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-283-247-10

Query Match 96.1%; Score 3065; DB 15; Length 614;
Best Local Similarity 99.7%; Pred. No. 2e-188;
Matches 585; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MKVEREIAILKLIIEHPHVLKLDVYENKYLVLVLEHVS GGELFDYLVKKGLRTPKEARK 60
Db 1 MKVEREIAILKLIIEHPHVLKLDVYENKYLVLVLEHVS GGELFDYLVKKGLRTPKEARK 60
Qy 61 FFRQIISALDFCHSHSICHRLDKPENLLDEKNNIRIADFGMASLQVGDSDLLETSCGSPH 120
Db 61 FFRQIISALDFCHSHSICHRLDKPENLLDEKNNIRIADFGMASLQVGDSDLLETSCGSPH 120
Qy 121 YACPEVIRGEKYDGRKADVWSCGVILFALLVGLPFDNDNRLQLLEKVRGVFHMHPFIP 180
Db 121 YACPEVIRGEKYDGRKADVWSCGVILFALLVGLPFDNDNRLQLLEKVRGVFHMHPFIP 180
Qy 181 PDCQSLRLGMIEVDAAARLTLEHIOKHIWYIGGKNEPEPEQIPRKVQIRSLPSLEDIDP 240
Db 181 PDCQSLRLGMIEVDAAARLTLEHIOKHIWYIGGKNEPEPEQIPRKVQIRSLPSLEDIDP 240
Qy 241 DVLDSMHSGLCFDRDNKLLQDLLSEENQEKMIYFLLDRKERYPSQDEDLPRNEIDP 300
Db 241 DVLDSMHSGLCFDRDNKLLQDLLSEENQEKMIYFLLDRKERYPSQDEDLPRNEIDP 300

Db 241 DVLDSMHSGLCFDRDNKLLQDLLSEENQEKMIYFLLDRKERYPSQDEDLPRNEIDP 300
Qy 301 PRKRVDSFPLNRHGRKRRPERKSMELSVTDGSGVPARRAEMAHOGRSISGASSGL 360
Db 301 PRKRVDSFPLNRHGRKRRPERKSMELSVTDGSGVPARRAEMAHOGRSISGASSGL 360
Qy 361 STPSLSSPRVTPHPSRGSPPLTPKGTVPHTPKESPAGTNPPTPPSSPSVGVVPMWRARLN 420
Db 361 STPSLSSPRVTPHPSRGSPPLTPKGTVPHTPKESPAGTNPPTPPSSPSVGVVPMWRARLN 420
Qy 421 SIKNSFLGSPRFRHRKLOVPTPEMSNLTPSSSPELAKKSWFGNFISLEKEEQIFVVIKD 480
Db 421 SIKNSFLGSPRFRHRKLOVPTPEMSNLTPSSSPELAKKSWFGNFISLEKEEQIFVVIKD 480
Qy 481 KPLSSIKADIHAFLSIPSLSHSVISQTSFRAEYKATGGPAVFOKPVKFOVDIITYTEGGE 540
Db 481 KPLSSIKADIHAFLSIPSLSHSVISQTSFRAEYKATGGPAVFOKPVKFOVDIITYTEGGE 540
Qy 541 AQKENGISYVFTLLSGPSRRFRKRVVETIQALLSTHDPAPAAQLHSD 587
Db 541 AQKENGISYVFTLLSGPSRRFRKRVVETIQALLSTHDPAPAAQLHSD 587

RESULT 9
US-09-842-582-2
; Sequence 2, Application US/09842582
; Patent No. US20020155570A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Meyers, Rachel
; TITLE OF INVENTION: 2246, NOVEL PROTEIN KINASE MOLECULES AND
; TITLE OF INVENTION: USES THEREFOR
; FILE REFERENCE: 38155-20054.00
; CURRENT APPLICATION NUMBER: US/09/842,582
; CURRENT FILING DATE: 2001-04-25
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 674
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-842-582-2

Query Match 96.1%; Score 3065; DB 10; Length 674;
Best Local Similarity 99.7%; Pred. No. 2.2e-188;
Matches 585; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MKVEREIAILKLIIEHPHVLKLDVYENKYLVLVLEHVS GGELFDYLVKKGLRTPKEARK 60
Db 61 MKVEREIAILKLIIEHPHVLKLDVYENKYLVLVLEHVS GGELFDYLVKKGLRTPKEARK 120
Qy 61 FFRQIISALDFCHSHSICHRLDKPENLLDEKNNIRIADFGMASLQVGDSDLLETSCGSPH 120
Db 121 FFRQIISALDFCHSHSICHRLDKPENLLDEKNNIRIADFGMASLQVGDSDLLETSCGSPH 180
Qy 121 YACPEVIRGEKYDGRKADVWSCGVILFALLVGLPFDNDNRLQLLEKVRGVFHMHPFIP 180
Db 181 YACPEVIRGEKYDGRKADVWSCGVILFALLVGLPFDNDNRLQLLEKVRGVFHMHPFIP 240
Qy 181 PDCQSLRLGMIEVDAAARLTLEHIOKHIWYIGGKNEPEPEQIPRKVQIRSLPSLEDIDP 240
Db 241 PDCQSLRLGMIEVDAAARLTLEHIOKHIWYIGGKNEPEPEQIPRKVQIRSLPSLEDIDP 300
Qy 241 DVLDSMHSGLCFDRDNKLLQDLLSEENQEKMIYFLLDRKERYPSQDEDLPRNEIDP 300
Db 301 DVLDSMHSGLCFDRDNKLLQDLLSEENQEKMIYFLLDRKERYPSQDEDLPRNEIDP 360
Qy 301 PRKRVDSFPLNRHGRKRRPERKSMELSVTDGSGVPARRAEMAHOGRSISGASSGL 360
Db 361 PRKRVDSFPLNRHGRKRRPERKSMELSVTDGSGVPARRAEMAHOGRSISGASSGL 420


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QY 361 STPLSSPRVTPHPSGRGSLPTPKGTPTVHTPKESPAGTNPPTPPSPSVGGVFWPWRARLN 420
DB 421 STPLSSPRVTPHPSGRGSLPTPKGTPTVHTPKESPAGTNPPTPPSPSVGGVFWPWRARLN 480
QY 421 SIKNSFLGSPRFRHRKQLQVPTPEEMSNLTPSSPELAKSWFGNFIISLEKEEQIFVWIKD 480
DB 481 SIKNSFLGSPRFRHRKQLQVPTPEEMSNLTPSSPELAKSWFGNFIISLEKEEQIFVWIKD 540
QY 481 KPLSSIKADIIVHAFSLIPSLSHSVISQTSFRAEYKATGGPAVFOKPKVQFVDIITYTEGGE 540
DB 541 KPLSSIKADIIVHAFSLIPSLSHSVISQTSFRAEYKATGGPAVFOKPKVQFVDIITYTEGGE 600
QY 541 AQKENGISYVFTLLSGSPRRFRKRVVETIQALLSTHDPAPAAQHLSD 587
DB 601 AQKENGISYVFTLLSGSPRRFRKRVVETIQALLSTHDPAPAAQHLSE 647

RESULT 10
US-10-283-247-7
; Sequence 7, Application US/10283247
; Publication No. US20030119037A1
; GENERAL INFORMATION:
; APPLICANT: NEELAM, Beena et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001304
; CURRENT APPLICATION NUMBER: US/10/283,247
; CURRENT FILING DATE: 2002-10-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 674
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-283-247-7

Query Match 96.1%; Score 3065; DB 15; Length 674;
Best Local Similarity 99.7%; Pred. No. 2.2e-188;
Matches 585; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKVEREIAILKLIIEHPHVLKLDHVVYENKKYLYLVLEHVS GGELFDYLVKKGR LTPKEARK 60
DB 61 MKVEREIAILKLIIEHPHVLKLDHVVYENKKYLYLVLEHVS GGELFDYLVKKGR LTPKEARK 120
QY 61 FFRQIISALDFCHSHSICHRLDKPENLLDEKNNIRIADFGMASLQVGD SILETSCGSPH 120
DB 121 FFRQIISALDFCHSHSICHRLDKPENLLDEKNNIRIADFGMASLQVGD SILETSCGSPH 180
QY 121 YACPEVIRGEKYDGRKADVWSCGVILFALLVGLALPDDDNLRQLLEKVKRGVFMHPHPI 180
DB 181 YACPEVIRGEKYDGRKADVWSCGVILFALLVGLALPDDDNLRQLLEKVKRGVFMHPHPI 240
QY 181 PDCOSLLRGMIENVDAARLTLEHIOKHIWIIGKNVEPEEQIPRKVQIRSLPSLEDIDP 240
DB 241 PDCOSLLRGMIENVDAARLTLEHIOKHIWIIGKNVEPEEQIPRKVQIRSLPSLEDIDP 300
QY 241 DVLDMSHSLGCFDRDNKLLQDLLSEENQEKMIYFLLLDKERYPSQDEDLPPRNEIDP 300
DB 301 DVLDMSHSLGCFDRDNKLLQDLLSEENQEKMIYFLLLDKERYPSQDEDLPPRNEIDP 360
QY 301 PRKRVDSFPLNRHGKRRPERKSMVLSVTDGSGVPARRAIEAQAHQGRSRSISGASSGL 360
DB 361 PRKRVDSFPLNRHGKRRPERKSMVLSVTDGSGVPARRAIEAQAHQGRSRSISGASSGL 420
QY 421 STPLSSPRVTPHPSGRGSLPTPKGTPTVHTPKESPAGTNPPTPPSPSVGGVFWPWRARLN 420
DB 481 STPLSSPRVTPHPSGRGSLPTPKGTPTVHTPKESPAGTNPPTPPSPSVGGVFWPWRARLN 480
QY 481 SIKNSFLGSPRFRHRKQLQVPTPEEMSNLTPSSPELAKSWFGNFIISLEKEEQIFVWIKD 480
DB 541 SIKNSFLGSPRFRHRKQLQVPTPEEMSNLTPSSPELAKSWFGNFIISLEKEEQIFVWIKD 540
QY 541 AQKENGISYVFTLLSGSPRRFRKRVVETIQALLSTHDPAPAAQHLSD 587
DB 601 AQKENGISYVFTLLSGSPRRFRKRVVETIQALLSTHDPAPAAQHLSE 647
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QY 481 KPLSSIKADIIVHAFSLIPSLSHSVISQTSFRAEYKATGGPAVFOKPKVQFVDIITYTEGGE 540
DB 541 KPLSSIKADIIVHAFSLIPSLSHSVISQTSFRAEYKATGGPAVFOKPKVQFVDIITYTEGGE 600
QY 541 AQKENGISYVFTLLSGSPRRFRKRVVETIQALLSTHDPAPAAQHLSD 587
DB 601 AQKENGISYVFTLLSGSPRRFRKRVVETIQALLSTHDPAPAAQHLSE 647

RESULT 11
US-10-283-247-8
; Sequence 8, Application US/10283247
; Publication No. US20030119037A1
; GENERAL INFORMATION:
; APPLICANT: NEELAM, Beena et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001304
; CURRENT APPLICATION NUMBER: US/10/283,247
; CURRENT FILING DATE: 2002-10-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 674
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-283-247-8

Query Match 96.1%; Score 3065; DB 15; Length 674;
Best Local Similarity 99.7%; Pred. No. 2.2e-188;
Matches 585; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKVEREIAILKLIIEHPHVLKLDHVVYENKKYLYLVLEHVS GGELFDYLVKKGR LTPKEARK 60
DB 61 MKVEREIAILKLIIEHPHVLKLDHVVYENKKYLYLVLEHVS GGELFDYLVKKGR LTPKEARK 120
QY 61 FFRQIISALDFCHSHSICHRLDKPENLLDEKNNIRIADFGMASLQVGD SILETSCGSPH 120
DB 121 FFRQIISALDFCHSHSICHRLDKPENLLDEKNNIRIADFGMASLQVGD SILETSCGSPH 180
QY 121 YACPEVIRGEKYDGRKADVWSCGVILFALLVGLALPDDDNLRQLLEKVKRGVFMHPHPI 180
DB 181 YACPEVIRGEKYDGRKADVWSCGVILFALLVGLALPDDDNLRQLLEKVKRGVFMHPHPI 240
QY 181 PDCOSLLRGMIENVDAARLTLEHIOKHIWIIGKNVEPEEQIPRKVQIRSLPSLEDIDP 240
DB 241 PDCOSLLRGMIENVDAARLTLEHIOKHIWIIGKNVEPEEQIPRKVQIRSLPSLEDIDP 300
QY 241 DVLDMSHSLGCFDRDNKLLQDLLSEENQEKMIYFLLLDKERYPSQDEDLPPRNEIDP 300
DB 301 DVLDMSHSLGCFDRDNKLLQDLLSEENQEKMIYFLLLDKERYPSQDEDLPPRNEIDP 360
QY 301 PRKRVDSFPLNRHGKRRPERKSMVLSVTDGSGVPARRAIEAQAHQGRSRSISGASSGL 360
DB 361 PRKRVDSFPLNRHGKRRPERKSMVLSVTDGSGVPARRAIEAQAHQGRSRSISGASSGL 420
QY 361 STPLSSPRVTPHPSGRGSLPTPKGTPTVHTPKESPAGTNPPTPPSPSVGGVFWPWRARLN 420
DB 421 STPLSSPRVTPHPSGRGSLPTPKGTPTVHTPKESPAGTNPPTPPSPSVGGVFWPWRARLN 480
QY 421 SIKNSFLGSPRFRHRKQLQVPTPEEMSNLTPSSPELAKSWFGNFIISLEKEEQIFVWIKD 480
DB 481 SIKNSFLGSPRFRHRKQLQVPTPEEMSNLTPSSPELAKSWFGNFIISLEKEEQIFVWIKD 540
QY 481 KPLSSIKADIIVHAFSLIPSLSHSVISQTSFRAEYKATGGPAVFOKPKVQFVDIITYTEGGE 540
DB 541 KPLSSIKADIIVHAFSLIPSLSHSVISQTSFRAEYKATGGPAVFOKPKVQFVDIITYTEGGE 600
QY 541 AQKENGISYVFTLLSGSPRRFRKRVVETIQALLSTHDPAPAAQHLSD 587
DB 601 AQKENGISYVFTLLSGSPRRFRKRVVETIQALLSTHDPAPAAQHLSE 647
```

RESULT 12

US-10-283-247-5
; Sequence 5, Application US/10283247
; Publication No. US20030119037A1
; GENERAL INFORMATION:
; APPLICANT: NEELAM, Beena et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; THEREOF
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001304
; CURRENT APPLICATION NUMBER: US/10/283,247
; CURRENT FILING DATE: 2002-10-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 636
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-283-247-5

Query Match 95.7%; Score 3050; DB 15; Length 636;
Best Local Similarity 96.2%; Pred. No. 1.9e-187;
Matches 586; Conservative 1; Mismatches 0; Indels 22; Gaps 1;

Qy 1 MKVEREIAILKLIIEHPHVLKLDHVVYENKKYLYLVLEHVSQGGELFDYLVKGRITPKARK 60
Db 1 MKVEREIAILKLIIEHPHVLKLDHVVYENKKYLYLVLEHVSQGGELFDYLVKGRITPKARK 60

Qy 61 FFRQIISALDFCHSHSICHRLDKPENLLDEKNNIRIADFQWASLQVDSLSLETSCGSPH 120
Db 61 FFRQIISALDFCHSHSICHRLDKPENLLDEKNNIRIADFQWASLQVDSLSLETSCGSPH 120

Qy 121 YACPEVIRGEKYDGRKADWVSCGVTILFALLVQALPFDDNNLRQLLEKVRGVFMPHFIP 180
Db 121 YACPEVIRGEKYDGRKADWVSCGVTILFALLVQALPFDDNNLRQLLEKVRGVFMPHFIP 180

Qy 181 PDCQSLRGMIEVDAARLTLEHQQHLYWYIGGKNEPEPEPIPRKQVIRSLPSLEIDP 240
Db 181 PDCQSLRGMIEVDAARLTLEHQQHLYWYIGGKNEPEPEPIPRKQVIRSLPSLEIDP 240

Qy 241 DVLDSMHSGLCFDRNKLQDLLSEENQEKMIYFLLLDRKERYPSQDEDELPNRNEIDP 300
Db 241 DVLDSMHSGLCFDRNKLQDLLSEENQEKMIYFLLLDRKERYPSQDEDELPNRNEIDP 300

Qy 301 PRKRVDSPLNRHGKRRPERKSMVLSVTDGSGSPVPARRAIEAQAQSG 348
Db 301 PRKRVDSPLNRHGKRRPERKSMVLSVTDGSGSPVPARRAIEAQAQSG 360

Qy 349 -----RSRSISGASSGLSTSPSSPRVTPHPSPRGSPPLTPKGTPTKESPA 398
Db 361 EAHQFQSKEDRSRISGASSGLSTSPSSPRVTPHPSPRGSPPLTPKGTPTKESPA 420

Qy 399 TPNPTPSSPSVGVVPMRRLNSIKNSFLGSPRFRHRLKQVPTPEMSNLTPSSPELAK 458
Db 421 TPNPTPSSPSVGVVPMRRLNSIKNSFLGSPRFRHRLKQVPTPEMSNLTPSSPELAK 480

Qy 459 KSWFGNFTLSLEKEQIFVVIKDKPLSSIKADIVHAFSLIPSLSHSVISQTSFRAYKATG 518
Db 481 KSWFGNFTLSLEKEQIFVVIKDKPLSSIKADIVHAFSLIPSLSHSVISQTSFRAYKATG 540

Qy 519 GPAVFQKPVKFQVDITYTTEGGAQKENGIVSVTFTLLSGPSRRFRKRVETIQALLSTHD 578
Db 541 GPAVFQKPVKFQVDITYTTEGGAQKENGIVSVTFTLLSGPSRRFRKRVETIQALLSTHD 600

Qy 579 PPAQAHLSD 587
Db 601 PPAQAHLSE 609

RESULT 13

US-10-195-072-4

; Sequence 4, Application US/10195072
; Publication No. US20030092036A1
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies
; TITLE OF INVENTION: Full-Length Serine Protein Kinase in Brain and Pancreas
; FILE REFERENCE: 16U 101 C2
; CURRENT APPLICATION NUMBER: US/10/195,072
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: US 09/930,181
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-195-072-4

Query Match 95.0%; Score 3028; DB 15; Length 585;
Best Local Similarity 100.0%; Pred. No. 4.3e-186;
Matches 577; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 YLVLEHVSQGGELFDYLVKGRITPKARKFFROIISALDFCHSHSICHRLDKPENLLDE 91
Db 9 YLVLEHVSQGGELFDYLVKGRITPKARKFFROIISALDFCHSHSICHRLDKPENLLDE 68

Qy 92 KNNIRIADFQWASLQVDSLSLETSCGSPHYACPEVIRGEKYDGRKADWVSCGVTILFALLV 151
Db 69 KNNIRIADFQWASLQVDSLSLETSCGSPHYACPEVIRGEKYDGRKADWVSCGVTILFALLV 128

Qy 152 GALPFDDNNLRQLLEKVRGVFMPHFIPDPCQSLRGMIEVDAARLTLEHQQHLYWYI 211
Db 129 GALPFDDNNLRQLLEKVRGVFMPHFIPDPCQSLRGMIEVDAARLTLEHQQHLYWYI 188

Qy 212 GGNKEPEPEPIPRKQVIRSLPSLEIDPDLDSMHSGLCFDRNKLQDLLSEENQEK 271
Db 189 GGNKEPEPEPIPRKQVIRSLPSLEIDPDLDSMHSGLCFDRNKLQDLLSEENQEK 248

Qy 272 MIYFLLLDRKERYPSQDEDELPNRNEIDPDKRVDSPLNRHGKRRPERKSMVLSVTDG 331
Db 249 MIYFLLLDRKERYPSQDEDELPNRNEIDPDKRVDSPLNRHGKRRPERKSMVLSVTDG 308

Qy 332 GSPVPARRAIEAQAQSGRSISGASSGLSTSPSSPRVTPHPSPRGSPPLTPKGTPTVHT 391
Db 309 GSPVPARRAIEAQAQSGRSISGASSGLSTSPSSPRVTPHPSPRGSPPLTPKGTPTVHT 368

Qy 392 PKESPAGTPTNPTPSSPSVGVVPMRRLNSIKNSFLGSPRFRHRLKQVPTPEMSNLTP 451
Db 369 PKESPAGTPTNPTPSSPSVGVVPMRRLNSIKNSFLGSPRFRHRLKQVPTPEMSNLTP 428

Qy 452 SSPELAKSWFGNFIISLEKEQIFVVIKDKPLSSIKADIVHAFSLIPSLSHSVISQTSFR 511
Db 429 SSPELAKSWFGNFIISLEKEQIFVVIKDKPLSSIKADIVHAFSLIPSLSHSVISQTSFR 488

Qy 512 ABEKATGPAVFQKPVKFQVDITYTTEGGAQKENGIVSVTFTLLSGPSRRFRKRVETIQ 571
Db 489 ABEKATGPAVFQKPVKFQVDITYTTEGGAQKENGIVSVTFTLLSGPSRRFRKRVETIQ 548

Qy 572 QLLSTHDPAAQHLSDTTNCMMMTGRLSKCGIIPKS 608
Db 549 QLLSTHDPAAQHLSDTTNCMMMTGRLSKCGIIPKS 585

RESULT 14

US-10-195-071-4
; Sequence 4, Application US/10195071
; Publication No. US20030096271A1
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies
; TITLE OF INVENTION: Full-Length Serine Protein Kinase in Brain and Pancreas
; FILE REFERENCE: 16U 101 C1
; CURRENT APPLICATION NUMBER: US/10/195,071
; CURRENT FILING DATE: 2002-07-15

;; PRIOR APPLICATION NUMBER: US 09/930,181
;; PRIOR FILING DATE: 2001-08-16
;; NUMBER OF SEQ ID NOS: 18
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 4
;; LENGTH: 585
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-195-072-4

Query Match 95.0%; Score 3028; DB 15; Length 585;
Best Local Similarity 100.0%; Pred. No. 4.3e-186;
Matches 577; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	32	YLVLHVSGGELFDYLVKKGRLTPEARKFQIISALDCHSHSICHRLKPENLLDE	91
DB	9	YLVLHVSGGELFDYLVKKGRLTPEARKFQIISALDCHSHSICHRLKPENLLDE	68
QY	92	KNNIRIADFGWASLQVGSLLTSCGSPHYACPEVIRGEKYDGRKADWVSCGVLFPALLV	151
DB	69	KNNIRIADFGWASLQVGSLLTSCGSPHYACPEVIRGEKYDGRKADWVSCGVLFPALLV	128
QY	152	GALPFDNDNLQQLLEKVKRGVFMHPHFIPDPQCSLLRGMIEVDAAKRLTLEHIQKHIWI	211
DB	129	GALPFDNDNLQQLLEKVKRGVFMHPHFIPDPQCSLLRGMIEVDAAKRLTLEHIQKHIWI	108
QY	212	GKKEPEPEQIPRKVQIRSLPSLEDIDPDVLSMHSILGCFDRNKLQDLLSEENOEK	271
DB	189	GKKEPEPEQIPRKVQIRSLPSLEDIDPDVLSMHSILGCFDRNKLQDLLSEENOEK	248
QY	272	MIYFLLLDKERYPSQEDDLPPRNEIDPPRKRVDSPMLNRHGRKRRPERKSMEVLSVTDG	331
DB	249	MIYFLLLDKERYPSQEDDLPPRNEIDPPRKRVDSPMLNRHGRKRRPERKSMEVLSVTDG	308
QY	332	GSPVARRAIEMAHQGRSISGASSGLSTPSLSSPRVTPHPSRGSPLTPKGTVPVHT	391
DB	309	GSPVARRAIEMAHQGRSISGASSGLSTPSLSSPRVTPHPSRGSPLTPKGTVPVHT	368
QY	392	PKESPAQTNPPTSSPSVGVVPMRRLNSIKNSFLGSPRHRKLOVPTPEEMSNLTPE	451
DB	369	PKESPAQTNPPTSSPSVGVVPMRRLNSIKNSFLGSPRHRKLOVPTPEEMSNLTPE	428
QY	452	SSPELAKKSWFGNFIISLEKEEQIFVWIKDKPLSSIKADIVHAFSLPSLSHSVISQTSFR	511
DB	429	SSPELAKKSWFGNFIISLEKEEQIFVWIKDKPLSSIKADIVHAFSLPSLSHSVISQTSFR	488
QY	512	AEYKATGAPAVFQKPVKQVDITYTEGGEAQKENGISYVTFLLSGPSRRRFRKRVVETIQ	571
DB	489	AEYKATGAPAVFQKPVKQVDITYTEGGEAQKENGISYVTFLLSGPSRRRFRKRVVETIQ	548
QY	572	QLLSTHDPAAQHLSDTTNCMEMMTGRLSKGIIPKS	608
DB	549	QLLSTHDPAAQHLSDTTNCMEMMTGRLSKGIIPKS	585

RESULT 15
US-10-195-072-17
; Sequence 17, Application US/10195072
; Publication No. US20030092036A1
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies
; TITLE OF INVENTION: Full-Length Serine Protein Kinase in Brain and Pancreas
; FILE REFERENCE: 16U 101 C2
; CURRENT APPLICATION NUMBER: US/10/195,072
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: US 09/930,181
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 603
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-195-072-17

Query Match 94.6%; Score 3015; DB 15; Length 603;
Best Local Similarity 99.7%; Pred. No. 3.1e-185;
Matches 574; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY	12	LIEHPHVLKLDVYENKYLVLVSHVSGGELFDYLVKKGRLTPEARKFFQIISALDF	71
DB	1	LIEHPHVLKLDVYENKYLVLVSHVSGGELFDYLVKKGRLTPEARKFFQIISALDF	60
QY	72	CHSHSICHRLDKPENLLDCKNNIRIADFGWASLQVGSLLTSCGSPHYACPEVIRGK	131
DB	61	CHSHSICHRLDKPENLLDCKNNIRIADFGWASLQVGSLLTSCGSPHYACPEVIRGK	120
QY	132	YDGRKADWVSCGVLFPALLVGVGALPDDNDNLROLLEKVKRGVFMHPHFIPDQCQSLRGM	191
DB	121	YDGRKADWVSCGVLFPALLVGVGALPDDNDNLROLLEKVKRGVFMHPHFIPDQCQSLRGM	180
QY	192	EYDAARRLTLEHIQKHIWIYGGKNEPEPEQIPRKVQIRSLPSLEDIDPDVLSMHSILG	251
DB	181	EYDAARRLTLEHIQKHIWIYGGKNEPEPEQIPRKVQIRSLPSLEDIDPDVLSMHSILG	240
QY	252	FRDRNKLQDLLSEENOEKMIYFLLLDKERYPSQEDDLPPRNEIDPPRKRVDSPMLN	311
DB	241	FRDRNKLQDLLSEENOEKMIYFLLLDKERYPSQEDDLPPRNEIDPPRKRVDSPMLN	300
QY	312	RHGRKRRPERKSMEVLSVTDGSGSPVARRAIEMAHQGRSISGASSGLSTPSLSSPRVT	371
DB	301	RHGRKRRPERKSMEVLSVTDGSGSPVARRAIEMAHQGRSISGASSGLSTPSLSSPRVT	360
QY	372	PHPSRGSPLTPKGTVPVHTPKESPAQTNPPTSSPSVGVVPMRRLNSIKNSFLGSPR	431
DB	361	PHPSRGSPLTPKGTVPVHTPKESPAQTNPPTSSPSVGVVPMRRLNSIKNSFLGSPR	420
QY	432	FHRKLOVPTPEEMSNLTPESSPELAKKSWFGNFIISLEKEEQIFVWIKDKPLSSIKADIV	491
DB	421	FHRKLOVPTPEEMSNLTPESSPELAKKSWFGNFIISLEKEEQIFVWIKDKPLSSIKADIV	480
QY	492	HAFSLPSLSHSVISQTSFRAEYKATGGPAVFOKPVKQVDITYTEGGEAQKENGISYVT	551
DB	481	HAFSLPSLSHSVISQTSFRAEYKATGGPAVFOKPVKQVDITYTEGGEAQKENGISYVT	540
QY	552	FTLLSGPSRRRFRKRVVETIQALLSTHDPAAQHLSD	587
DB	541	FTLLSGPSRRRFRKRVVETIQALLSTHDPAAQHLSE	576

Search completed: November 26, 2003, 12:11:03
Job time : 27.7304 secs

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OM protein - protein search, using sw model

Run on: November 26, 2003, 11:58:31 ; Search time 15.7053 Seconds
(without alignments)
1799.622 Million cell updates/sec

Title: US-10-054-579-2

Perfect score: 3497

Sequence: 1 MTSTGKGGGAHQYVGPYR.....TNCMEMTGRLSKCGIIPKS 668

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_AA*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pap:**
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pap:**
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pap:**
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pap:**
- 5: /cgn2_6/ptodata/1/iaa/ECTUS_COMB.pap:**
- 6: /cgn2_6/ptodata/1/iaa/backfiles.pap:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3497	100.0	668	US-09-930-181-2	Sequence 2, Appli
2	3028	86.6	585	US-09-930-181-4	Sequence 4, Appli
3	3015	86.2	603	US-09-930-181-17	Sequence 17, Appl
4	796.5	22.8	745	US-09-523-849-36	Sequence 36, Appl
5	793.5	22.7	724	US-09-984-890-2	Sequence 2, Appli
6	792.5	22.7	722	US-09-984-890-4	Sequence 4, Appli
7	790.5	22.6	722	US-08-817-832B-32	Sequence 32, Appl
8	768.5	22.0	729	US-08-677-298-2	Sequence 2, Appli
9	768.5	22.0	729	US-09-523-849-33	Sequence 33, Appl
10	764.5	21.9	793	US-09-523-849-32	Sequence 32, Appl
11	749	21.4	776	US-09-523-849-34	Sequence 34, Appl
12	749	21.4	779	US-08-817-832B-31	Sequence 31, Appl
13	729.5	20.9	552	US-08-557-006C-40	Sequence 40, Appl
14	720.5	20.6	633	US-08-557-006C-43	Sequence 43, Appl
15	718.5	20.5	345	US-09-101-146-1	Sequence 1, Appli
16	694.5	19.9	257	US-07-857-224B-6	Sequence 6, Appli
17	681	19.5	257	US-09-101-146-1	Sequence 1, Appli
18	680	19.4	149	US-09-930-181-18	Sequence 18, Appl
19	670.5	19.2	604	US-09-523-849-35	Sequence 35, Appl
20	599.5	17.1	631	US-09-579-664B-11	Sequence 11, Appl
21	523	15.0	290	US-09-734-673-4	Sequence 4, Appli
22	523	15.0	334	US-09-523-849-31	Sequence 31, Appl
23	520.5	14.9	252	US-07-857-224B-26	Sequence 26, Appl
24	515.5	14.7	436	US-09-734-673-2	Sequence 2, Appli
25	515.5	14.7	436	US-09-523-849-2	Sequence 2, Appli
26	506.5	14.5	260	US-07-857-224B-27	Sequence 27, Appl
27	501	14.3	353	US-08-688-988-31	Sequence 31, Appl

28	491.5	14.1	556	4	US-09-800-960-4	Sequence 4, Appli
29	490	14.0	363	3	US-08-688-988-30	Sequence 30, Appl
30	488.5	14.0	260	3	US-07-857-224B-28	Sequence 28, Appl
31	485	13.9	339	3	US-08-688-988-13	Sequence 13, Appl
32	485	13.9	351	3	US-08-688-988-28	Sequence 28, Appl
33	485	13.9	565	4	US-09-800-960-2	Sequence 2, Appli
34	481	13.8	354	3	US-08-688-988-29	Sequence 29, Appl
35	471.5	13.5	359	3	US-08-688-988-32	Sequence 32, Appl
36	469.5	13.4	1037	4	US-09-428-711A-21	Sequence 21, Appl
37	467.5	13.4	339	3	US-08-688-988-2	Sequence 2, Appli
38	466.5	13.3	295	1	US-07-951-715A-23	Sequence 23, Appl
39	466.5	13.3	295	2	US-08-459-448A-23	Sequence 23, Appl
40	466.5	13.3	295	3	US-08-459-595A-23	Sequence 23, Appl
41	466.5	13.3	295	3	US-08-459-504B-23	Sequence 23, Appl
42	466.5	13.3	295	3	US-08-459-444-23	Sequence 23, Appl
43	466.5	13.3	295	4	US-09-547-422-23	Sequence 23, Appl
44	463.5	13.3	433	2	US-08-913-050A-7	Sequence 7, Appli
45	463.5	13.3	433	2	US-08-749-902-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-09-930-181-2
Sequence 2, Application US/09930181
Patent No. 6455292
GENERAL INFORMATION:
APPLICANT: Origene Technologies
TITLE OF INVENTION: Full-Length Serine Protein Kinase in Brain and Pancreas
FILE REFERENCE: 160 101 V1
CURRENT APPLICATION NUMBER: US/09/930,181
CURRENT FILING DATE: 2001-08-16
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 668
TYPE: PRT
ORGANISM: Homo sapiens
US-09-930-181-2

Query Match 100.0%; Score 3497; DB 4; Length 668;
Best Local Similarity 100.0%; Pred. No. 3.4e-251;
Matches 668; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MTSTGKGGGAHQYVGPYRLEKTLGKGQGLVGLGVHCVTCQKVAIKIVNREKLSVVL	60
Db	1	MTSTGKGGGAHQYVGPYRLEKTLGKGQGLVGLGVHCVTCQKVAIKIVNREKLSVVL	60
Qy	61	MKVEREIAILKLEIHPHVLKLDVYENKYLVLVLEHVSGLGELFDYLVKGRLLTPKEARK	120
Db	61	MKVEREIAILKLEIHPHVLKLDVYENKYLVLVLEHVSGLGELFDYLVKGRLLTPKEARK	120
Qy	121	PFROIISALDFCHSHSICHRLDKPENLLDEKKNIRIADFGMASLQVDSLETSCGSPH	180
Db	121	PFROIISALDFCHSHSICHRLDKPENLLDEKKNIRIADFGMASLQVDSLETSCGSPH	180
Qy	181	YACFEVIRGEKIDCKADVNSCGVILFALLVGLPFPDDNLRQLLEKVKRGVFMHPFIP	240
Db	181	YACFEVIRGEKIDCKADVNSCGVILFALLVGLPFPDDNLRQLLEKVKRGVFMHPFIP	240
Qy	241	PDCQSLLRGMIEVDAAARLLTLEHIQKIWIYIGKNPEPEQPIPRKQVIRSLPSLEIDP	300
Db	241	PDCQSLLRGMIEVDAAARLLTLEHIQKIWIYIGKNPEPEQPIPRKQVIRSLPSLEIDP	300
Qy	301	DVLDSMSLGCFRDRNKLQDLSSEENQEKMIYFLLDRKERYPSQDEDLPPRNEIDP	360
Db	301	DVLDSMSLGCFRDRNKLQDLSSEENQEKMIYFLLDRKERYPSQDEDLPPRNEIDP	360
Qy	361	PRKVDSPMLNRHCKRRPERKSMELSVTDGGSVPARRAITEMAQHGQSRSSISGASSGL	420
Db	361	PRKVDSPMLNRHCKRRPERKSMELSVTDGGSVPARRAITEMAQHGQSRSSISGASSGL	420

5962312

QY 421 STGPLSPRVTPHPSPRGSLPTPKGTVPVHTPKESPAGTNPPTPPSPSPVGGVPMARLN 480
DB 421 STGPLSPRVTPHPSPRGSLPTPKGTVPVHTPKESPAGTNPPTPPSPSPVGGVPMARLN 480
QY 481 SIKNSFLGSPRRHRKLVQVTPPEMSNLTPESSPELAKSWFGNFISLEKEQIFVVIKD 540
DB 481 SIKNSFLGSPRRHRKLVQVTPPEMSNLTPESSPELAKSWFGNFISLEKEQIFVVIKD 540
QY 541 KPLSSIKADIVHAPLSIPSLSHSVISOTSPRAEYKATGGPAVKFQVDFVITTEGGE 600
DB 541 KPLSSIKADIVHAPLSIPSLSHSVISOTSPRAEYKATGGPAVKFQVDFVITTEGGE 600
QY 601 AQKENGYSYVFTLLSGSPRRFRKRVETIOAQLSTHDDPPAAQHLSDTTNCMEMMTGRLS 660
DB 601 AQKENGYSYVFTLLSGSPRRFRKRVETIOAQLSTHDDPPAAQHLSDTTNCMEMMTGRLS 660
QY 661 KCGIIPKS 668
DB 661 KCGIIPKS 668

RESULT 2
US-09-930-181-4
; Sequence 4, Application US/09930181
; Patent No. 6455292
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies
; TITLE OF INVENTION: Full-Length Serine Protein Kinase in Brain and Pancreas
; FILE REFERENCE: 160 101 VI
; CURRENT APPLICATION NUMBER: US/09/930,181
; CURRENT FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-930-181-4

Query Match 86.6%; Score 3028; DB 4; Length 585;
Best Local Similarity 100.0%; Pred. No. 1.7e-216;
Matches 577; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 92 YLVLEHVS GSGELFDYLVKKGRLTPKEARKFPRIISALDFCHSHSICHRLKPNLLDE 151
DB 9 YLVLEHVS GSGELFDYLVKKGRLTPKEARKFPRIISALDFCHSHSICHRLKPNLLDE 68
QY 152 KNRIADFGMASLQVGDLSLETSCGSPHYACPEVIRGEKYDGRKADVWSCGVILFALLV 211
DB 69 KNRIADFGMASLQVGDLSLETSCGSPHYACPEVIRGEKYDGRKADVWSCGVILFALLV 128
QY 212 GALPDDNLRQLLEKVKRGVFMHPHFTPPDCQSLLRGMIEVDAARLTLEHIQKHIWYI 271
DB 129 GALPDDNLRQLLEKVKRGVFMHPHFTPPDCQSLLRGMIEVDAARLTLEHIQKHIWYI 188
QY 272 GKGNEPEQIPRKVQIRSLPSLEIDDPDVLDSMHSIGCFRDRNKLQDLLSEENQEK 331
DB 189 GKGNEPEQIPRKVQIRSLPSLEIDDPDVLDSMHSIGCFRDRNKLQDLLSEENQEK 248
QY 332 MIYFLLDRKERYPSQEDLPPRNEIDPPRKVDSPMLNHRGKRRPERKSMVLSVTDG 391
DB 249 MIYFLLDRKERYPSQEDLPPRNEIDPPRKVDSPMLNHRGKRRPERKSMVLSVTDG 308
QY 392 GSPVARRAIEMAHQGRSRISGASSGLSTSPSSPRVTPHPSPRGSLPTPKGTVPHT 451
DB 309 GSPVARRAIEMAHQGRSRISGASSGLSTSPSSPRVTPHPSPRGSLPTPKGTVPHT 368
QY 452 PKESPAGTNPPTPPSPSPVGGVPMARLNSIKNSFLGSPRRHRKLVQVTPPEMSNLTPE 511
DB 369 PKESPAGTNPPTPPSPSPVGGVPMARLNSIKNSFLGSPRRHRKLVQVTPPEMSNLTPE 428
QY 512 SSPELAKSWFGNFISLEKEQIFVVIKDPLSSIKADIVHAPLSIPSLSHSVISOTSFR 571

DB 429 SSPELAKSWFGNFISLEKEQIFVVIKDPLSSIKADIVHAPLSIPSLSHSVISOTSFR 488
QY 572 ABYKATGGPAVKFQVDFVITTEGGEAQKENGYSYVFTLLSGSPRRFRKRVETIOA 631
DB 489 ABYKATGGPAVKFQVDFVITTEGGEAQKENGYSYVFTLLSGSPRRFRKRVETIOA 548
QY 632 QLLSTHDDPPAAQHLSDTTNCMEMMTGRLSKCGIIPKS 668
DB 549 QLLSTHDDPPAAQHLSDTTNCMEMMTGRLSKCGIIPKS 585

RESULT 3
US-09-930-181-17
; Sequence 17, Application US/09930181
; Patent No. 6455292
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies
; TITLE OF INVENTION: Full-Length Serine Protein Kinase in Brain and Pancreas
; FILE REFERENCE: 160 101 VI
; CURRENT APPLICATION NUMBER: US/09/930,181
; CURRENT FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 603
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-930-181-17

Query Match 86.2%; Score 3015; DB 4; Length 603;
Best Local Similarity 99.7%; Pred. No. 1.6e-215;
Matches 574; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 72 LIEHPVLKLDVYENKYLVLVLEHVS GSGELFDYLVKKGRLTPKEARKFPRIISALDF 131
DB 1 LIEHPVLKLDVYENKYLVLVLEHVS GSGELFDYLVKKGRLTPKEARKFPRIISALDF 60
QY 132 CHSHSICHRLKPNLLDEKNRIADFGMASLQVGDLSLETSCGSPHYACPEVIRGEK 191
DB 61 CHSHSICHRLKPNLLDEKNRIADFGMASLQVGDLSLETSCGSPHYACPEVIRGEK 120
QY 192 YDGRKADVWSCGVILFALLVGLPDDNLRQLLEKVKRGVFMHPHFTPPDCQSLLRGM 251
DB 121 YDGRKADVWSCGVILFALLVGLPDDNLRQLLEKVKRGVFMHPHFTPPDCQSLLRGM 180
QY 252 EVDAARLTLEHIQKHIWYIGGKNEPEQIPRKVQIRSLPSLEIDDPDVLDSMHSIG 311
DB 181 EVDAARLTLEHIQKHIWYIGGKNEPEQIPRKVQIRSLPSLEIDDPDVLDSMHSIG 240
QY 312 FRDRNKLQDLLSEENQEKMIYFLLDRKERYPSQEDLPPRNEIDPPRKVDSPMLN 371
DB 241 FRDRNKLQDLLSEENQEKMIYFLLDRKERYPSQEDLPPRNEIDPPRKVDSPMLN 300
QY 372 RHGKRPERKSMVLSVTDGSPVARRAIEMAHQGRSRISGASSGLSTSPSSPRVT 431
DB 301 RHGKRPERKSMVLSVTDGSPVARRAIEMAHQGRSRISGASSGLSTSPSSPRVT 360
QY 432 PHPSRGSLPTPKGTVPVHTPKESPAGTNPPTPPSPSPVGGVPMARLNSIKNSFLGSP 491
DB 361 PHPSRGSLPTPKGTVPVHTPKESPAGTNPPTPPSPSPVGGVPMARLNSIKNSFLGSP 420
QY 492 FHRKLVQVTPPEMSNLTPESSPELAKSWFGNFISLEKEQIFVVIKQPLSSIKADIV 551
DB 421 FHRKLVQVTPPEMSNLTPESSPELAKSWFGNFISLEKEQIFVVIKQPLSSIKADIV 480
QY 552 HAFLSIPSLSHSVISOTSPRAEYKATGGPAVKFQVDFVITTEGGEAQKENGYSVT 611
DB 481 HAFLSIPSLSHSVISOTSPRAEYKATGGPAVKFQVDFVITTEGGEAQKENGYSVT 540
QY 612 FTLLSGSPRRFRKRVETIOAQLSTHDDPPAAQHLSD 647
DB 541 FTLLSGSPRRFRKRVETIOAQLSTHDDPPAAQHLSD 576

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RESULT 4
US-09-523-849-36
; Sequence 36, Application US/09523849
; Patent No. 6458561
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Molteni, Angela
; APPLICANT: Magnaghi, Paola
; APPLICANT: Bosotti, Roberta
; APPLICANT: Scacheri, Emanuela
; APPLICANT: Isacchi, Antonella
; APPLICANT: Hodgson, Dave
; TITLE OF INVENTION: HUMAN NIM1 KINASE
; FILE REFERENCE: PC-0009 US
; CURRENT APPLICATION NUMBER: US/09/523,849
; CURRENT FILING DATE: 2000-03-13
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PERL Program
; SEQ ID NO 36
; LENGTH: 745
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: GenBank Accession No. 6458561 gi749794
US-09-523-849-36

Query Match      22.8%; Score 796.5; DB 4; Length 745;
Best Local Similarity 29.1%; Pred. No. 6.4e-51;
Matches 224; Conservative 120; Mismatches 243; Indels 183; Gaps 21;

Qy 10 AQHAQYVGPYRLKTLGKGTGLVKGVCVTCOKVAIKIVNRKLSGLVLMKVERIAI 69
Db 11 ADEQPHIGNYRLKTLGKGNFAKVKLARHILITGEVAVKIIDKTQLNSSSLQKLFREVI 70

Qy 70 LKLEHPHVLKLDHYENKYLVLVLEHVSQGLFDYLVKKGRLTPKEARKFPRQIISAL 129
Db 71 MKVLNHPNIVKLFVETETKTLVLMVEASGGEVDFYLVAGRMKEKEARAKFRQIVSAV 130

Qy 130 DFCHSHSICHRLDKPENLLIDKKNIRIADFGMASLQVDSLLTSCGSPHYACPEVIRG 189
Db 131 QYCHQKFIVHRDLKAENLLDADNMIKIADFGFNEFTGKNGKLTFCGSPYAAPELFGQ 190

Qy 190 EKYDGRKADVWSCGVILFALLVGLALPDDNLRQLLEKVKRGVFMHPHFIPPCQSLRG 249
Db 191 KKYDGPVDVWSLGVILYTLVSGSLPFDGQNLKELRERVLGKRYIPFYMTDCENLLKK 250

Qy 250 MIEVDAARRLTLEHIQKHIWYIGGKNEPEPEQIPRKVQIRSLPSLEDIDPDVLDMSHL 309
Db 251 FLILNPSKRGTLQIMKDRMNVGHEDDE-----LKPVEPELPDYK--DPRRTELVMVM 302

Qy 310 GCFDRNKLLODLSSEENQEKMIYFLLIDRKERYPSQDEDELPNREID----- 359
Db 303 GYTREE---IQDSLVGQRYNEVMATYLLLGYSSELEGDTITLKPSPADLTNSAQPFS 359

Qy 360 -----PPRKRVDS-----PMLNRHGK-----RRPE-----RKS----- 383
Db 360 HKVQSVSANPKQRRFSDQAGPAIPTSNYSYKKTQSNNAENKRPEDRESGRKASTAKV 419

Qy 384 -----EVLSTVDG-----GSPVPARRAJEMA--QHGQSRISIG--A 416
Db 420 PASPLPLGLERKKTTPSTNSVLSTNRSNRSPLLERASLQASIQNGKDSLTPGSGRA 479

Qy 417 SSGISTSLSPRTVTPH-----PSPRGSLPTPKGTPVHTPKESA-- 457
Db 480 STASASAASARPRQHKQMSASVHPNKAAGLPTTESNCVPRPSTAPQRPVVASPSAH 539

Qy 458 -----GTNPNT-----PPSSPSVGVVWRRLNS 481
Db 540 NISSGGAPDRTNPRGVSSRSTFHAGQLRQVRDQONLPGYVTPASPSGHSQGRGASGS 599

Qy 482 IKNSFLGSPRFRHRLQVP--TPPEMSNLTP-----BSSPELAKSW--FG 523
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Db 600 IFSKF--TSKFVRNLNPEPSKORVETLAPHHVVGSGNDKEKEEFREAKPRSLRFTWSMK 657
Qy 524 NFISLEKEEQIFVVIKDKPLSSIKADIVHAFISIPLSLSHVISQTSFRAEYKATGPAVF 593
Db 658 TTSSMEPNEMREIRKVLVDANSQCSLHEKYMULL--CMHGTGPHGDF----- 702
Qy 584 QKPVKFOVDITYTEGGEAQKENGIVSVTFTLLSGPSRRFRKRVVETIQAOL 633
Db 703 ---VQMEMEVC-----KLPRLSLNGVRPKRISGTSMAFKNIASKIANEL 743

RESULT 5
US-09-984-890-2
; Sequence 2, Application US/09984890
; Patent No. 6492156
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001306
; CURRENT APPLICATION NUMBER: US/09/984,890
; CURRENT FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 724
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-984-890-2

Query Match      22.7%; Score 793.5; DB 4; Length 724;
Best Local Similarity 29.8%; Pred. No. 1e-50;
Matches 216; Conservative 115; Mismatches 248; Indels 145; Gaps 19;

Qy 10 AQHAQYVGPYRLKTLGKGTGLVKGVCVTCOKVAIKIVNRKLSGLVLMKVERIAI 69
Db 44 ADEQPHIGNYRLKTLGKGNFAKVKLARHILITGEVAVKIIDKTQLNSSSLQKLFREVI 103

Qy 70 LKLEHPHVLKLDHYENKYLVLVLEHVSQGLFDYLVKKGRLTPKEARKFPRQIISAL 129
Db 104 MKVLNHPNIVKLFVETETKTLVLMVEASGGEVDFYLVAGRMKEKEARAKFRQIVSAV 163

Qy 130 DFCHSHSICHRLDKPENLLIDKKNIRIADFGMASLQVDSLLTSCGSPHYACPEVIRG 189
Db 164 QYCHQKFIVHRDLKAENLLDADNMIKIADFGFNEFTGKNGKLTFCGSPYAAPELFGQ 223

Qy 190 EKYDGRKADVWSCGVILFALLVGLALPDDNLRQLLEKVKRGVFMHPHFIPPCQSLRG 249
Db 224 KKYDGPVDVWSLGVILYTLVSGSLPFDGQNLKELRERVLGKRYIPFYMTDCENLLKK 283

Qy 250 MIEVDAARRLTLEHIQKHIWYIGGKNEPEPEQIPRKVQIRSLPSLEDIDPDVLDMSHL 309
Db 284 FLILNPSKRGTLQIMKDRMNVGHEDDE-----LKPVEPELPDYK--DPRRTELVMVM 335

Qy 310 GCFDRNKLLODLSSEENQEKMIYFLLIDRKERYPSQDEDELPNREIDPPRKRVDSP- 368
Db 336 GYTREE---IQDSLVGQRYNEVMATYLLLGYSSELEGDTITLKPSPADLTNSAQPFS 392

Qy 369 -MLNRHGKRRPERKSMVLSVTDGSGVPA-----RRAIMAQHGQSRRS 412
Db 393 HKVQSVSANPKQRRFSDQAGPAIPTSNYSYKKTQSNNAENKRPEDRESGRKASS 448

Qy 413 ISGASSGLSTSP---LSSPRVTPHS-----PRGSL----- 441
Db 449 -----TAKVPASPLPLGLERKKTTPSTNSVLSTNRSNRSPLLERASLQASIQNGKOS 504

Qy 442 PTPKGTVPVHTPK-----ESPAGTPNPT-----PPSS 467
Db 505 TAPQRPVVASPSAHNITSSSGGADRTNPRFGVSSRSTFHAGQLRQVRDQONLPGYVTPAS 564

Qy 468 PSVGVVWRRLNSIKNSFLGSPRFRHRLQVP--TPPEMSNLTP----- 510
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Db 565 PSCHSQRRGASGSIKFP--TSKVRNRLNEPESKDRVETLRLPHVVGSGNDKEKEPR 622
QY 511 ESSPELAKSW-FGNFISLEKEQIFWIKDKPLSSIKADIVHAFISLSLSHVSISQTS 569
Db 623 EAKPRSLRTWMTKTTSSMEPNEMREIRKVLNDANSQSELHEKYMLL--CMHGTGHEB 680
QY 570 FRAEYKATGPAVFQKPVKFOVDITVTEGGEAQKENGIVSVTFTLLSGPSRRFRKRVETI 629
Db 681 F-----VQWEMEVC-----KLPRLSLNGVRFRKRSIGTSMAPKNTASKI 718
QY 630 QAQL 633
Db 719 ANEL 722
RESULT 6
US-09-984-890-4
; Sequence 4, Application US/09984890
; Patent No. 6492156
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CLO01306
; CURRENT APPLICATION NUMBER: US/09/984,890
; CURRENT FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 722
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-984-890-4

Query Match 22.7%; Score 792.5; DB 4; Length 722;
Best Local Similarity 30.2%; Pred. No. 1.2e-50;
Matches 217; Conservative 115; Mismatches 251; Indels 135; Gaps 18;
QY 10 AQHAQVGPVRLKTLGKGTGLVGLVHCVTQKVAIKIVNREKLSVLMKVEREIAI 69
Db 44 ADEQPHIGNYRLTKTGKGNFAKYLARHILTGKEVAVKIIDTKQLNSSLQKLFREVI 103
QY 70 LKLTIEHPVLKLDHVVENKYLVLVLEHVSQGGELFDYLVKKGRLTPKEARKFQRIISAL 129
Db 104 MKVLNHNIVKLFEVETETKTLVLMVYASGEVFDYLVHGRMKEKARAKFRQIVSAV 163
QY 130 DFCSHSICHRLDKPENLLDKNNIRIADFGMASLQVSDLSLETSCGSPHYACPEVIRG 189
Db 164 QYCHQKFIHVRDLKAENLLDADNMNIADFGFSNEFTFGNKLDTCGSPPYAAPLFOG 223
QY 190 EKYDGRKADVWSCGVILFALLVGLPDDNLRQLLEKVKRGVFMHPHFIPDQCSSLRG 249
Db 224 KKYDGPVDVMSGLVILYTLVSGSLPDGQNLKELRERVLGRKYRIPFYMTDCENLLKK 283
QY 250 MIEYDAARRLTLEHIQKHIWYIGKNEPEPEQIPRKVQVRSLSLEDIDPDVLDMSHSL 309
Db 284 FLILNPSKRGTLQIMKDRWNVGHEDD-----LKPVEPLPDYK--DPRTELVMVM 335
QY 310 GCFDRNKLQDLSEENKMTYFILLDRKERYPSQEDDLPNRNEID-----SSPRVTPH 359
Db 336 GYTREE---IQDSLVGQRYNEVMATYLLGYKSSLEGGDTITLTPRPSADLTNSSAPSPS 392
QY 360 -----PPRKEVDS-----PMLNRHCK-----RPE-----RKSMEVLSVTD 390
Db 393 HKVQSVSAMPKQRRSDQAVPAIPTNSYSKTKQSNNAENKRPETGRKASTAKVP- 451
QY 391 GGSVPARRAIEAQAHQGRSRSISGASGLSTSP-----SSPRVTPH 433
Db 452 -ASPLPGLDRKTTFTSTNSVLTSTNSRNSPLDRASLQASIQNGKSDTAPQVPV 510
QY 434 PSRGSPLPTPKGPPVHTPKESPAGT-----PNPTPPSSPSVGGV 473

Db 511 ASPSAHNIISSSGADRT--NFRGVSSRSTFHAGLQVRDQQLPGVTPASFGHSQ 568
QY 474 PWRALNISKNSFLGSPRHRKLOVP--TPREMSNLTP-----ESSPEL 516
Db 569 GRRGASGSIKFP--TSKVRNRLNEPESKDRVETLRLPHVVGSGGTDKKEKEFRAPRS 626
QY 517 AKSW-FGNFISLEKEQIFWIKDKPLSSIKADIVHAFISLSLSHVSISQTSFRAEYK 575
Db 627 LRFTWSMTTSMENEMREIRKVLNDANSQSELHEKYMLL--CVHGTGHENP----- 679
QY 576 ATGGAFAVFQKPVKFOVDITVTEGGEAQKENGIVSVTFTLLSGPSRRFRKRVETIQAOL 633
Db 680 -----VQWEMEVC-----KLPRLSLNGVRFRKRSIGTSMAFKNIASKIANEL 720
RESULT 7
US-08-817-832B-32
; Sequence 32, Application US/08817832B
; Patent No. 6579691
; GENERAL INFORMATION:
; APPLICANT: MANDELKOW, Eckhard, et al.
; TITLE OF INVENTION: NO. 6579691el Protein Kinase (NPK-110)
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 S. Wacker Drive, 6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: US
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/817,832B
; FILING DATE: 28-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: NO PCT/EP95/04258
; FILING DATE: 30-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94 11 7122.5
; FILING DATE: 28-OCT-1994
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 722 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-817-832B-32

Query Match 22.6%; Score 790.5; DB 4; Length 722;
Best Local Similarity 30.2%; Pred. No. 1.7e-50;
Matches 217; Conservative 115; Mismatches 251; Indels 135; Gaps 18;
QY 10 AQHAQVGPVRLKTLGKGTGLVGLVHCVTQKVAIKIVNREKLSVLMKVEREIAI 69
Db 44 ADEQPHIGNYRLTKTGKGNFAKYLARHILTGKEVAVKIIDTKQLNSSLQKLFREVI 103
QY 70 LKLTIEHPVLKLDHVVENKYLVLVLEHVSQGGELFDYLVKKGRLTPKEARKFQRIISAL 129
Db 104 MKVLNHNIVKLFEVETETKTLVLMVYASGEVFDYLVHGRMKEKARAKFRQIVSAV 163
QY 130 DFCSHSICHRLDKPENLLDKNNIRIADFGMASLQVSDLSLETSCGSPHYACPEVIRG 189
Db 164 QYCHHKKFIHVRDLKAENLLDADNMNIADFGFSNEFTFGNKLDTCGSPPYAAPLFOG 223
QY 190 EKYDGRKADVWSCGVILFALLVGLPDDNLRQLLEKVKRGVFMHPHFIPDQCSSLRG 249
Db 224 KKYDGPVDVMSGLVILYTLVSGSLPDGQNLKELRERVLGRKYRIPFYMTDCENLLKK 283

APPLICANT: Bandman, Olga
APPLICANT: Molteni, Angela
APPLICANT: Magnaghi, Paola
APPLICANT: Scaccheri, Emanuela
APPLICANT: Scaccheri, Emanuela
APPLICANT: Isacchi, Antonella
APPLICANT: Hodgson, Dave
TITLE OF INVENTION: HUMAN NIM1 KINASE
FILE REFERENCE: PC-0009 US
CURRENT APPLICATION NUMBER: US/09/523,849
CURRENT FILING DATE: 2000-03-13
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PERL Program
SEQ ID NO 34
LENGTH: 776
TYPE: PRT
ORGANISM: Rattus norvegicus
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: GenBank Accession No. 6458561 g5672676
US-09-523-849-34

Query Match 21.4%; Score 749; DB 4; Length 776;
Best Local Similarity 31.5%; Pred. No. 2.2e-47;
Matches 214; Conservative 87; Mismatches 223; Indels 156; Gaps 20;

Qy 4 TGKGGGAQAQYGVYRLEKTLGKGTGLVGLVHVCVTCQKVAIKIVNRKLSVLMKV 63
Db 12 TGTGGQKPLRVGYDVERTLGKGNFVAVKLAHRVTKTQVAIKIDKTLDSNLEKI 71
Qy 64 ERETAIKLLEHVLKLVHVDYENKYLVLVLEHVSGLFDPYLVKGRITPKEARF 123
Db 72 YREVLKMLNHPNIIKLYQVMEKMDLYIVTEFAKNGEMFDYLTNGHLSSEAR 131
Qy 124 QIISALDFCHSHSICRDLKENLLEKKNIRIADFGMASLQVDSLLTSCSPHYAC 183
Db 132 QILSAVEYCHNHVHRLDKTENLLDGNMDIKLADFGNFYKPGFPLTWCSPYAA 191
Qy 184 PEVIRGEYDKRQADVMSGCVILFALLVGLVFPDDNLRLEKVKRGVFMHPFIPDC 243
Db 192 PEVEGEGYEGPQLDINSGLVVLVCGSLPFGPNLPTLRQVLRGRFRIFPFMSQDC 251
Qy 244 QSLRGMIEVDAAARLTLEHVKHVIWIGGKNEPEP---EQIPRKVQIRSLPSLEIDP 300
Db 252 ETLIRRLVMDPAKRITIAQIRCHRW-----QADPTLLQDDPAFSMQGYTSLGDYNE 306
Qy 301 DVLSMHSGLCFRDRNKLQDLLESEENQEKMIYFLILDR-----KERYPSQDEDLPPR- 355
Db 307 QVLGIMQALGI--DRQRTVBSLQNSYNHFAAIYILLERLREHRSQPSRATPAPARQ 364
Qy 356 -----NEI---DPPRKRVDSPP-----LNRHGKRRP----- 378
Db 365 POLRNSDLSLLEVQEIILPCDPPRPSLLCPOQALQSVLQAEIDCDLHSLQPLFPFLD 424
Qy 379 -----ERKSMVELSVTDGSPVPARRAIMAHGQSRSSISGASGLST-----S 423
Db 425 TNCSGVFRHRSISPSLLDTAISEARQGSLEBEQVEQPLPGSTCKRRHTLAERVSTHS 484
Qy 424 PLSSPRVTPHSPRGSPLTPKGT-----VHTKESPA-----TNPPTSPSPSVGG 472
Db 485 PLNPPCIIVSSSAVSP---SEGTSBDSCLPFSASEGPAAGGLGGLATPGLLGTSPP 537
Qy 473 VPMARLNSIKNSFLGSPFRHRRKLQVPTPEMNS-----LTPESPE----- 515
Db 538 -----VRLAS-----PFLGS-----QSATPVLSQAGLGATVLPVFSQEGRRASDTSLT 582
Qy 516 -----LAKSWFGNFISSLEKEQIFVVKOKPLSSIKADIVHAPLSIPSLSHSVIS 566
Db 583 QGLKAFRQOLKRNARTKGLGLNK-----IKGLARQV-C 615
Qy 567 QTSFRAEYKATGGPAVQKP 586
Db 616 QSSIRG-----SRGGMSTFHTP 632

RESULT 12

US-08-817-832B-31
Sequence 31, Application US/08817832B
Patent No. 6579691
GENERAL INFORMATION:
APPLICANT: MANDELKOW, Eckhard, et al.
TITLE OF INVENTION: No. 6579691el Protein Kinase (NPK-110)
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 S. Wacker Drive, 6300 Sears Tower
CITY: Chicago
STATE: Illinois
COUNTRY: US
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,832B
FILING DATE: 28-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP95/04258
FILING DATE: 30-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94 11 7122.5
FILING DATE: 28-OCT-1994
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 779 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-817-832B-31

Query Match 21.4%; Score 749; DB 4; Length 779;
Best Local Similarity 32.4%; Pred. No. 2.2e-47;
Matches 192; Conservative 94; Mismatches 186; Indels 120; Gaps 15;

Qy 15 YVGPYLEKTLGKGTGLVGLVHVCVTCQKVAIKIVNRKLSVLMKVRETAILKLE 74
Db 42 HIGNYRLQTKIGKGNFVAVKLAHRVTGTREAVKIIDKTLNFTSLQKLFREVRIMKILN 101
Qy 75 HPHVLKLVHVDYENKYLVLVLEHVSGLFDPYLVKGRITPKEARFQRIISALDFCHS 134
Db 102 HPNIVKLFVEIETEKTLVMEYASGGEVDFYLVHGRMKKEARAKFRQIVSAVQYCHQ 161
Qy 135 HSIHCHDLKPENLLEKKNIRIADFGMASLQVDSLLTSCSPHYACPEVIRGEYDKG 194
Db 162 KCIVHRLDKAENLLDADNMNIKIADFGSPNEFTVGNKLDITFCGSPPYAAPELPQGGKYDG 221
Qy 195 RKADVMSGCVILFALLVGLVFPDDNLRLEK-VKRGVFMHPFIPDCQSLRGMIEV 253
Db 222 PEVDVMSGLVLTLSVLSLFPDQNLKELRERSCLRGKRVFPVFMSTDCENLLKLLVL 281
Qy 254 DAARRLTLEHVKHVIWIGGKNEPEPQIPRKVQIRSLPSLEIDPDLSDMSHSLGCFR 313
Db 282 NPIKRGSLQEKIMDRWMNVGHEBEE-----LKPSEPELDLNDAKRIDIMVTMGFAR 333
Qy 314 DRNKLQDLLESEENQEKMIYFLILDRK----- 341
Db 334 DE---INDALVSKQYDEVMTATYILGRKPPFEGSGSLSSGNLCQSRPSSDLNNTLQS 390
Qy 342 -----ERYPSQDEDLPP-----RNEIDPPRKV-DSPMLNRHGK 375
Db 391 PAHLKVQRTISANQKORRFSHDHAGSIPPAVSVYTKRQANSVESEKQEWKDTARLGS 450
Qy 376 RR-----PERKSMVEV---LSVTGGSFPVARRAI-----EMAQHGQRS 410

Db 451 TTGSKSEVTASPLVGDRKKSAGSPNNVYSGSMTRNTYVCERSTDRYAALQNGRDS 510
Qy 411 RSTSGASSGLSTS-----PLSSPRVTPHSPRGSP-----LPTPK-GTPVHTPKESA 457
Db 511 SLTMSGASSMSTGTVASAGSPARPRHQKSMSTSGHPKIVTLPTTKDGEAYRP----- 565
Qy 458 GTENPTPPSPSPVGGV----PWEARL---NSIKNSFLGSPRFHRRKLQVPTP 502
Db 566 GTAQRPVPAASPSAHSISASPTDTRTPRGSSRSSTHGEQLRERSAAYSGP 617

RESULT 13
US-08-557-006C-40
; Sequence 40, Application US/08557006C
; Patent No. 6258547
; GENERAL INFORMATION:
; APPLICANT: Beri, Rajindar K.
; APPLICANT: Carling, David
; APPLICANT: Forder, Robert A.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING AMP-ACTIVATED PROTEIN KINASE
; FILE REFERENCE: NGAP/PHM37588/UST
; CURRENT APPLICATION NUMBER: US/08/557,006C
; CURRENT FILING DATE: 1996-03-06
; PRIOR APPLICATION NUMBER: PCT/GB94/01093
; PRIOR FILING DATE: 1994-05-20
; PRIOR APPLICATION NUMBER: GB 9310489.1
; PRIOR FILING DATE: 1993-05-21
; PRIOR APPLICATION NUMBER: GB 9318010.7
; PRIOR FILING DATE: 1993-08-31
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 40
; LENGTH: 552
; TYPE: PRT
; ORGANISM: Rat
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)..(1747)
; OTHER INFORMATION: Full length cDNA sequence fragment of Human AMPK -
; OTHER INFORMATION: fragment begins at nucleotide 24 and ends with
; OTHER INFORMATION: nucleotide 1765
US-08-557-006C-40

Query Match 20.9%; Score 729.5; DB 3; Length 552;
Best Local Similarity 29.8%; Pred. No. 4e-46;
Matches 197; Conservative 103; Mismatches 217; Indels 143; Gaps 22;

Qy 16 VGPYRLEKTLGKGTGLVKLVGCHVCTCKVAIKIVNREKL-SESVLMKVEREIAILKLE 74
Db 13 IGHVYLGDTLGVGTGKVKIGEHQLTGKVAIKINRQKIRSLDVGVGKIKREIQNLKLF 72
Qy 75 HPHVLKLDHVENKYLVLVLEHVSGLFDYLVKKGRLTPKEARKFPROIISALDFCHS 134
Db 73 HPHIILKQVISTPTDFFWMEYVSGSELDYICKHGRVEVEARRUFQQLSLSAVDYCHR 132
Qy 135 HSIHRDLKPENLLDEKNRIADFGMASLQVGSLSLETSCGSPHYACPEVIRGEKYDG 194
Db 133 HMVVRDLKPENLLDAQMNKADFGLSNMMSDGEFLRTSCGSPNYAAPEVIRGLYAG 192
Qy 195 KADVWVSCGVILFALLVQALPDDDNLRLQLLEKVRGVFHPHPIPPDCQSLLRGMIEVD 254
Db 193 PEVDIWSGVILYALLCGTLFPDDSHVPTLFPKIRGGVFYIPEVLNRSIATLLMHMLQVD 252
Qy 255 AARRLTLEHIQKHIWIGGKNEPEPEQIPRKVQIRSLPSLEDDIPDVLDS-----MHS 308
Db 253 PLKRATIKDIRHEWF-----KQDLPVSL-----FPEDPSYDANVIDEAVEKCEK 299
Qy 309 LGCFDRNRKLLQLLAS-EEENQKMIYFILLDRKERYPSQDE-----DLPPRNEIDPPRK 363
Db 300 PEC--TESEVMNSLYSGDPQDLAVAYHLIIDNR-RINNQASEFYLAASSPTG----- 349
Qy 364 RVDSPMLNRHGKRRPERKSMELVSLVTDGSGVPARRAIEAQAHQGRSRSISGASSGLSTS 423

Db 350 -----SPMD-----DMAMH----- 358
Qy 424 PLSSPRVTPHSPRGSP-----LPTPKGTPVHTPKESPAGTNPPTPSSPSVGGVPMPEARLNS 481
Db 359 --IPGLKPHPE-RMPPLIADSPKA-----RCPDLALNTTKPKSLAVKAKWHLGIRS 408
Qy 482 IKNSFLGSPRFHRRKLQVPTPEMSNL-----TPESSPELAKKSWFCNFISLEKEEQIFV 537
Db 409 QSKPYDIMAENVYRAMKQLDFEKKVYNAYHLRVRKNPVT-----GNVYKMSL--QLYLV 460
Qy 538 IKDKPLSSIKADIVHAFSLISPSLSHVSISQTSFRAYEKATGGPAVFPQKPFQVDITYTE 597
Db 461 -----DNRSYLLDFKSIDDEVVEQRSGSTPQRSASAGLHRP-RSSVDSSTA 508
Qy 598 GGEAQKENGIIYSVTFTLLSGSPRRFRKVVETIQALLSTHDPAAQHLSDDTTN-CWEMMT 656
Db 509 NHS-----LSG-----SLTGSUTGSTLSASPRLGSHNTMDFEMCASLIT 548

RESULT 14
US-08-557-006C-43
; Sequence 43, Application US/08557006C
; Patent No. 6258547
; GENERAL INFORMATION:
; APPLICANT: Beri, Rajindar K.
; APPLICANT: Carling, David
; APPLICANT: Forder, Robert A.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING AMP-ACTIVATED PROTEIN KINASE
; FILE REFERENCE: NGAP/PHM37588/UST
; CURRENT APPLICATION NUMBER: US/08/557,006C
; CURRENT FILING DATE: 1996-03-06
; PRIOR APPLICATION NUMBER: PCT/GB94/01093
; PRIOR FILING DATE: 1994-05-20
; PRIOR APPLICATION NUMBER: GB 9310489.1
; PRIOR FILING DATE: 1993-05-21
; PRIOR APPLICATION NUMBER: GB 9318010.7
; PRIOR FILING DATE: 1993-08-31
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 43
; LENGTH: 633
; TYPE: PRT
; ORGANISM: Yeast
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(633)
; OTHER INFORMATION: Yeast SNF1 polypeptide
US-08-557-006C-43

Query Match 20.6%; Score 720.5; DB 3; Length 633;
Best Local Similarity 33.6%; Pred. No. 2.2e-45;
Matches 158; Conservative 109; Mismatches 152; Indels 51; Gaps 11;

Qy 15 YGYPYRLEKTLGKGTGLVKLVGCHVCTCKVAIKIVNREKLSVLM-KVEREIAILKLI 73
Db 51 HIGNYQIVTKTGLSGSPGKVLAYHTTTGQKVALKIINKKVLAKSDMQGRIEREISYRL 110
Qy 74 EHPVLKLDHVENKYLVLVLEHVSGLFDYLVKKGRLTPKEARKFPROIISALDFCH 133
Db 111 RHPHILKLDHVENKYLVLVLEHVSGLFDYLVKKGRLTPKEARKFPROIISALDFCH 169
Qy 134 HSIHRDLKPENLLDEKNRIADFGMASLQVGSLSLETSCGSPHYACPEVIRGEKYD 193
Db 170 RHKIVHRDLKPENLLDEHNLNVIADFGLSNIMTDGNFLKTCGSPNYAAPEVIRGLYA 229
Qy 194 GRADVWVSCGVILFALLVQALPDDDNLRLQLLEKVRGVFHPHPIPPDCQSLLRGMIEV 253
Db 230 GPEVDIWSGVILYVLMCRLPDDESIPLVFNKISNGVYTLFPKLSFGAAGLKKRLIV 289
Qy 254 DAARRLTLEHIQKHIWIGG-----KNEPEPEQIPRKVQIRSLPSLEDDIPDVL 303
Db 290 NPLNRISIHIMQDDWFKVDLPYLLPPDLKPHPEENENNDSKCGSSPDNDIEDNLV 349

Qy 304 DSMHSLGCFRDRNKLQDLSEEE-----NOKMIYFLLDRKERYPSOE-----DEDLPP 354
Db 350 NILSSTWGY-EKDIYESLESSEDTPAFNEIRDAYMLIKENKSLIKOMKANKSVSDLDLT 408
Qy 355 RNEIDPP-----RKRVDSPLNRHKGRRERKSRMEVLSVTDGSGSPVARRALEMA 404
Db 409 FLSQSPPTFOQSKSHQSKQSDVHTAKQHARM-----ASAITQORTYHQS 454
Qy 405 QHGORSRSISGASSGLSTPLSSPRV--TPHSPRGSPLTPKGPVHTPK 453
Db 455 PFMDQYKE---EDSTVILPISLQIHRANLMAQGSAAAS-KISPIVTKK 500

RESULT 15

US-09-101-146-1
; Sequence 1, Application US/09101146
; Patent No. 6124125
; GENERAL INFORMATION:
; APPLICANT: Dartmouth College, St. Vincents Institute of
; APPLICANT: Medical Research, Kemp et al.
; TITLE OF INVENTION: No. 6124125e1 AMP Activated Protein Kinase
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jane Massey Licata, Esq.
; STREET: 66 E. Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: USA
; ZIP: 08053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PC
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: WORDPERFECT 6.0 FOR WINDOWS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/101,146
; FILING DATE: October 7, 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PN7450
; FILING DATE: 8 JAN 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: DC-0050
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (856) 810-1515
; TELEFAX: (856) 810-1454
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 345
; TYPE: Amino acid
; TOPOLOGY: Linear
US-09-101-146-1

Query Match 20.5%; Score 718.5; DB 3; Length 345;
Best Local Similarity 42.5%; Pred. No. 1.4e-45;
Matches 150; Conservative 63; Mismatches 107; Indels 33; Gaps 7;
Qy 16 VGPYRLKTKGQGTGLVKLVGCVTCQKVAIKIVNREKLSVLMKVREIALLKLIH 75
Db 12 IGHVILGDTLGVGTGKVGKVBELTGHKAVKILNRQKIRLDVVVGKIRREIQNLKLF 71
Qy 76 PHVLKLDHVVYENKYLVLVLEHVSGLGELFDYLVKKGLRTPKEARKFQIISALDFCHSH 135
Db 72 PHILKLVQVISTPDSIDFMVMEYVSGGELFDYICKNGRLDEKESRRLFQQILSGVDYCHRH 131
Qy 136 SICHRLDKPENLLDEKKNIRIADFGMASLQVGSLLSETSCGSPHYACPEVIRGEKYDGR 195
Db 132 MVVHRDLKPFENVLLDAHNNAKIADFGLSNMWSDGEFLRTSCGSPNYAAPEVISGELYAGP 191
Qy 196 KADVWSCGVILFALLVGLALPFDDNNLRQLLEKVKRGVPHMHPHFIPDCQSLLRGMIEYDA 255

Db 192 EVDIWSGVLVYALLCGTLFPDDDHVPTLFKKICDGFYTPQYLNPSVLSLLKMLQVDP 251
Qy 256 ARELTLEHIOKHIIWYIGGKNEPEPEQPIPRKVOIRSLPSLED--IDPDVLSM----- 306
Db 252 MKGATIKDIREHEWF-----KQDLP-KYLFPEDPSPYSSTMIIDDEALKEVCEKPECS 301
Qy 307 --HSLGCFRDRNKLQDLSEEEENQEKMIYFLLDRKERYPSOEDEDL---PP 354
Db 302 EESVLSCLYNRNH--QDPLA-----VAYHLIIDNRIRIMNEAKDFYLATSP 345

Search completed: November 26, 2003, 12:03:21
Job time : 18.7053 secs